

TGGCTCGAAC CACCGACCTC ACGCTTATCA GGGCTCGCTC TAACCAGCTG AGCTATAGGC 60  
 CATTAATTTG AATGAACAAA CATTCAAAAC TGAATACAAT ATGTCACGTT ATTCCGCATC 120  
 5 TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC GCACCTTCCG 180  
 ATACGGCTAC CTTGTTACGA CTTCAACCCCA ATCATTGTGTC CCACCTTCGA CGGCTAGCTC 240  
 10 CTAAAAGGTT ACTCCACCGG CTTCCGGGTGT TACAACTCT CGTGGTGTGA CGGGCGGTGT 300  
 GTACAAGACC CGGGAACGTT ATTCACCGTA GCATGCTGAT CTACGATTAC TAnCGATTCC 360  
 AGCTTCATGT AGTCGAGTTT GCAGACTACA ATnCGAACTG 400

(2) INFORMATION FOR SEQ ID NO: 3821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3821:

TATTAAATTA ATGGTGGGCC TAAnTGGACT CGAACCACCG ACCTCAGCT TATCAGGCGT 60  
 GCGCTCTAAC CAGCTGAGCT ATAGGCCCAT TAATTTGAAT GAACAAACAT TCAAACTGA 120  
 30 ATACAATATG TCACGTTATT CCGCATCTTC TGAAGAAGAT GTTCCGAATA TATCCTTAGA 180  
 AAGGAGGTGA TCCAGCCGCA CCTTCCGATA CGGCTACCTT GTTACGACTT CACCCCAATC 240  
 ATTTGTCCCA CCTTCGACGG CTAGCTCCTA AAAGGTTACT CCACCGGCTT CGGGTGTAC 300  
 35 AAActCTCGT GGTGTGACGG GCGGTGTGTA CAAGACCCGG GAACGTATTC ACCGTAGCAT 360  
 GCTGATCTAC GATTACTnAG CAnTTCCAGC TTCCATGnTA 400

(2) INFORMATION FOR SEQ ID NO: 3822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3822:

TCTACCAACT GAGCTAATGG CTCTAATGGC TGGGCTAGCT GGATTCTGAAC CAACGAGTGA 60  
 50 CGGATAAAGT CCGTTGCCTT ACCGCTTGGC TATAGCCCAA TATATAGATG GnGGAGGGGG 120  
 GCAGATTCTGA ACTGCCGAAC CCGAAGAGCG GATTACAGT CCGCCGCGTT TACCACTTCG 180

GAACCGCCGA CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA TTCTCCAAAA 300  
 TAATGACTCC TACGGA CTG AACCCGTGTT ACCGCCGTGA AAGGGCGGTG TCTTAACCGC 360  
 5 TTGACCAAGG AGCCATGCTC CACAGTAGGA TTCGAACTAA 400

(2) INFORMATION FOR SEQ ID NO: 3823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3823:

AAC TTGCCTC TTTAGGTACA GCATGAGGCC CTAGGAAAGT ATGTTTCATG TCTAAATCAT 60  
 20 ATTTCTCAGC TAAACGATTA GACACTTTCA ATTGCTTCAG TTCATTTTCT CTATCTAATC 120  
 CATAACCACT CTTACTTTCA ACTGCAnGCA CGCCGTGTTT AATCATAGTA AGCAAATCAT 180  
 GCTCTGCTTT TTTAAACAAG TCATCTTCGG ATGTTTCTCT AGTAGCATT ACGGTAGATA 240  
 25 ATATGCCACC ACCCATTTCT AATATTTCAA GGTAAGACTT ACCTGGACGT TTTAATGACA 300  
 TCTCATGTTT TCGAGATCCA CCAAATGThA AATGGGGTAT GTGGCATCTA CTAAGCCGGG 360  
 GGACACTAnC TTTCCCACTA GGCATCAATC G 391

(2) INFORMATION FOR SEQ ID NO: 3824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3824:

ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT CTCTGGATCA 60  
 AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA 120  
 45 GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAT CCTACAGGAA 180  
 ACGCGTTATT AATCTTGTGG AGTGTCTTT CGAACACTGA GCGATTATTT CTTATGAATT 240  
 CAAGCTTATT TAAAACTCTT TATCACTCG GTTTTGCTTG GTAAAATCTA TATTTTACTT 300  
 50 ACnTATCTAG TTTTCAATGT ACAATTCTTT TTAGTCAAGC GCTCGCATAA GCAATATCAC 360  
 TTTGAACCAA AAAAGATTGG AAGGTGAAAT AAACATTCAA 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3825:

```

10 ATCGATAACA TGACATAACT CATGCTGGGT TTCCCCATTC GGAAATCTCT GGATCAAAGC      60
   TTACTTACAG CTCCCCAAAG CATATCGTCG TTAGTAACGT CCTTCATCGG CTTCTAGTGC      120
15 CAAGGCATCC ACCGTGCGCC CTTAATAACT TAATCTATGT TTCCATCCTA CAGGAAACGC      180
   GTTATTAATC TTGTGAGTGT TCTTTGGAAC ACTAGCGATT ATTTCTTATG AATTCAAGCT      240
   TATTTAAAC TCTTTATTCA CTCGGTTTTG CTGGTAAAT TCTATATnTT ACTTACTTAT      300
20 CTAGTTTTCA ATGTACAATT TCTTTTTAGT CAAGCGCTCG CATAAGCAAT ATCACTTTAA      360
   CCAAAAAATA TTTGAATGTh AAATAAACAT TCAAACTGA      400

```

(2) INFORMATION FOR SEQ ID NO: 3826:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3826:

```

35 TCACTCACCG CAGATTTTTA AGTCTGTGTC GTCTGCCAGT TCCGCCACCC CGGCACTATA      60
   AAAATGGAGC AGAAGACGGG ATTCGAACCC GCGACCCCAA CCTTGGCAAG GTTGTATTCT      120
   ACCGCTGAAC TACTTCTGCA TATGCGGGTG AAGGGAGTCG AACCCCCACG CCGTAAGnCT      180
40 TAGATCCTAA GTCTAGTGCG TCTGCCAATT CCGCCACACC CGCAAATGGT GAGCCATAGA      240
   GGATTCGAAC CTCTGACCCT CTGATTAAAA GTCAGATGCT CTACCAACTG AGCTAATGGC      300
   TCTTCCATGG TGCCGGCCAG AGGATTTGAA CCCCCAACCT TATTGGTTAC AAGTCAGTTG      360
45 CTCTTACCAA TTGAGCTAGG nCGGCAATAT GTTAAGATTA      400

```

(2) INFORMATION FOR SEQ ID NO: 3827:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3827:

AGTGGTGGAA TGGTCTTAAA AGTTGGTGGT CTAACCTTTAG AGAAGACCAA AAGAAGAAAA 60  
 5 GTGATAAATA CGCTAAAGAA CAAGAAGAAA CAGCTCGTAG AAACAGAGAA AATATAAAGA 120  
 AATGGTTTGG AAATGCTTGG GACGGCGTAA AAATAAAAC TGGTGAAGCC TTTAGTAAAA 180  
 10 TGGGCAGAAA TGCTAATCAT TTTGGCGGCG AAATGAAAAA AATGTGGAGT GGAATCAAAG 240  
 GAATTCCAAG CAAATTAAGT TCAAGTTGGA GCTCAGCCAA AAGTTCTGTA GGATATCACA 300  
 CTAAGGCTAT AGCTAATTAG TACTGGTAAA ATGGTTTGGG AAAGCTTGGC CAATCTGTTA 360  
 15 AATTCGACTA CAGGAAGTAT TTACATTCAA ACTAGGCAAA 400

## (2) INFORMATION FOR SEQ ID NO: 3828:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3828:

TCTCAGTTCC AGTGTGGCCG ATCACCTCT CAGGTCGGCT ATGCATCGTT GCCTTGGTAA 60  
 25 GCCGTTACCT TACCAACTAG CTAATGCAGC GCGGATCCAT CTATAAGTGA CAGCAAGACC 120  
 30 GTCTTTCACT TTTGAACCAT GCGGTTCAAA ATATTATCCG GTATTAGCTA CGGTTTCCCG 180  
 AAGTTATCCC AGTCTTATAG GTAGGTTATC CACGTGTTAC TCACCCGTCC GCCGCTAACA 240  
 35 TCAGAGAAGC AAGCTTCTCG TCCGTTGCT CGACTTGCAT GTATTAGGCA CGCCGCCAGC 300  
 GTTCATCCTG AGCCAGGATC AAACCTCTCA TAAAAATTAT GATGTTGANT AGCTCATAAA 360  
 TACTAAATAA TGTGTGTAAT TATAGTACGT TTTTGAAAT 400

## (2) INFORMATION FOR SEQ ID NO: 3829:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3829:

CAAGCGCCAT GACATCATAA CTTTCTTGCA CAAGATATGT GAACGGCGGT GTTGATCCTA 60  
 50 GATTCGTGGC ATGCATACGC AAACCATTTT CTTCAATTAC TTCACCAAGG CGTTTAAAT 120

ATTGATAAAA CCTTGATGTG TTTCGTGTCA ATGACATACC ATATCGACTA GGTACCTTTT 240  
 TAGAATGTTG ATTAATCACA ACAAATATCA TGGCAAGGTC ATCTTCAAAA TGATTGCGATT 300  
 5 CAAGTGGGAR sGGCATATGA CGTCTCATCA CtATACCCTt TnTnCCCATT CTGCAAATnC 360  
 ACCCATAAAT ACTACGGGAC GGAGAACCCG TACCCATTTT 400

(2) INFORMATION FOR SEQ ID NO: 3830:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3830:

GGGTACTAAG ATGTTTCAGT TCTCCGGGTG TGCCTTCTGA TATGCTATGT ATTACATAT 60  
 CGATAACATG ACATAACTCA TGCTGGGTTT CCCCATTCGG AAATCTCTGG ATCAAAGCTT 120  
 ACTTACAGCT CCCCAAAGCA TATCnCGTTA GTAACGTCCT TCATCGGCTT CTAGTGCCAA 180  
 25 GGATCCACCG TGCGCCCTTA ATAACTTAAT CTATGTTTCC ACCATTTTTTA TAAGTCAAAC 240  
 GCTCACATAC GGCTTCGTTT TCATTATTTT AAATGCTCAT TTACATAAGT AAATCTGCT 300  
 TTAAAATAAT TAACTCATT GTCTGCTAAA CGTTTTCTTT TATAAAAAGA TTAAACGCG 360  
 30 TTATTAATCT TGTGAGTGGT CCTTCGAACA CTAGCGATnA 400

(2) INFORMATION FOR SEQ ID NO: 3831:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3831:

AAATGCGGCT CATCGCATCC ATTTTTTGCC TGGCAACGTT CTACTCTAGC GGAACGTAAG 60  
 45 TTGGCTACCA TCGTCGCTAA AGACCTTTCT TGACTTGTGA CAATCGCTTG CTTCTTTCCT 120  
 CTCCTTCGGC TCTCGCTTAC TCATTTAGCT CTACTAAACT CGTTGCGCTC TTTTCTCGTT 180  
 TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT 240  
 50 TTGACGTTTT AGACATAAAA AAAAGAGACC TTGCGGTCTC AATGCGGCTC ATCGCATCCA 300  
 TTTTTTGCCT GGGCAACGTT CTACTCTAGC GGAACGTAAT TGGGCTACCA TCGACGCTAA 360

## (2) INFORMATION FOR SEQ ID NO: 3832:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3832:

AGCTTATTTT AAAACGTCGT TTATTCAC TC TGGTTTGGCT TGGTAAAATC TATATTTTAC	60
TTACTTATCT AGTTTTCAAT GTACAATTTC TTTT TAGTCA AGCGCTCGCA TAAGCAATAT	120
CACTTTAAACC AAAAAATATT TGAATGTAA ATAACATTC AAAACTGAAT ACAATATGTC	180
ACATTATTCC GCATCTTCTG AAGAAGATGT TCCGAATATA TCCTTAGAAA GGAGGTGATC	240
CAGCCGCACC TTCCGATACG GCTACCTTGT TACGACTTCA CCCC AATCAT TTGTCCCACC	300
TTCGACGGCT AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG	360
TGTGACGGGC GGTGTGTACA AGACCCGGGA ACGTATTTCA	400

## (2) INFORMATION FOR SEQ ID NO: 3833:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3833:

TTTTCTTCTG GTAAAATATC TGCAATAACA GTATCTATGC CTACTTGTTT TGCAATGGCT	60
TGAGCAGTGT TTTTATTATC GCCAGTTAAC ATGGCAACTT CAATGCCCAT ATCATGCAAT	120
TGTATTATAG CATCTTTGGC ATGATCTTTG ACAGTATCTG CCACTGCAAT GATACCAGTT	180
AATGAATAAT TAACAGCAAT GAGCATAGCA GTTTTACCAT CTCGTTTATA ATGTGTTAAA	240
TCATCAGAAA TATGCTTAGG CAAGCTAATA TCATTGTCAG CCATTAATAT ACGGGTTACC	300
AACCAATATA TGGTGATGAT CAATCCGTGG CTTCAATACC ATGGCCAGGT ACCGCTTAA	360
AGTTGTTGTC TCAGTTAATA TTAATTGCTT TCCTTTTGCA	400

## (2) INFORMATION FOR SEQ ID NO: 3834:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3834:

5    nAATTATATG GACCTTGCAG GACTCGAACC TGCgACCGAA CGGTTATGAG CCGTTAGCTC       60  
       TAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TnGCGGnnGA       120  
       GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC       180  
 10    CGCCTTATAT AGTTTGTAAG TAATATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC       240  
       TGCGTGCAAA GCAGGCGCTC TCCAGCTGA GCTAAGCCCC CATAATAATT ACAGTATATC       300  
       GGGAAGACAG GATTCTGAACC TGCgACCCCT TGGTCCCAAA CCAAGTGCTC TACCAAGCTG       360  
 15    AGCTACTTCC CGTATAATTA ACGCGCCCGA TAGGAGTCGA                               400

## (2) INFORMATION FOR SEQ ID NO: 3835:

## (i) SEQUENCE CHARACTERISTICS:

- 20       (A) LENGTH: 400 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: double  
        (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3835:

      AATAACAATT GCGCCACTAA AACTCAAAAT TTCCACCACC AACATCCAAA TTATCAACAT       60  
 30    CGCAACATAA CCAATGTGA TAATAAATCT ATTACACAAA GAGATAAATT ACTTATGCAA       120  
       AGGCGGAGGA ATCACATGTC TATTACTGAA AAACAACGTC AGCAACAAGC TGAATTACAT       180  
       AAAAAATTAT GGTCGATTGC GAATGATTTA AGAGGGAACA TGGATGCGAG TGAATTCCGT       240  
 35    AATTACATTT TAGGCTTGAT TTTCTATCGC TTCTTATCTG AAAAAGCCGA ACAAGnATAT       300  
       GCAGATGCCT TGTCAGGTGA AGACATCACG TATCnAGAAG CGTGCGCAGA TGAAGAATAT       360  
 40    CGTGAAGACT TnAAAAGCAG GAATTAATTG GTTCAAGTCG                               400

## (2) INFORMATION FOR SEQ ID NO: 3836:

## (i) SEQUENCE CHARACTERISTICS:

- 45       (A) LENGTH: 400 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: double  
        (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3836:

55    CTAATCGCAT CTTTTTCAAT CTAAGTGGGT TTGTGACAAA CTTACTGAAC TTAGTGCCAT       60

ATTATAGCCG AATGCCCAAA ATAGATTTTG ACGAATATTA CGAATGGTTG CTTTACTTGC 180  
 ATAAATGGCT TTAGGAATAA GCATCAAGTC GCCACCAAGA ATAGTAATAT CAGCTGCTTC 240  
 5 AATGGCAACT TCTGTACCTG TACCAATGGC GATACCGATA TCAGCTTTAA CTAAATGCAG 300  
 GTGCATCATT TACACCGTCA CCAACCATCG CAACCTTCTT ACCTGTTGGC TGTAGTTTCG 360  
 10 CAATTGTGGC AGCTTTTTnG TTCCGGnGAA AATATCnGGC 400

## (2) INFORMATION FOR SEQ ID NO: 3837:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3837:

AGAGCGGATT TACAGTCCGC CGCGTTTACC ACTTCGCTAC CCCTCCAGCT TATTCATATA 60  
 ATTTAATAAT CAAAATGGTG GAGAATGACG GGTTCGAACC GCGACCCTC TGCTTGTAAG 120  
 25 GCAGATGCTC TCCCAGCTGA GCTAATTCTC CAAAATAATG ACTCCTACGG GACTCGAACC 180  
 CGTGTTACCG CCGTGAAAGG GCGTGTCTTA ACCGCTTGGA CCAAGGAGCC ATGGCTCAAC 240  
 30 AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 300  
 TGTGGGATTA ATATTATGCC TGGCAACGTT CTACTCTAGC GGAAGTAAn TCGGACTACC 360  
 ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGG 400

## (2) INFORMATION FOR SEQ ID NO: 3838:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3838:

AATCGCTTGC TTCTTCTC TCCTTCGGCT CTCGCTTACT CATTAGCTC TACTAAACTC 60  
 GTTGGCGTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA GCCATTTTTC 120  
 50 TTTGTGTTTA TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180  
 ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT ACTCTAGCGG AAGTAATTGG 240  
 55 GCTACCATCG ACGCTAAGAA CCTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCTCTT 300

TCAGATCCAA ACGTTTTCAa TCGnCCAAGC CAATTTGCCT

400

(2) INFORMATION FOR SEQ ID NO: 3839:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3839:

TTACGGCCGC CGTTTACTGG GGCTTCGATT CGTAGCTTCG CAGTAGAcrc GACTCCTCTT 60  
 AACCTTCCAG CACCGGGCAG GCGTCACCCT gATAcATCAC CTTACGGTTT AGCAGAGACC 120  
 TGTGTTTTTG ATAAACAGTC GCTTGGGCCT ATTCACTGCG GCTCTTCTGG GCGTTAACCC 180  
 TAAAGAGCAC CCCTTCTCCC GAAGTTACGG GGTCATTTTG CCGAGTTCCT TAACGAGAGT 240  
 TCGCTCGCTC ACCTTAGAAT TCTCATCTTG ACTACTGTG TCGGTTTGCG GTAGGGcACC 300  
 TATTTTCTAT CTAGAGGCTT TTCTCGGCAG TGTGAAATCA ACGACTcGag GACACAATGT 360  
 CTTCTCCCCA TCACAGtTCA GCCTTgAACG rGTaCCGGAT TTGnCTAATG ATTCAG 416

(2) INFORMATION FOR SEQ ID NO: 3840:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3840:

AAGTTAGGCT ACCATCCTCG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60  
 TCCTCTCCTT CGGCTCTCGC TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT 120  
 CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT 180  
 TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTCACGGT CTCAAACCTG CCTGGCAACG 240  
 TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 300  
 GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 360  
 CTCGTTGGnG CTCTTTTTTCT CGGTTTnGTC AGAnTTCAAA 400

(2) INFORMATION FOR SEQ ID NO: 3841:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3841:

	CGCGACTGAn GAATACAATG nCTACGATAA CTAAACCCAA TCAATCTTTT CATTCTATCA	60
10	ATTCTTTTCA AAATCTTCAC TATATATCAT TAATGTCTAC GTATGAATCT AGCTAGAACA	120
	TTCCCTAGCG TTTGAATCAC TTGGACAATA ATGACTAATA CAATAACGGT AATAATAATG	180
	ACCGTCGTAT CAAATCTTTG ATAACCATAC ACTAAAGCTA AGTCTCCTAT ACCACCACCG	240
15	CCAACAGCTC CTGCCATCGC CGTACTTCCA ATAAGTCCAA TAATCGCAGT GGTAATTGCT	300
	AATACTAACG AACCTAAAGC TTCAGGAATT AAAAAATATC TAATGATTG TAGTGGTGAA	360
20	GCGCCCATCG CTTTCGCCGC TTCAATAATC CCCTCGTCTA	400

(2) INFORMATION FOR SEQ ID NO: 3842:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
25	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3842:

	TCGCGATTCTG CGTGTTGAGA AATCATCGGC ATCGCGTCAT TCAATGATTC ATATGCATCT	60
	AAAGCAATAG AAGATAATGT GTCTGGCACA TATACCCATG CCAACGTATC AGTAGACGTA	120
35	TGATGTTCTG CTACCGCAAA AACAGTTGTC TCTGGAATAT ACACACCTGA TTGTTTTAAT	180
	CCTTGCTCTGA CATTTGGACG ATTACATATC ATCGCTAATA ACTTAGCATT AAAACCGCTT	240
	GATGCGCCAC CACAAGCCCC ACATTCAAGT GATGCATGAT GTGGATTATT GTGAGAATGA	300
40	CTAGCATGAC CTGCTAACAC AACGAACGGC GCAAATGCTT CGGkTAAATC CATCAATTTC	360
	AACGCTgTAA CGCGAATCAA TTGCTCTGCT CAGTAAATCC	400

45

(2) INFORMATION FOR SEQ ID NO: 3843:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
50	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3843:

GCCAACATCC TAGTTGTCTG GGCAACGCCA CATCCTTTTC CACTTAACAT ATATTTTGGG 120  
 ACCTTAGCTG GTGGTCTGGG CTGTTTCCCh GTCGAACACG GACCTTATCA CCCATGTTCT 180  
 5 GACTCCCAAG TTAAATTAAT TGGACATTCG GAGTTTGTCT GAATTCGGTA ACCCGAGAGG 240  
 GGCCCCCTCGT CCAAACAGTG CTCTACCTCC AATAATCATC ACTTGAGGCT AGCCCTAAAG 300  
 10 CTATTTCCGA GAGAACCAGC TATTTCCAGG TTCGATTGGG AATTCTCCGC TAACCTCAGT 360  
 TCATCCGnTC ACTTTCAACG TAAnTCGGGT CGGGTCTCCA 400

## (2) INFORMATION FOR SEQ ID NO: 3844:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 469 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3844:

ACTTTTACTT GCTGCGCCTC CAGCCAAACC TGCTGTTCCA GCACCGATCG CTGCACCTTT 60  
 25 TTTGCCATTA TGATGATCTT TAGACTTATC TTGAGACGCT TTATCCTCAG TCGAGTTATT 120  
 CGCCTTGCCA GAATTACTTT TGTTTTGAGC GTCATTTGAA TGTTTCTTAG CTTTAGAAGC 180  
 30 AGCCATTGCA CCAGCTGCAC CTGCAACACC TGCTGTTCCA GCACCAATAG CTGCTGCTTT 240  
 TTTACCATTA TGATGTTCTT TAGGTTTCATC TTGATCTTGT TTTACAGAAT CATTATCATG 300  
 TTCATTTTTC GATGTTTCTG ATTGGTTAGC ACCTGTTGTA AAATATGGTT TAGGTTGCTG 360  
 35 AGATGTTC A GCTTCACTCT TATCAGAAAC TGTTGAATGC TCAGTGTAT TTTCTGCATT 420  
 TTTAATAGTA TCGTGTITAn CCATTGTCCT CGAATGGGTT CnGGATGTG 469

## (2) INFORMATION FOR SEQ ID NO: 3845:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3845:

GCTTCACTAC CAAGTGAAGA AGTTGCTGAA ACTCCTGCAG CACCTGCAnC AGTAACATTA 60  
 50 GAAGGCGACT TCCCAGAAAC AACTGAAAAA ATCCCTGCTA TCGGTAGAGC AATTGCGnAA 120  
 CATGGnTTTA ACTCTAAGCA TACTGCACCT CATGTAACAT TAATGGATGA AATTGATGTT 180

TTAACATTCT TACCTTATGT TGTAAAGCA CTTGTTTCTG CATTGAAAAA ATACCCAGCA 300  
 CTTAACACTT CATTCAATGA AGAAGCTGGT GAAATCGTTC ATAAACATTA CTGGGAATAT 360  
 5 CGGTATTGCA GCAGACACTG ATAGAGGATT ATTAGTACCT 400

## (2) INFORMATION FOR SEQ ID NO: 3846:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3846:

TTAAGCTACC ATCCTCGCTA AGAACCTTTC TTGACTTGTG ACAATCGCTT GCTTCTTTCC 60  
 20 TCTCCTTCGG CTCTCGCTTA CTCATTAGC TCTACTAAAC TCGTTGCGCT CTTTTCTCGT 120  
 TTCGTCAGAT TCAAACGTTT TCACCTCGCC AAGCCATTTT TCTTTGTGTT TACTTTTTAT 180  
 25 TTTGACGTTT TAGACATAAA AAAAGAGACC TCACGGTCTC AACTTGCCTG GCAACGTTCT 240  
 ACTCTAGCGG AACGTAAGTT GGGCTACCAT CGTCGCTAAA GACCTTTCTT GACTTGTGAC 300  
 AATCGCTTGC TTCTTCTCTC TCCTTCGGCT CTCGCTACT CATTAGCTC TACTAAACTC 360  
 30 GTTGGCGCTC TTTTCTCGGT TCGTCAGATT CAAACGGTTT 400

## (2) INFORMATION FOR SEQ ID NO: 3847:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3847:

ATCGTCAACT TATTATTAGA CGATGTACAA GTTACATTAG AAAAAAAGG TATTACGATG 60  
 GACGTTTCTC AAGATGCGAA AGATTGGTTA ATTGAAGAAG GCTATGATGA AGAATTAGGT 120  
 45 GCACGTCCAT TAAGACGTAT TGTGAACAG CAAGTACGTG ACAAATTAC AGATTACTAT 180  
 TTAGATCATA CAGACGTAA ACATGTGGAT ATAGATGTTG AGGGATAACG AATTAGTCGT 240  
 50 AAAAGGTAAT TAACGACACT TTAACATATC GCGCATCAA AATGAGCATC AGGTCGCCCT 300  
 TGCCTGTGGC TCATTTTTTT GAATTATTTT CCTGGGAAAA TGATTCGCTG TGTGCTGTTC 360  
 TGTTCACCA ACAATCACGA TTGAATGTGC ACATGTGACC 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3848:

TTTAAACTC TTTATTCAC	CGGTTTGGCT TGGTAAATC	TATATTTTAC TTACTTATCT	60
AGTTTTCAAT GTACAAATA	TGGTGGGCCT AAGTGGACTC	GAACCACCGA CCTCACGCTT	120
ATCAGGCGTG CGCTCTAAC	AGCTGAGCTA TAGGCCCAT	TTTTTGAATG TTAAATAAAC	180
ATTCAAACT GAATACAATA	TGTCACGTTA TTCCGCATCT	TCTGAAGAAG ATGTTCCGAA	240
TATATCCTTA GAAAGGAGG	TATCCAGCCG CACCTTTCCG	ATACGGCTAC CTTGGTnACG	300
ACTTCACCCC AAATCATTTG	TCCCACCTTC GACGGCTAGC	TCCTAAAAGG TTACTCCACC	360
GGCTTCGGGn GTTACAACT	CTCGTGGGTG TGACnGGCGG		400

(2) INFORMATION FOR SEQ ID NO: 3849:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3849:

GTCTCAACTT GCCTGGCAAC	GTTCTACTCT AGCGGAACGT	AAGTTGGCTA CCATCGTCGC	60
TAAAGACCTT TCTTGACTTG	TGACAATCGC TTGCTTCTTT	CCTCTCCTTC GGCTCTCGCT	120
TACTCATTTA GCTCTACTAA	ACTCGTTGCG CTCTTTTCTC	GTTTCGTCAG ATTCAAACGT	180
TTTCACTTCG CCAAGCCATT	TTTCTTTGTG TTTACTTTTT	ATTTTGACGT TTTAGGCATA	240
AAAAAAAGAG ACCTTGCGGT	CTCAATGCGG CTCATCGCAT	CCATTTTTTG CCTGGCAACG	300
TTCTACTCTA GCGGAACGTA	AGTTGGCTAC CATCGTCGCT	AAAGACCTTT CTTGACTTGT	360
GACAATCGCT TGCTTCTTTC	CTnTCCTTCG GCTCTCGCTT		400

(2) INFORMATION FOR SEQ ID NO: 3850:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 463 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3850:

	GTCTACTAAT GTTACAACCA CACCTGATTa ATTGCTTTTT TAGCAGTAAT TGCCACATCT	60
5	GTGTGACGAT AATGATATGC GACAGTTAAT AATTTGTGAT TTTTATTAGC CGCTTCAATC	120
	ATGCGATCAC ACTCTTCCGT CGTCATCGCC ATTGGCTTTT CACACAATAC ATGGACACCA	180
10	TGGTTCAATG CTTCTATAGA AAGATCAGCA TGGAATTTAT TAGGTGTACA AATGACCACC	240
	GCATCAACAA GTTTAAACAG CTCGCTAGGT GTCTCAACTG CATGAGGTAT ATTAAAGCGC	300
	TTGCAACAT CAATCATCTG CACTGTATTA ATATCTTGTA CTGCAACTAA TGAGACTGTG	360
15	TCTTTGAGTT TCAGCAATGC TGGAATATGA CGGTCTTGTT CAATACCACC AACAACTATG	420
	CACACCAACT TTTAAaTTTG TnCATGATGT GCCnGCTTn CCG	463

## (2) INFORMATION FOR SEQ ID NO: 3851:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3851:

30	TATGCTCTAA TGCTGGGCTT AGTGGATTCTG ACCAACGAGT GACGnAGTCA AAGTCnGTTG	60
	CTTTACGCTT GGCTATAGCC CCAATATATA GATGTTGGAG GGGGCAGATT CGAACTGCCG	120
	AACCCGAAGG AGCGGATTTA CAGTCCGCCcG CGTTTAGCCA CTTGCTACC CCTCCAGCTT	180
35	ATTCATATAA TTTAATAATC AAAATGGTGG AGAATGACGG GTTCGAACCG CCGACCCTCT	240
	GCTTGTAAGG CAGATGCTCT CCCAGCTGAG CTAATTCTCC AAAATAATGA CTCCTACGGG	300
	ACTCGAACCC GTGTTACCGC CGTGAAAGGG CgtGTcTTAA CCGCTTGACC AAGGAGCCAT	360
40	GGCTCaCAGG TAGGACTCGA ACCTACGACC GATCGGTTAA CAGCCGATAG CTCTACCACT	420
	GAGCTACTGT GGaTTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTtCG	480
	GACTrACCAT CGACGCTgAA GGAGCTTAAa CTTCTGTGTT CgGCATGGGa ACAGGTGTGA	540
45	CCTCCTTGCT ATAGTCACCA GACATATGGA ATGTGAATTT GATGACATTG CAAAAnTAGn	600
	TTAGTAAGTA AAAGTGGATT TTGGnTTn	628

## (2) INFORMATION FOR SEQ ID NO: 3852:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3852:

5 TAAAGATTTA AAAGTAGCTG TTATTGGnAC AGGTCGAATT GGCCGTGTAG TAGCCGATAT 60  
 ATTTGCCAAT GGTATCAAA GTGATGTGGT CGCATACGAC CGTTTCCTAA TGCTAAAATT 120  
 GCAACGTATG TCGATTACAA AGATACGATT GAGGAAGCGG TTGAAGGTGC TGATATCGTG 180  
 10 ACATTACATG TACCTGCAAC GAAATATAAT CATTATCTAT TTAATGCTGA ATTATTTAAA 240  
 CATTTTAAAA AGGGCGCnTA TTTGTCAATT GTGCGAGAGG TTCTTTAGTA GGATACTAAG 300  
 GCGTTATTAG ACGCATTAGA CAATGGTGTG ATTAAAGGTG CAGCACTTgn TTACGTATGG 360  
 15 ATTTGGAACG GCAAACTTTT TCCCAAGTGG TCCAAAGGGG 400

## (2) INFORMATION FOR SEQ ID NO: 3853:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3853:

25 TCTTAAACAT TAGCCACAGC TAATTGTGAC TTA AAAATAG GAATACATGA GTAA AACTCA 60  
 30 TCATAAGAAA TACTAATTTT TATAGAAAA GTATTACTTT ATCGTTGTCC CACCCCAACT 120  
 TGCACATTAT TGTAAGCTGA CTTTCCGCCA GCTTCTGTGT TGGGGCCCCG CCAACTTGCA 180  
 CATTATTGTA AGCTGACTTT TCGTCACTTG CTGTGTTGGG GCCCCGCCAA CTTGCACATT 240  
 35 ATTGTAAGCT GACTTTTCGT CACTTnCTGT GTTGGGGCCC CGCCAACTTG CATTGTCTGT 300  
 AGAAATTGGG AATCCAATTT CTGCTATGTT GGGGCCCA CCCC AACTnC GCATTGCCTG 360  
 TAGAATTTCT TTTGAAATT CTCTGTGTTG GGGGCCCA 400

## (2) INFORMATION FOR SEQ ID NO: 3854:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3854:

50 GTGCAATCTG CGTTAACAAA TGTAATCGT GTCAATGAGC GATTAACGCA AGCAATTAAT 60



GAAATCAATA nATCAGTAAC TACTGATGGT ATGACACAAT CATCAATCCA AGCATATGAA 180  
 AATGCTAAAC GTGCGGGTCA AACAGAATCA ACAAATGCAC AAAATGTTAT TAACAATGGT 240  
 5 GATGCGACTG ACCAACAAAT TGCCGCAGAA AAAACAAAAG TAGAAGAAAA ATATAATAGC 300  
 TTAAACAAG CAATTGCTGG ATTAnCTCCA GACTTGGCAC CATTACAAAC TGCAAAAnCT 360  
 CAGTTGCAAA TGnTATTGTC AGCCACGAGT ACGGCTGGTA 400

(2) INFORMATION FOR SEQ ID NO: 3855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3855:

TGTGTGAAAA ACCAATGGCT GAAAACGACA GCAGAAGCTC AAAAAATGAT AGATACAGCT 60  
 AAATCAACAG GTAAAAAATT AACAATAGGT TATCAAAATC GTTCCGAGC AGATAGTCAA 120  
 25 TTTTACATC AAGCAGCGCA ACGTGCGGAC TTAGGAGACA TTTACTTCGG AAAGGCACAT 180  
 GCCATTCGTC GTCGAGCAGT ACCAACATGG GGTGTCTTTC TAGACGTAGT AAGCTCAAGG 240  
 TGGAGGACCA TTAATCGATA TCGGTACACA CGCTTTAGAT TTAACGTTAT GGATGATGGA 300  
 30 TAnTTATGGA ACCAGAATCA GTGATGGGTT TCAACATTCC ATAAATThAA TAAACAGCCT 360  
 CATGCGGGCA AACGCTTGGG GTTTCAGGnG TTCCAGATGG 400

(2) INFORMATION FOR SEQ ID NO: 3856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3856:

CGTTCTCAAT AGAATGATTT AAATCTTCGA TTTCTTTATC TAAATGACTA CCAATTAAAT 60  
 CTATTTCTTC TATTGTTAAA TCGTATCTC CATCTTCTTT TATCTCTGGT ATTATTTTTT 120  
 CTTCAACTAA GTCACGATAT AATGTTTTTG AATTTTCGTT CAATTCGAT TCGTGATTTT 180  
 50 GAATACTTTT CTTCCACACA AATGTATATC TATTGGCATT AGCTTCTACT TTTGTACCAT 240  
 CAATAAAAAT TGAATTATTA TCAATAAGAT TTTGCTTTAA ACATTGACTA TGGAAC TGAA 300

TATAAGAAGG nGGTTGGAnC nTGAGCGAAC CACAnCATCC

400

## (2) INFORMATION FOR SEQ ID NO: 3857:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 381 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3857:

15	GGCATACCAT GGTCAAACGC GTGATGATCA AGTAACATCA CATGTTCAAC ATATTTTGA	60
	AGTTGTGAAT GCACATGGTA AACATTTTGT TGCATTACCA CGTGAAGATG AAGATATTGC	120
	AAAATGGCAG GCACAAGGTG TACAAACATT TATTTTAGGT GATGATCGCG GAAAAATATA	180
20	TCGCCATTTA AGTGCATCTC TAGCGACGTC TAAACAGAAA GGGGATGAAG GCTAATGCGT	240
	AAAGTTCAAC CTGTTATTGA ACAATTAAAA GCACAATCTC ATCCAGTTTG TCATTAnATC	300
	TATGATTTAG TCGGACTGGG ACATCATTTG CAnCATATTA CATCGnCCTT GCCGAGTAAT	360
25	TGTCAAATGT ACTATGCAAT G	381

## (2) INFORMATION FOR SEQ ID NO: 3858:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3858:

	GCATGAAGCC CCCCTCAAGA TGAGATTTCC CAACTTCGGT TATAAGATCC CTCAAAGATG	60
40	ATGAGGTAA TAGGTTTCGAG GTGGAAGCAT GGTGACATGT GGAAGCTGAC GAATACTAAT	120
	CGATCGAAGA CTTAATCAAA ATAAATGTTT TGCGACAATT CACTTTTACT TACTATCTAG	180
	TTTTGAATGT ATAAATTACA TTCATATGTC TGGTGACTAT AGCAAGGAGG TCACACCTGT	240
45	TCCCATGCCG AACACAGAAG TTAAGCTCCT TAGCGTCGAT GGTAGTCGAA CTTACGTTCC	300
	GCTAGAGTAG AACGTTGCCA GGCAAAAAAT GGATGCCGAT GGAGCCGCAT TGAGACCGCA	360
50	GGnCTnTTTG TTTTTTATGT CTAAAACGTC CAAATTAAnA	400

## (2) INFORMATION FOR SEQ ID NO: 3859:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 573 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3859:

	GTTTATTAAT CGTGTCATTA GCATCTTTAT AATTGCTTCT AATCGTATTC AAATCACCTA	60
10	ATGTAAATC TGTTTAACA TTATTTTGAA TTTCATTCAT GCATCTGAAT CTGAATCGCT	120
	ATCTGAATCT GAGTCGTTGT CTGAGTCCGA nTCGCTATCT GAnTCGAGT CGCTGTCTGA	180
	ATCTGAATCG CTATCCGAGT CTGAGTCGCT ATCTGAGTCT GAGTCGCTAT CTGAATCTGA	240
15	ATCGCTGTCT GAGTCTGAAT CGCTATCTGA GTCTGAATCG CTGTCCGAAT CTGAGTCGCT	300
	ATCTGAATCT GAATCGCTAT CTGAATCTGA GTCGTTGTCT GAGTCCGAAT CGCTATCTGA	360
20	ATCTGAGTCG CTATCTGAGT CTGAGTCGCT ATCTGAATCT GAGTCGCTGT CTGAATCTGA	420
	ATCACTGTCT GAGTCTGAGT CGCTGTCTGA AGTCTGAATC GCTGTCAGAA TCTGAGTCGC	480
	CAACTGAGTC TGAATCTGAA TCACTGGTCT GAGTCCGAAT CGCnATCTGA ATCnGAATCG	540
25	CnAACCGAGT CCGAAGCCGC nAATCCGAAT CTG	573

(2) INFORMATION FOR SEQ ID NO: 3860:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3860:

	GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG GATCGAACCG	60
40	CTGACCTCCT GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC ATAATAATTA	120
	CAGTATATCG GGAAGACAGG ATTCGAACCT GCGACCCCTT GGTCCCAAAC CAAGTGCTCT	180
	ACCAAGCTGA GCTACTTCCC GTATAATTAA CGCGCCCGAT AGGAGTCGAA CCCATAACCT	240
45	CTTGATCCGT AGTCAAACGC TCTATCCAAT TGAGCTACGG GCGCATATGT TTTTATTGnA	300
	AAATGGTGCC GAGGnACCGG GAATCGGAAC CGGTACGGTT GATnCACTCA CCGGCAGGAT	360
50	TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGnGC	400

(2) INFORMATION FOR SEQ ID NO: 3861:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3861:

5 TGTTCGACT AAACCATTAC CTATCGCACA TATGACGAAA CCAATGATAA CTGCAATGAC 60  
 ATATTGTGAT GCCAATAATT GAGTCATGCT AATAATAGTG ATGCCGATGA CAGGGAACAA 120  
 CGGACCAATG ATGAGCATCA ATTTGCCACC GAAACGTAAT GTTGCTTTTT CACCTAAACG 180  
 10 AATCATCGCA ACTGCCACAA TGGCATATGG CAATGTAACA nGTCCAGATT GCGCACTGAT 240  
 AAACCAAGGT GTGTTTGAGC ATATATGAAA AAGACCACTG TTACGCCTAG ACCGCTATTT 300  
 AAAACAAAGT TATTTAAAAA TGCACCAATG GAACGGACGG TTGCGTAATA CTGGAGAAnt 360  
 15 CAATAAAAGG TACTTCCATG TCCGACGTTT CGATGGATGG 400

## (2) INFORMATION FOR SEQ ID NO: 3862:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3862:

25 GTGCGCATGG GAACTATCAA GCTTTGAAGA TGTGGTACTA CATGCGTTGA ATTAGGGATC 60  
 30 GGTACTTTAT ATGAAGACGT GCTGCTTCCA TTAAATGAGT GATGCGATT TGGCATGAAG 120  
 GTCACCTTAA ATGTACATTG TTGTAATAAA ATTGCCTATA AATTTTtagC ACATAAAATA 180  
 AGAGGAGCCA ACCATTGTGA GACTATAACA ACGGTTGGCT CTTTAATTGT AAAAAGAAAA 240  
 35 CCATACGCTA TCGGTATGGT TCAGAAAAGG TCTACCATTG TCACCAAAAA TGCATCTCTA 300  
 CGTGCTAGAA TAAATATTGG TCAGCCAACC AAAATAATCC ACACGGGGAG ATGCTATTTA 360  
 40 ATGTCCTCCT GACACCAACA GTTAGCACCA TACAAAATGG 400

## (2) INFORMATION FOR SEQ ID NO: 3863:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3863:

50 TCGGCAAGCC ATTTTCTTT GTGTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAA 60

CTAGCGGAAC GTAAGTTGGC TACCATCGAC GCTAAGAACC TTTCTTGACT TGTGACAATC 180  
 GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG 240  
 5 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACCT CGCCAAGCCA TTTTCTTTG 300  
 TGTTCGCTTT TTTTGTGAC GTTTTAGACA TAAAAAAAG AGACCTTGCG GTCTCAAATG 360  
 10 CGGCTCATCG CATnCATnT TGCCGGCAAC GTTCTACTCT 400

(2) INFORMATION FOR SEQ ID NO: 3864:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3864:

GTACTATAGA ATTAAAGAAT TATAAAAATA TAATCCTGAT TAGCTTGTTG TCAAGTCATC 60  
 GTTCATAATG AAGATATCAC GTTCAATTGT ATTGTTTGTT TATGGGAAAT GAATTAATGT 120  
 25 AATAGTATAT GTATGCGGTT ACATAAAAAG CGAACATCTA ACCTGATATT TAAATGAACC 180  
 TGACGCTCAA TCAACTAATT TACAACCGTA TTTTATAAT CAACCATAAA GGAGGAGATA 240  
 GAAAATGAAT AGTGCAAAT TGATTGATCA CACTTTATTG AAGCCTGAGT CAACACGTAC 300  
 30 GCAAATCGAT CCAAATCATC GATGAAGCGA AGCATACCAT TTAAATCTG TATGTGTGAA 360  
 TCCAACGCAT GTTAAAnGTG CCAGCAGAGC GACTAGCTGG 400

(2) INFORMATION FOR SEQ ID NO: 3865:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3865:

GCAGCACGTC TTCATATAAA GTACCGATCC CTAATTC AAC GCATGTAGTA CCACATCTTC 60  
 AAAGCTTGAT AGTTCCCATG CGCACACCAC GTTTCATACT AGCTATGCGA GCTCAACTTG 120  
 50 GTTCATAAAC TCTTTAATAT AAGTCAATGT TTCAACCATC GCTGGTGGTC TTGGCACATG 180  
 TCCTTCTGCC ATTTGATAAA ATGTTTCATG CGTGGCACCT TTAACTCTA GTTGGTCCGC 240  
 TAAATAATAC GCATGATGAA TACCAACTTG CTGGTCTTTC CCTCCATGTA CAATTAATAT 300

TTTTTTCGGA TGACCAATCA TTCTTCGTAG CATGCCTCTT

400

## (2) INFORMATION FOR SEQ ID NO: 3866:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3866:

AAGTCAATAA CTTTTTTTAT CTTGTCCATT TTATTTTTTA ACCAAAATTT GATTAAAAAA 60  
 CTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAAGTTCGA nCTACCATCG ACGCTAAGGA 120  
 GCTTAACTTC TGTGTTCCGC ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA 180  
 TATGAATGTA ATTTATACAT TCAAAACTAG ATAGTAAGTA AAAGTGATTT TGCTTCGCAA 240  
 AACATTTATT TTGATTAAGT CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT 300  
 GCTTCCACCT CGGAACCTAT TAACCTCATC ATCTTTGGAG GGGATCTTAT AACCGGAGGT 360  
 TGGGGnAAAT CTCATCTTGA GGGGGGGCTT CCAGGCTTAG 400

## (2) INFORMATION FOR SEQ ID NO: 3867:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3867:

CACCTATAAT CGTTTTAATC GATGGGGGGA CGCATAGGGA TAGGCGAnGT GnCGATTGGA 60  
 TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC GGTACTCGTT AAGGCTGAGC 120  
 TGTGATGGGG AGAAGACATT GTGTCTTCGA GGTGTTGAT TTCACACTGC CGAGAAAAGC 180  
 CTCTAGATAG AAAATAGGTG CCCGTACCGC AAACCGACAC AGGTAGTCAA GATGAGAATT 240  
 CTAAGGTGAG CGAGCGAACT CTCGTTAAGG AACTCGGCAA AATGACCCCG TAACTTCGGG 300  
 AAGAAGGGTG CTCTTTAAGG TTAACGCCCA GAAGAGCCGC ATGAATAGGC CCAAGCGACT 360  
 GTTTAntCAA AACACAGTCT CTGCTAAACC TAAGGATGTA 400

## (2) INFORMATION FOR SEQ ID NO: 3868:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 383 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3868:

TTCTTTGGAA ATAGTAACGT TGAAGTTGTA CTCACTGGTG ATACATTGA TCACTGTTA	60
GCTGAAGCTT TAACTTATAC AAGTGAACAT CAAATGAnCT TTATAGATCC ATTCAATAAT	120
GTTCATACAA TTTCTGGACA AGGTACGCTT GCTAAAGAAA TGCTAGAACA AGCAAAGTCT	180
GACAATGTTA ACTTTGATTA TCTATTTGCC GCAATTGGTG GTGGCGGTTT AATTTTCAGGT	240
ATTAGTACTT ACTTTAAAAC CTATTCACCT ACCACGnAAA TTATAGGTGT TGAACCTTCA	300
GGTGCCAAAGT AGTATGTGAT GGAATCTGTT GTGAAATATT CAGGTAGTCA CATTGCCCTA	360
AnTCGATAAA TTTGTGGACG GTG	383

(2) INFORMATION FOR SEQ ID NO: 3869:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3869:

CTAAGCTTAA GGGTTGCGCT CGTTGCGGGA CTTAACCCAA CATCTCACGA CACGAGCTGA	60
CGACAACCAC CACCTGTCAC TTTGTCCCCC GAAGAAGnGC TCTATCTCTA GATTGTCAAA	120
GGATGTCAAG ATTTGGTAAG GTTCTTCGCG TTGCTTCGAA TTAAACCACA TGCTCCACCG	180
nTTGTGCGGT TCCCCGTCAA TTCCTTTGAG TTTCAACCTT GCGGTCGTAC TCCCCAGGCG	240
GAGTGCTTAA TGC GTTAnTG CCAGCACTAA GGGGCGGAAA CCCCCTAACA CTTAGCACTC	300
ATCGTTTACG GCGTGGACTA CCAGGGTATC TAATCCTGTT TGATCCCCAC GGTTTCGCAC	360
ATCAGCGTCA TTTACAGACC AGAAAGTCGn CTTCGGCAAT	400

(2) INFORMATION FOR SEQ ID NO: 3870:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 377 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3870:

GTGTGCCTTC TGATATGCTA TGTATTACACA TATCGATAAC ATGACATAAC TCATGCTGGG 120  
 TTTCCCCATT CGGAAATCTC TGGATCAAAG CTTACTTACA GCTCCCCAAA GCATATCGTC 180  
 5 GTTAGTAACG TCCTTCATCG GCTTCTAGTG CCAAGGCATC CACCGTGC GC CCTTAATAAC 240  
 TTAATCTATG TTTCCATCCT ACAGGAAACG CGTTATTAAT CTTGTGAGTG TTCCTTCGAA 300  
 CATGAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCCTTATTC ACTCGGTTTT 360  
 10 GCTTGGTAAA AGCnnGn 377

## (2) INFORMATION FOR SEQ ID NO: 3871:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3871:

ATAACGTTGC CCCTCCCATG TATATCCTAC CCAAACATGA CCATCTTGTA ACATCACTTC 60  
 25 TGTATAATCA CAATACCCAC CAGGTTGGAA CTGATAACCC ACTGGACAAG ATAAGAATGG 120  
 CCCCACTTTT CTTACTGTGA TTGGTTGATT GCCGTTGTG AATCTAGCAC TTTCTTCCAT 180  
 GTAGTAAGTA CCATATTTAT TACGTTTTCCA TGCACTTGCA ACTGGTTTAA CTGTATTACT 240  
 30 TGAAGCGCTT GACTCATTAG AGACAGTGGC AACCGGTATT TTACCATCCA TGTACGCCCT 300  
 AAATCTGCTT GATAAAGTAG TCTTTTAAGT TGCAACCGCT TGTCTTCTGG GCAATAGACC 360  
 GCGAGTTACn GGGGTCCAAA CCCnTGGTGT AAAAnCGAAC 400  
 35

## (2) INFORMATION FOR SEQ ID NO: 3872:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3872:

CGCTACACTA CGAGACCATT AGTAAACGC AGGAAGAGGG ATTCGAACCC CCGCGAGCCG 60  
 TTAAGCCCCT GTCGGTTTTT AAGACCGATC CCTTCAGCCG GACTTGGGTA TTCCTCCAAA 120  
 50 ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG TTATGAGCCG TTAGCTCTAA 180  
 CCAACTGAGC TAAAGGTCCT AAATATAATT TTACAATAA TAAATAGTGG CGGTGGAGGG 240

GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG GGATCGAACC GCTGTACCTC 360  
 CTGCGTGCAA ACGGGCGCTC TTCCCAGCTG nAGCTAAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3873:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3873:

ACAGCTCACG GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA 60  
 CCATCGTCGC TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCTTCG 120  
 GTCTCGCTTA CTCATTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGTT TCGTCAGATT 180  
 CAAnnGTTTT CAATCGCCAA GCCATTTTTC TTTGTGTTTA CTTTTTATTT TGACGTTTTA 240  
 GGCATAAAAA AAAGAGACCT TCGGGTCTCA AnTGCGGCTC ATCGCATCCA TTTTTGCTT 300  
 GGCAACGTTT TACTCTAGCG GAAnTAAGTT GGGCTACCAT CGTCGCTAAA GACCTTTCTT 360  
 GACTTGTGAC AATCGCTTGC TTCTTCTCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC 420  
 TACTAAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACITCGCCAA 480  
 GCCATTTTTC TTTGTGTTTA CTTnTnATTT TGACGTTTTA GACATAAAAA AAAGAGACCT 540  
 TCGGGTCCAA ATCGGGGCTC ATCGCATCCA TTTTTGCTT GGGC 584

(2) INFORMATION FOR SEQ ID NO: 3874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3874:

TTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAnTTGG CTACCATCGT CGCTAAAGAC 60  
 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCTCTCC TTCGGCTCTC GCTTACTCAT 120  
 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 180  
 TCGCCAAGCC ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAA 240  
 GAGACCTTGC GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGCA ACGTTCTACT 300

GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG CTTACTCATT

400

## (2) INFORMATION FOR SEQ ID NO: 3875:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3875:

TCTGCTAATT TAAAAATGAT ATTTTCTATC TTTTCTTTAT TATTAACGTC TAATGCACTG 60  
 GTCGATTCAT CTAATAAAAG AATATCCGGT GTATACATCA GTTGGCGCGC TATAGCAATT 120  
 CTTTGCCGCT CACCACCCGA CATATTTTCC ACTTCCGAAC TTAATTGATA ATGTCCCAAA 180  
 CCGACATCTT TAATTAATTG CTTTGCACGT TTTCTATCAA ATTTATCATT ACGTGCAAGT 240  
 GATGGGAATA TCATGTTATC TTCAATCGGT CACCAAACAA GTCACTTTGC TGCATCAAAT 300  
 AACTGATTCTG TTGACGCCAA TTCTTCCGGG GCATAATnCA TATAGGGGTT ACCTTAAAAA 360  
 TAAAGGTCCT CCACTAGTTG GCCTAnACnA ATTACATAAn 400

## (2) INFORMATION FOR SEQ ID NO: 3876:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3876:

AGATAGACTT TCTGGTGAAG ATACACGTGA AGGTATGACA GCAATTATAT CTATCAAACA 60  
 TGGTGATCCT CAATTGGAAG GTCAAACGAA GACAAAATTA GGTAATTCTG AAGTGCCTCA 120  
 AGTTGTAGAT AAATTATTCT CAGAGCACTT TGAACGATTT TTATATGAAA ATCCACAAGT 180  
 CGCACGTACA GTGGTTGAAA AAGGTATTAT GGCGGCACTG CACGTnTTGC TGCGAAAAAA 240  
 GCGCGTGAAG TAACACGTCC GTAAATCAGC GTTAGATGTA GCAAGCCTTC CAGGTAAATT 300  
 AGCCGATTGC TCTAGTAAAA GTCCTGAAGA ATGTGAGATT TCTTAGTCGA AGGGGCTCTG 360  
 CCGGGGGGTC TACAAAATCT GGTCGTGACT CTAGACCGCA 400

## (2) INFORMATION FOR SEQ ID NO: 3877:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3877:

	ACCAATTTCT CTTTGTATC CGCCATCTTT AAATAATTTT ACTGCTCTAG CATGAGCCAC	60
10	CATCATGTTA TGTGATTGGA ATACTTTTTC AAAATCATAT TTAATACCTG GAGGGAATTT	120
	ACCTACTAAA TATTGACCAT CACCAATAGG TCCAATTTCA TTGAATGTAG TCCAATATTT	180
	TACTTCTGGG AATTCTTTAA AACAAATATTC AGCATAATCT ACAAAGTAGT CAATCGTTTT	240
15	ACGnTTTAGA AAATCGCCAT CTTTGGTGGT ACACTTCTGG GnGTATCAAA ATGnTGCAAT	300
	GTTACAAATG GTTCAACATG ACGGTTTATG GnCACTCTGC AAATAACCTT ATGGTAATAC	360
20	TCAACACCTT AGGGGTAAAC TTCGGCCATA TCCCTTTTGG	400

(2) INFORMATION FOR SEQ ID NO: 3878:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
25	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3878:

	ATTAAAGCAG TTTCTGGATC TGGTAAAAAT GGTCGTATTA CAAAAGAAGA TGTAGATGCA	60
	TACTTAAATG GTGGTGCACC AACAGCTTCA AATGAATCAG CTGCTTCACT AACAAAGTGAA	120
35	GAAGTTGCTG AAACCTCTGC AGCACCTGCh GCAGTTAACA TTAGAAGGCG ACTTCCCAGA	180
	AACAACTGGA AAAAATCCCT GGCTATGCGT AGAGCAATTG CGAnAACATG GGTTTAACTC	240
40	TAAGCATACT GCACCTCATG TAACATTAAT GGATGAAATT GGATGTTCAA GCATTATGGG	300
	GATCACCGTA AGAAATTTAA AGAAATCGCG GCTGAACAAG GTACTAAGTT AACATTCTTA	360
	CCTTATGTTG TTAAnGCACT GTTTTCGGCA TGGnAAAAAT	400

45

(2) INFORMATION FOR SEQ ID NO: 3879:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
50	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3879:

TTGTGTTTAC TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 120  
 TCGGGCTCAT CGCATCCATT TTTTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTG 180  
 5 GCTACCATCG ACGCTAAGAA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTT 240  
 CTTGGGCTCT CGCTTACTCA TTTAGCTCTA CTAACTCGT TCGGCTCTTT TCTCGTTTCG 300  
 TCAGATTCAA ACGTTTCACT TCGCAAGCCA TTTTCTTTG TGTGCTTTT ATTTGACGTT 360  
 10 TAGACATAAA AaAAGAnCCT TCGGnCTCA ATGCGGCCAT 400

## (2) INFORMATION FOR SEQ ID NO: 3880:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3880:

TAGGTGTAAG TCCTGCGATT CGATCTGGAC CATATTTTTT TATTGTATAC AGTAATTGTG 60  
 25 CTGCGATTAT CTCTGTAACG TCTTTCCAAT TTGAACGCAC GTGCCCTCCC ATACCTCGGG 120  
 CTTGCTTATA TTGTTTGGCT TTGTCTTCAT TTTCAACAAT AGACGCCCCAT GCAGCAACGC 180  
 GATTACCATT GTTTTCTTCT AATGCTTCAG TCCATAAATC CCAGAGTTTT CCACGAATAT 240  
 30 ATGGATATTG ATTCGAAGCG GACTGTATCA TACCAAGAGA ATGACGCACT CGTGGACATC 300  
 CTCTCGGTCA TATTCAGGCA TATCCGGACA CAACTTGGAT AGCAGTTGTG ATTTCCAGG 360  
 AATCACACCA TTTCACAAAC TTCCAGACAT GGCTGACAGT 400  
 35

## (2) INFORMATION FOR SEQ ID NO: 3881:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3881:

TGAGTAGCGA AAGACGGGTG AGAATCCCGT CCACCGATTG ACTAAGGTTT CCAGAGGAAG 60  
 50 GCTCGTCCGC TCTGGGTTAG TCGGGTCCTA AGCTGAGGCC GACAGnGTAG GCGATGGATA 120  
 ACAGGTTGAT ATTCCTGTAC CACCTATAAT CGTTTAAATC GATGGGGGGA CGCAGTAGGA 180  
 TAGGCGAACG TGCGATTGGA TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC 240  
 55

TCACACTGCC GAGAAAAGCC TCTAAGATAA GAAAATTAGG TGCCCGTACC GCAAACCGAC 360  
 ACAGGTAGTC CAAGATGGAG AnTCTnAAGG TGGAGCGAGC 400

(2) INFORMATION FOR SEQ ID NO: 3882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3882:

CATCCCCAAC TTGCACATTA TTGTAAGCTG ACTTTTCGTC ACTTCTGTGT TGGGGCCCTC 60  
 ACCCCAACTC GCATTGCCTG TAGAATTTCT TTTGAAATT CTCTGTGTTG GGGCCCCTGA 120  
 CTAGAATTGA AAAAAGCTTG TTACAAGCGC ATTTTCGTTC AGTCAACTAC TGCCAATATA 180  
 ACTTCGTAGA GCATAGAATA TTGATTTATG TCCCAGCCTG AGTTAATTTT CTATAAAAGT 240  
 ATATTTAATT TCGGTTTATA CCGTCAAAC TCACTTTAGC TTTGTCAAAC CCCTTTCTAT 300  
 TAAGTTTCA GAAATAAACC TATCTTAAAA TATAAAAAAA TCGAGAATTC GTAGTTTAAT 360  
 AACGAAATTC TCGTTCTTAT CCTTTTGaAT aTACTCAATT TTCCACAAAA ACAACAAGT 420  
 AGTATATCTG TTCTAGCTAC TAGAATGACA TACTACTTGT TATTAAAATA CTTAACATAA 480  
 CTTTATTAGT TATCTTTnTT CTCTATATTT CTACGTGGAC TGACGCTTTT CAnGAATGTC 540  
 AGATTCATAA TCCTCTGGT TGGACTCCTG GATATATTCT TGGTAAGCGG ATGGTTTATT 600  
 CGGAGTCAA 609

(2) INFORMATION FOR SEQ ID NO: 3883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3883:

ATATATTGGC GGACATAACG ATGTACTAGC AGGTGTCGTA ACCGTCAAAG ATGAATCACT 60  
 CGCGCAACAG TTGTTTGATT TTCACAACAT GACTGGCGCA ACACTTTCAC CAATAGATAG 120  
 TTATTTGTTG TTACGTGGAC TTAAAACTTT GCATTTACGC ATTGAGCGTG CGCAATCAAA 180  
 CGCTAGAAAA CTTGCTAAAA AATGTCAGTC ACTTCAAGCA ATTGACGAAt ACTaTATAGC 240

GAAAATTTAG ACATTTGcAT TTTTGCAGAA AGTTTAGGAg GTACkGAAAC ATTAGTGACC 360  
 TTCCCTTACA CCCAAACACT GTTGATATGC CAGT 394

(2) INFORMATION FOR SEQ ID NO: 3884:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3884:

CGATTAATGA ATTAACAGAA TACGGACCAG AAACGATAAC ACCAGGTCAT CGAGACGAAT 60  
 TTGATCCGAA GTTACCAACA GGAGAGAAAG AGGAAGTTCC AGGTAAACCA GGAATTAAGA 120  
 ATCCAGAAAC AGGAGACGTG TTAGACCACC GGTGATTAG CGTAACAAAA TATGGACCTG 180  
 TAAAAGGAGA CTCGATTGTA GAAAAAGAAG AAATTCCATT CAAGAAAGAA CGTAAATTTA 240  
 ATCTGATTT AGCACCAGGG ACAGAAAAAG TAACAAGAGA AGGACAAAAA GGTGAGAAGA 300  
 CAATAACGAC GCCAACACTA AAAANTCCAT TAACTGGAGA ATTATTAGTA AAGGTGATCG 360  
 AAAGAGGAAT CACAAAAGTT CCnTTTATGA TTAACAGATA 400

(2) INFORMATION FOR SEQ ID NO: 3885:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3885:

TGAGCGGATT ATTTCTTATG AATTCAAGCT TATTTAAAC TCTTTATTCA CTCGGTTTTG 60  
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGC 120  
 CTAAGTGGAC TCGAACACC GACCTCACGC TTATCAGGCG TCGCTCTAA CCAGCTGAGC 180  
 TATAGGCCCA TTTTTTTGAA TGTAAATAA ACATTCAAAA CTGGAATACA ATATGTCACG 240  
 TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG 300  
 CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC 360  
 GACGGCTAGC TCCCAAAGG GTACTnCCAn CGGGnTTCGG 400

(2) INFORMATION FOR SEQ ID NO: 3886:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3886:

10 TACGGTAGGT GGCAAGCAGT TATCCnGGAA TTATTGGGCG TAAAGCGCGC GTAGGGGTTT 60  
 TTTTAAGTCT GATGTGAAAG CCCACGGCTC AACCGTGGAG GGTCAATTGA AACTGGAATn 120  
 CTTGAGTGCA GAAGAGGAAA GTGGAATTCC ATGTGTAGCG GTGAAATGCG CAGAGATATG 180  
 15 GAGGAACACC AGTGGCGAAG GCGACTTTCT GGTCTGTAAC TGACGCTGAT GTGCGAAACG 240  
 TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC GTAAACGATG AGTGCTAAGT 300  
 20 GTTAGGGGGT TTCCGCCCTT TTAGTGCTGC AGCTAACGCA TTTAAGCACT CCGCCTGGGG 360  
 GAGTTACGAC CGCAAAGTTT GGAAACTCAA AGGGAATTGG 400

## (2) INFORMATION FOR SEQ ID NO: 3887:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3887:

35 ATTTTTTAAT TTTCATGCAA ATTTTTAAGC ACCATATAAT GCCTACCAAA TTTCAATAAT 60  
 CTTTGTTGCC GTTTAAATAA TGTGAATGTC AATAAATTCT CCAAACCTAGT CGAAAATAAA 120  
 GGGAGTnGGA CATAAATCCC TAAAAAACA GCAGTAAGAT AATTTTCAAT TAGAAAATAT 180  
 40 CTTACTGCTG TTCTCTATTT ATACAATACT TCGTATTGAA TGGCTTCGCT TTCCnAGGGT 240  
 GCCGTCTCAG CCTCGGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC CATTAACTACT 300  
 ACGTATTAAC ATGGAATTTT ACTTTTACAT ACTTTAAAAA ATAAGnCACT TTGGCCAACT 360  
 45 TACTACTACCA TAGGAACCCT GGTAGGAATC CCCCAAATGn 400

## (2) INFORMATION FOR SEQ ID NO: 3888:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

ATACGACAAT CACAGCAATA ATAATTGCTT TAGAAAGTCG TGCCGAACTG GAACTTACAA 60  
 GTCTAGTTTCG AACACACACT GATGTGAGTG GTTTTATTTA TTTTAAACAT GAACAATCAG 120  
 5 ATAAGTTACT AGCATTAGCA AATATTATTA AATCAAAGGG CTTCGATTCA TAAAATTAAA 180  
 ACAATGATTA AAATTAGACG TGTAATGTT AAATTCTAAA ACGGAAATAA CCACCATCCC 240  
 10 ATTAAGCCAC TTTnATnGTT CAATCACTAT ATTTACACA GCTTCATTAA TAAACGACT 300  
 TGCTTCAACC CGCTTCAACT TCAACTGGCT TCAACTTCAG CCTACTTCAT TCAATnACAA 360  
 AACGAATCCG CTTTCATCCAA AATCAnCCAT TCTAACGCAC 400

(2) INFORMATION FOR SEQ ID NO: 3889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3889:

CCATGChAGA CGCATACATT GTaGCTTATG GgCGITCAGC gCAGCGAAmG aAAGCAAGGC 60  
 GCATTATTCC ACGAAAGACC TGATGATGTC GCAGCCAAAG TATTACAAGG CGTATTGAAA 120  
 30 CGTATTGACG GAAAATTCAA TAAGAATATG ATTGAAGATG TCATTGTTGG TACGGCTTTT 180  
 CCAGAAGGAT TACAAGGCCA AAACATTGCA CGAACGATTG CATTGCGTGC GGGATTATCT 240  
 GACACGGTAC CGGGTCAAAC AGTGAATCGC TACTGCTCAT CAGGATTACA AACCATCGCG 300  
 35 ATTGCAGCCA ATCAAATTAT GGCTGGTCAA GGAGATATAC TTGTAgCTGG TGGCGTTGAA 360  
 TTGATGAGTG CCGTACCAAT GGGTGGCAAC GAGCCCACAA ACAATCCaAC CTTwACAATA 420  
 tGaTGATATA GGTGCGTCCA TATnCTATG GGTTTnAAnT GCTGGAAAAT GTTAGCCTnC 480  
 40 CCAAT 485

(2) INFORMATION FOR SEQ ID NO: 3890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3890:

AGGCAGATGC TCTCCCAGCT GAGCTAATTC TCCAAATAA TGACTCCTAC GGGACTCGAA 60

AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 180  
 TGTGGGATTA ATATTATGCC TGGCAACGTT CTACTCTAGC GGAANTGAAT TCGGACTACC 240  
 5 ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT 300  
 ATAGTCACCA GACATATGAA TGTAAATTTAT ACATTCAAAA CTAGATAGTG AAGTAAAAGT 360  
 10 GGTTTTGCnT CGCAAAACAT TTATTTTgN 389

## (2) INFORMATION FOR SEQ ID NO: 3891:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3891:

CAGATGTTTA AGTCTGTGC GTCTGCCAGT TCCGCCACCC CGGCACTATA AAAATGGAGC 60  
 AGAAGACGGG ATTCGAACCC GCGACCCCAA CCTTGGCAAG GTTGTATTCT ACCGCTGAAC 120  
 25 TACTTCTGCA TATGCGGGTG AAGGGAGTCG AACCCCCACG CCGTAAGCTn AGATCCTAAG 180  
 TCTAGTGCgt CTGCCAATTC CGCCACACCC GCAAATGGTG AGCCATAGAG GATTGGAACC 240  
 TCTGACCCTC TGATTAAAAG TCAGATGCTC TACCAACTGG AGCTAATGGC TCTTCCATGG 300  
 30 TGCCGGCCAG AGGACTTGAA CCCCCAACCT ACTGGATTTA CAAGTCAGTT TGCTCTACCA 360  
 ATTGGAGCTA GGGCCGGGCA ATATGGTAAG AATAAATTGG 400

## (2) INFORMATION FOR SEQ ID NO: 3892:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3892:

CTCTCGGTGG TCGTGCTACA ACTGGTAAAA ATGTACATGT AGGGGCTGGC GCAGTATTAG 60  
 CAGGTGTGAT TGAACCCCTT AGTGCTTCAC CGGTTATAAT CGAGGATGAT GTATTAATCG 120  
 50 GTGCAAATGC AGTTATTTTA GAAGGTGTAC GTGTTGGTAA AGGTGCTATT GTTGCAGCTG 180  
 GCGCGATTGT GACACAAGAT GTACCAGCTG GTGCAGTTGT TGCTGGTACA CCTGCAAAAG 240  
 TGATTAAGCA AGCTTCTGAA GTACAAGATA CTAAAAAAGA GATTGTAGCA GCATTAAGAA 300

CCACChTAAT GGTnTAGCAT TGAATAAACT TATGnnCCCC

400

## (2) INFORMATION FOR SEQ ID NO: 3893:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3893:

GAATGTAGTT GTGGTAAATA CAAACGTGTT CGCTACAAAG GCATGGTCTG TGACAGATGT 60  
 GGAGTTGAAG TAACTAAATC TAAGTACGT CGTGAAAGAA TGGGTCACAT TGAACCTGCT 120  
 GCTCCAGTTT CTCACATTTG GTATTTCAAA GGTATACCAA GTCGTATGGG TATTATTACT 180  
 TGACATGTCA CCAAGAGCAT TAGAAGAAGT TATTTACTTT GCTTCTTATG TGTGTAGAT 240  
 CCAGGTCCAA CTGGTTTAGA AAAGAAAACCT TTATTATCTG AAGCTGAATT CAGAGATTAT 300  
 TATGATGAAA TACCCAGGTC AATTCGTTGC CAAAATGGG TGCCAGAAGG TCATTAAAAG 360  
 ATTTACTTGA AGnnGATTGA TnCTTGACGA GGGAACTTnA 400

## (2) INFORMATION FOR SEQ ID NO: 3894:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3894:

CACGTGAAGT TAGAGATACT TCATTACGTG TACCTCACGG CGCTGGCGGT ATCGTTCCTG 60  
 ATGTAAAAGT ATTCAATCGT GAAGAAGGCG ACGATACATT ATCACCTGGT GTAAACCAAT 120  
 TAGTACGTGT ATATATCGTT CAAAAACGTA AAATTCATGT TGGTGATAAG ATGTGTGGTC 180  
 GACATGGTAA CAAAGGTGTC ATTTCTAAGA TTGTTCTGA AGAAGATATG CCTTACTTAC 240  
 CAGATGGACG TCCGATCGAT ATCATGTTAA ATCCTCTTGG TGTACCATCT CGTATGAACA 300  
 TCGGACAAGT ATTAGAGCTA CACTTAGGTA TGGCTGCTaA AAATCTTGGT ATTCACGTTG 360  
 CATCACCAGT ATTTGacGGT GCaAACGrTG aCGATGTATG GTCAnCAATT GAAGAAGCTG 420  
 GTATGGCTCG TGATGGTAAA ACTGTACTTT ATCGATGGAC GTACCAGGTG ACCChTCCGA 480  
 TAACC 485

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 507 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3895:

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10 GAACAACATA CCTTTGTTTG TTGATTCTTC TCCACCTGTT TCAAGTAGTT CAGATTTCTT      60
   AGATTGTGGT TTTTLAGTTG GTGCCACTGc TTAAACCTTT TCATTGATT CAATAACAGG      120
   TGTACTACT TTACCTTGTT CCACTGGTTT AGAAGGCTTT TTAGGTTCTT CTTTGGCAGG      180
15 TGGTACTGGT TTACCAngTT CAGCTGGTAC CTCTGGTGTT GCGGGTGTTG GAGTTTCTGG      240
   CTCACTCGGC ACTTCTGGTG TCGGTGGTGT TGGTGTTC CC GGCTCACTTG GTACTTCTGG      300
20 TGTGGTGGGc GTTGGTGTTC COGGCTCACT TGGTACTTCT GGTGTCGGTG GCGTTGGtGG      360
   CACGATTGGA gGTGTTGTAT CTCTTCAAT CGTTTGTGA CCTTCATTTT GGGCCGCTTA      420
   CTTTGGGAA GTGTATCTTC TTCAAAGTCA AACTAATGT GGTCCACCGG AATTGATAAC      480
25 TGGGGTTAAC CTAAATTGG AACCTCC                                         507

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(2) INFORMATION FOR SEQ ID NO: 3896:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3896:

```

CTAGCGGAAG TAATTGGCTA CCATCGTCGC TAAAGACCTT nGgNgACTTG TGACAATCGC      60
40 TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG      120
   CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACTTCG CCAAGCCATT TTTCTTTGTG      180
   TTTACTTTTT ATTTTGACGT TTTAGGCATA AAAAAAGAG ACCTTGCGGT CTCAATGCGG      240
45 CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAAnGTA ATTGGGCTAC      300
   CATCGTCGCT AAAGACCTTT CTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG      360
   GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC                                         400

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(2) INFORMATION FOR SEQ ID NO: 3897:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3897:

	TTGAAGAAGA TCGCGATGAC TATACAATCA ATATCGAGTA TAATACCGAT TTATATCACT	60
10	CAGAAACAGT TCGTCACATG GGTAATCAAT GTATGATTAT GATTGATTAT ATTTTGAAGC	120
	ATCAAGATAC ACTACAAATT TGTGATATAC CAAACGGCAC GAGGAACTTC TAAATTGGGT	180
	CAATACGCAT GTTAACGATC GAATGCTTAA TGTCCCGGGA AATAAATCTA TCATAAGTTA	240
15	CTTTAATGAA GTTGTCTCAC GACAAGGTAA TCATGTTGCG CTAGTCATGA ATGAnTTGAC	300
	AATGACGTAT GAAACATTAC GCAACTATGT GGGATGCCAT TCGGCACATG CTCCTATCAA	360
20	ATGGTGTGGG CAATGGTCAA CGGGTTGCCT TGGTGTACAG	400

(2) INFORMATION FOR SEQ ID NO: 3898:

(i) SEQUENCE CHARACTERISTICS:

25	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3898:

	GAAATCAGTA TTAAAGCAGT TAATCCACAA GGGAAAGTGG TTAATACAGT TGGCTCTGGT	60
	GATAGTACAG TTGCAGGCAT GGTGGCTGGA ATTGCTTCAG GTTTAACGAT TGAAAAAGCA	120
35	TTCCAACAAG CAGTCGCATG CGGTACTGCC ACGGCATTTG ATGAGGACTT AGCAACACGG	180
	GACGCTATAG AAAAAATAAA ATCACAAGTT ACGATTAGCG TACTTGATGG GGAGTGAAAA	240
	TAATGAGAGT AACAGAGTTA TTAACAAAAG ATACAATAGC AATGGATTTA ATGGCAAATG	300
40	ACAAAAATGG TGTATTGAT GAGTTAGTAA ATCAATTAGA CCAAGCAGGT AAATTAAGTG	360
	ATGTCGCGTC ATTTAANGGA AGCGATTCAC CATCGnGATC	400

45

(2) INFORMATION FOR SEQ ID NO: 3899:

(i) SEQUENCE CHARACTERISTICS:

50	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3899:

CTAGCGGAAC GTAAGTTAGC TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC 120  
 GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG 180  
 5 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG 240  
 TGTTTACTTT TTATTTTGAC GTTTTAGACA TAAAAAAGA nACCTCACGG TCTCAACTTG 300  
 CCTGGCAACG TTCTACTTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC TnAAAGACCT 360  
 10 TTCTTGACT TGTGGACAAT CGGCTTGGCA nTCTTTnCTC 400

## (2) INFORMATION FOR SEQ ID NO: 3900:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3900:

TGCACGCGTA TCTGATGGTT GCTCAGTTGC ATCTACCCAA GGTAACCATT CCCTAAGTGA 60  
 25 ATTTCTTGAA CGATTGACTA AATTGAAAAG CGCTTCTGTG TCATGAGCTT CTAAAATTTT 120  
 TAATGTTATT TGTTCAATCA CTTTCATTCC AACATACCA TCACATCCTC ATTCAATTTT 180  
 CATATAATTC TGTAATTTAT CATTATAATA ACATATTAAT GTTACGCATT GTATCTTAAA 240  
 30 TTTGTTGTCC TTCCCCAACT TGCATTGCTT GTAGAATTC TTTTCGAAAT TCTCTATGTT 300  
 GGGGCCCCGn AACTTGCAAT GTCTGTAGAA ATTACGGACC CAATTTCTCT AGGTGGGGCC 360  
 CATCCCCAAC TTGCACATTA ATnGCAAGCn GACTTTCCGT 400

## (2) INFORMATION FOR SEQ ID NO: 3901:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3901:

TACTGCTGTT CACTTTTTAT AATACTTCTG AATGTCTTCA CTTATACTTC TAGTCACAGA 60  
 TTAAATAAT CAAAAGTGCA CATTATTAAA ATATCAATTT CAACTCAAT GCGGCTCATC 120  
 50 GCATTCATTT CTTGTCTCAA CGTTCTACTC TAGCGGAAGT AAGTTAGCTA CCATCCTCGC 180  
 TAAGAACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT 240

TTTCACTTCG CCAAGCCATT TTTCCTTGGT GGTTCACCTT TTAATTGGGA CGGTTTAGAC 360  
 ATAAAAAAG GGGACCTCAC GGGCCCAACT TGGCCTGGGC 400

(2) INFORMATION FOR SEQ ID NO: 3902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3902:

TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG 60  
 TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 120  
 GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 180  
 CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT 240  
 TTCTTTGTGT TTAATTTTGA TTTTGACGTT TTAGGCATAA AAAAAAGAGA CCTTGCGGTC 300  
 TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGGCAACG TTCTACTCTA GCGGGAACGT 360  
 AAGTTGGGCT ACCAAGCGCG GCTAAAGACC TTTCCTGGAC 400

(2) INFORMATION FOR SEQ ID NO: 3903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3903:

TTGTTATAAC GAAAACCATT AATAGATTTT TATTTGGTGA TTTCAAATCA TGAGACTGGG 60  
 ACAGAAATGA TGTTTTCATA AAAATTATTT CGTTGTTCCA CTCTCATGAT TTTTTTGATG 120  
 AAACATAATT ACATGATTGA TTGCATCATT TTGTTAAACA AGTGATTGCA AACCTGCCAT 180  
 TTCACACTGA AAATTTACAT AATAAGTGAC GATATTTTAC AAGTCATATA CAAATAACAT 240  
 ATATTGTAA ATAATTTTAC CTAATCTTAA CATTAAATTT ACAATTATAA GCGATAATCT 300  
 AAATATAAAG CTTATTTGAG GTGAAATAAT GGAAATGTCG GTTACAGAAG TCATTTTCTC 360  
 CTTTTTAGGT GGGTTTAGGG AATTTCCnTT ACGGCCTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3904:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3904:

10 CATAAGACAT AATCGCTAGT GTTCGAAAGA GCACTCACAA GATTAATAAC GCGTTTCCTG 60  
 TAGGATGGAA ACATAGATTA AGTTATTAAG GGCGCACGGT GGATGCCTTG GCACTAGAAG 120  
 CCGATGAAGG ACGTTACTAA CGACGATATG CTTTGGGGAG CTGTAAGTAA GCTTTGATCC 180  
 15 AGAGATTTCC GAATGGGGAA ACCCAGCATG AGTTATGTCA TGTTATCGAT ATGTGAATAC 240  
 ATAGCATATC AGAAGGCACA CCCGAGAGnC TGAAACATCT TAGTACCCGG AGGAAGAGAA 300  
 AGAAAATTTCG ATTCCCTTAG TAGCGGCGAG CGAAACGGGA AGAGCCCCAA CCAnCAAGCT 360  
 20 TGCTTGTTGG GGTGTAGGG CACTCTATAC GGAGTTACAA 400

## (2) INFORMATION FOR SEQ ID NO: 3905:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3905:

AACTAACATT ACAACATGCA TGTGAACAAT TAAAAACATA TTTTAAGTAG GTGAATGAAA 60  
 35 TGgTAAATGA ACAAATCATT GATATTTTcAG GTCCGTtAAA GGGCGAAATA GAAGTGCCGG 120  
 GCGATAAGTC AATGACACAC CGTGCAATCA TGTTGGCGTC GCTAGCTGAA GGTGTATCTA 180  
 CTATATATAA GCCACTACTT GGCGAaTtCG TCGTACgATG GaCATTtTTCC gACTGTtTAGG 240  
 40 TGTAGAAATC AAAGAAGATG ATGAAAAATT AGTTGTGACT TCCCCAGGAT ATCAATCTTT 300  
 TAACACGCCA CATCAAGTnT TGtTnTACAGG TAATTCCGGG TACGACAACA CGATTGATAG 360  
 TTTGGTTAAT GGGTTAAGTA TTGAAAGTGT TTTGTCCGG 399

45

## (2) INFORMATION FOR SEQ ID NO: 3906:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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TTCTTTAAAA ATAAACGCCT ATnCGTTATC GGTGGTGGTG ATTcAGCAGT AGAAGAGGGA 60  
 ACATTCTAAA CTAAATTTCG TGACAAAGTA ACAATCGTTC ACCGTCGTGA TGAGTTACGT 120  
 5 GCACAGCGTA TTTTACAAGA TAGAGCATTc AAAAATGATA AAATCGACTT TATTGGAGT 180  
 CATACTTTGA AATCAATTAA TGAAAAAGAC GGCAAAGTGG GTTCTGTGAC ATTAACGTCT 240  
 ACAAAAGATG GTTCAGAAGA AACACACGAG GCTGATGGTG TATTCATCTA TATTGGTATG 300  
 10 AACCATTAAc AGCGCCATTT AAnGCTTAGG TATTACnAAT GATGTTGGTT ATATTGTGAC 360  
 AAAGGTGGAT TGGCCAC 377

(2) INFORMATION FOR SEQ ID NO: 3907:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 502 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3907:

AATTAGGTAA TTCAAAATAA TATTAGCGCG GGATGGAGCA GTTCGGTAGC TCGTCGGGCT 60  
 CATAACCCGA AGTCGGTGGT TCAAATCCGC CTCCCGCAAT ACATAGTTTT TAATTTAATA 120  
 GGTCTCGTAG TGTAGCGrTT AACACGCCCTG CCTGTCAGCG AGAGATCGCG GGTTCGATTc 180  
 30 CCGTCGAGAC CGCCATTATT ATTACCATTA CGGTTCAgTA GCTCAGTTGG TAGAGCAATG 240  
 GATTGAAGCT CCATGTGTcG GCAGTTCGAC TCTGTCCtGa ACCATTCTTA ATTcATGGCG 300  
 GTTGTGGTGA AGTGGTTAAC ACATCGGATT GTGGTTCCGA CATTcGAGGG TTCGATCCCC 360  
 35 TTCAGCCGCC CCATAATCGT TTACATTAGC GGGTGTAGTT TAATGGcAAA ACCTCAGCCT 420  
 TCCAAGCTGA TGTTGTGGGk TtCGrTTCCC AtCAmCCnGy TCCaTaATTT CnAAnaATTC 480  
 40 CAACAGTAGC CGCAAGTnGG TA 502

(2) INFORMATION FOR SEQ ID NO: 3908:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3908:

AAAAAATGCA TCTCTACGTG CTAGAATAAA TATTGGTCAG CCAACCAAAA TAATCAACAC 60

TAAGTATCAT ATTGTCTTTG CACCTAAATA CAGAAGACAA GTGATATATG GAAAAATAAA 180  
 AAAAGATATA GGGATTATAT TCGTCAATT ATGTGAAAGA AAAGGTGTAG AGATAATTGA 240  
 AGCAGAGGCA TGTAAGATC ATATCCATAT GTTAGTTAGT ATACCACCCA AACTGGGGG 300  
 TATCATCATT TGTTGGGCTA TTTAAAAGGG AAAAAGTAGT TTAATGGATA TTTGGATAGA 360  
 CATGGCTAAC TTAAAGTATA GATATGGGAA ATAGGAAAGT 400

## (2) INFORMATION FOR SEQ ID NO: 3909:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3909:

GGTTTAACTA TTGAAGAAAA TGTGCCGACA ATTAACAAGA TAAAAAATGC GGTATATTCA 60  
 GCAGATAAAG CTTTACCTAA GATTAATGAC TTTGCGAATA AAATTGTATA TTTGAATAAC 120  
 CACCAAGCGG ATTTAGATAA ATATGCCAAT GATTTTAGAA AACTAGGAAA TTATAAAGGT 180  
 GATATTTTAG ATGCTCAGAA AAAATTAAAC GAGTCAATGG TGCTATTCCG CAACTTAATG 240  
 AAAAGGCTAA GTTGGATATT AGCTTTTAAA TAATTATATG CCGGAAAATT GGAAAAAGCG 300  
 TTTAAATTTT GCAGCTGGAT GACGTGCCAC GCGTTCCCT AAAATTAATC CAGGGCTTAA 360  
 CATTGCGAGT CCAGGTATTG GATCCAAGCT AATGGGGCCG 400

## (2) INFORMATION FOR SEQ ID NO: 3910:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3910:

TTACCCGATA TCGGGAAGGT ATCCACGAAG GTGAAATTGT AAAATGGTTT GTTAAAGCTG 60  
 GAGATACTAT TGAAGAAGAC GATGTTTTAG CTGAGGTACA AAACGATAAA TCAGTAGTAG 120  
 AAATCCCATC ACCAGCATCT GGTACTGTAG AAGAAGTTAT GGTAGAAGAA GGTACAGTAG 180  
 CTGTAGTTGG TGACGTTATT GTTAAATCG ATGCACCTGA TGCAGAAGAT ATGCAATTTA 240  
 AAGGTCATGA TGATGATTCA TCATCTAAAG AAGAACCTGC GAAAGAGGGA AGCGCCACAG 300

GCCATGCCTT CCAGTTACGT TAAATACGCA CGTGGAAAAG

400

(2) INFORMATION FOR SEQ ID NO: 3911:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3911:

CGTGTAnCTC	AAGTTATGGG	TCCTGTAATT	GATGTTGAT	TTGAACATAA	CGAATTCCTA	60
AAATTAATAA	CGCCTTGGTT	ATTGATGTGC	CTAAAGAAGA	AGGTACAATA	CAACTAACAT	120
TAGAAGTTGC	GCTGCAATTA	GGTGACGACG	TTGTTCTGAC	AATTGCGATG	GATTCAACTG	180
ATGGTGTCCA	AAGAGGCATG	GATGTAAAAG	ATACAGGCAA	AGAAATTAGT	GTACCTGTTG	240
GTGACGAAAC	ATTAGGTCGT	GTATTTAATG	TACTAGGTGA	AACAATTGAC	CTTAAAGAAG	300
AAATTAGTGA	TTCTGTTTCG	CGCGATCCTA	TCCATCGTTC	AAGCACCAGC	ATTCCGATGG	360
AACTTTTCAA	CAGAAGTTCC	AAATTTTGTAG	GnACAGGGTA			400

(2) INFORMATION FOR SEQ ID NO: 3912:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3912:

TTGTACAAGT	TGAAGAAAAA	TCAACACAAC	CAAAGGTTAG	AAAATTCAA	GATTTCCTA	60
GTAAATTTAA	TATAGCATCA	GAAGCTAAAG	AAAATGAACC	TATATCAGTC	ATTGGTTATC	120
CAAATCCTAA	TGGAAATAAA	CTACAAATGT	ATGAATCAAC	TGGTAAAGTA	TTATCAGTGA	180
ATGGGAATAT	AGTGTCTATG	GATGCAATTA	TTCAGCCTGG	TAGCTCTGGT	TCACCTATAT	240
TAAATAGTAA	ACACGANGCT	ATTGGTGTA	TCTATGCCGG	TAATAAGCCA	TCAGGTGAAA	300
GCACCAGAGG	GATTTGCTGT	TTATTTCTCT	CCTGAAATTA	AGAAATTCCA	TTGCAGATAA	360
TTTAGATAAA	TnATTAAGAC	CTANGACATT	CACCCAATCC			400

(2) INFORMATION FOR SEQ ID NO: 3913:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3913:

ACTCATTTAG	CTCTACTAAA	CTCGTTGCGC	TCTTTTCTCG	TTTCGTCAGA	TTCAAACGTT	60
TTCACTTCGC	CAAGCCATTT	TTCTTTGTGT	TTACTTTTAA	TTTTGACGTT	TTAGACATAA	120
AAAAAAGAGA	CCTTGCGGTC	TCAATGnGGC	TCATCGCATC	CATTTTTTGC	CTGGCAACGT	180
TCTACTCTAG	CGGAAGTAAG	TTGGCTACCA	TCGACGCTAA	GAACCTTTCT	TGACTTGTGA	240
CAATCGCTTG	CTTCTTTCCT	CTTCTTCGGC	TCTCGCTTAC	TCATTTAGCT	CTACTAAACT	300
CGTTGCGCTC	TTTTCTCGTT	TCGTCAGATT	CAAACGTTTT	CACTTCGCCA	AGCCATTTTT	360
CTTTGGGGTT	TGChnTTTGA	ATTTGGACGT	TTTAGACATA			400

(2) INFORMATION FOR SEQ ID NO: 3914:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3914:

TGGAATGAGC	GGATATAAGC	ATCTTTAGAT	AATGCACCAT	CAACTAATGG	ATATTTATGT	60
CCAGTTGGAC	GCCAGAAATC	ATAAACGTCT	TCAGTGTAAG	CAACAGCATC	TTCATTTAAT	120
GCCAAAATGC	TTGGATTATG	TGCAATAACC	ATCGCAACTG	nGCCACACCT	TGTGTTGGCT	180
CGCCGCCTGA	ATTCAATCCA	TAACGTGCTG	TATCTGTAGC	AATAACTAAT	ACTTTTTTCAT	240
TCGGTCTAGT	TGCTAAATAA	TCTTTAGCTA	ATTGAATTGC	TGGTGTGCA	GCATAACAAG	300
CTTCTTTCAT	TTCAAAGCAG	CGTGCAAAAG	GTTGGnATAC	CTAATAAGTT	GTGGAATTTG	360
nACAGCGGCT	GCTTTACGAA	TTCCAACGTC	TGATTCCAGT			400

(2) INFORMATION FOR SEQ ID NO: 3915:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 371 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3915:

TCTTTATTTA TCCAGTTTCA TAGTCAATGT TTAAAGCAAA ATCTTATTGA TGGTACAAAA 120  
 GTAGAAGCTA ATGCCAATAG GTATACATTT GTGTGGAAGA AAAGTATTCA AAATCACGAA 180  
 5 TCGAAATTGA ACGAaAATTC AAAAACATTA TATCGTGACT TAGTTGAAGA AAAAATAATA 240  
 CCAGAGATAA AAGAAGATGG AGATAGCGAT TTAACAATAG AnGAAATAGA TTTAATTGGT 300  
 AGTCATTAG ATAAAGAAAT CGAGGTTTAA ATCATTCTAT TGAGACGnGA TAGTACTCAA 360  
 10 ATTAGAAACA G 371

## (2) INFORMATION FOR SEQ ID NO: 3916:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3916:

ACCATGGACG ACGGTTAGGT TTATGAATGT TATTCCAAAT AGGTTTCATCT ATAAAATAGC 60  
 25 TTTAGTTGGA AAAGATGAGA AAAAATATAA AGATGGACCT TACGATAATA TCGATGTATT 120  
 TATCGTTTTA GAAGACAATA AATATCAATT GAAAAAATAT TCTGTCGGTG GCATCACGAA 180  
 GACTAATAGT AAAAAAGTTA ATCACAAAGT AGAATTAAGC ATTACTAAAA AAGATAATCA 240  
 30 AGGTATGATT TCACGCGATG TTTCAGAATA CATGATTACT AAGGAAGAGA TTTCCTTGAA 300  
 AGAGCTTGAT TTAAATTGA GAAACAACT TATTGAAAAA CAGATCTTTA CGGTAAACATG 360  
 GGTCAGGAC AATCGTATTA AATGAAAACG GGGGAATATA 400

## (2) INFORMATION FOR SEQ ID NO: 3917:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3917:

GAGGAAATTA TTAACCTTnC GCATCGTATG GGCCnTGAAG GAATAACAaC CTTTAGACCT 60  
 GGAGATTGAG CTAAATACC TTCTAAGTTA TCTGCGTGTA ATTCTGGTGT GTGTACGCCA 120  
 50 CCACCAAATG GGCTACGAAT TGTTACAGGT GCAGTTTTAG TACCGCCTGA ACGGAAACGA 180  
 GTACGTGCAA TTTGTCCAGC AATCGCATCA AATACTTCGA ATACGAAACC TAAGAATTGT 240

GATTCAGCTA AAGGTGTATC GAATACTCTA TCTTCACCAA ATTCTTTTGT TAGTCCTTCA 360  
 GTAACACGGA AAACACCGCC GTTAACACCA ACGTCTTCAC CAnAATnAAA AC 412

(2) INFORMATION FOR SEQ ID NO: 3918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3918:

ATAGATTGCT GAGTGACAAT ACTTCAGGAn TCGCATATGC AGGCCCAATA CCCATAATTT 60  
 TCGGGTCAAC GCCTACTGCC TTAAAACCAA CGAATCGTGC AATAGGTGTC ACGCCGAGTT 120  
 CTTTCACTTT ATCTCCAGAC ATTAAAACTA CAAATCCTGC ACCATCAGAA AGTGGGGCAG 180  
 ATGTTCTCTG AGTCATAGTG CCGTCAGCTT TAAATACTGT ACGTAATTTG GCTAATGCCT 240  
 CCATCGTGGT GTCAGGGCGT ATnAAATTCA TCTTGGTCAA AGATATTTGT GTGTACTTTT 300  
 GGTCTGCGT TTGTATATTC AACTGAGTTT ACTTGTATTG GGATnATTTC ATCTTTGGAA 360  
 CCGACCATCA CCGTGTGCGT TCATAGGCAC GTTGATGnAC 400

(2) INFORMATION FOR SEQ ID NO: 3919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3919:

CAAGGGCAAC AAGGTGGCAA CGGCAATTAT TTAGAACAAA TTGGTCGTAA CCTTACnAAG 60  
 AAGCACGTGA CGGTTTATTA GATCCAGTCA TTGGTCGTGA TAAAGAAATT CAAGAAACTG 120  
 CTGAAGTTTT AAGTAGACGA ACTAAAAACA ATCCTATATT AGTTGGAGAA GCTGGTGTG 180  
 GTAAAACTGC GATTGTTGAA GGTTTAGCAC AGGCAATCGT TGAAGGAAAT GTACCAGCAG 240  
 CAATCAAAGA CAAAGAAATT ATTTCTGTAG ACATTTTCATC ATTAGAAGCT GGAACGCAAT 300  
 ATCGTGGTGC TTTTGAGGAA AATATTCCAA AATTAATCGA GGTGTTAAnc TTCACAAATG 360  
 CCGTACTATC TTTGATGAAn CCATCAATTA TCGGTTTCAGT 400

(2) INFORMATION FOR SEQ ID NO: 3920:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3920:

10 CTTATCCCGT CCACACATAG CTACCCAGCT ATGCCGTTGG CACGACAACT GGTACACCAG 60  
 AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACAGCTC CTCTCAAATT TCCTACGCCC 120  
 ACGACGGATA GGGACCGAAC TGTCTCACGA CGTTCTGAAC CCAGCTCGCG TACCGCTTTA 180  
 15 ATGGGCGAAC AGCCAAGnCC TTGGGACOGA CTACAGCCCC AGGATGCGAT GAGCCGACAT 240  
 CGAGGTGCCA AACCTCCCCG TCGATGTGAA CTCTTGGGGG AGATAAGCCT GTTATCCCCG 300  
 GGGTAGCTTT TATCCGTTGA GCGATGGCCC TTCCATGCGG GAAnCAACGG ATTCACTAAA 360  
 20 GTCCGTCTTT TCGAACCTGG CTCGGACTTG TAGGTCTCGG 400

## (2) INFORMATION FOR SEQ ID NO: 3921:

25

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3921:

CGGGTTGGGC AGGTATGTTG TATTACCGTT CACAGCAGCA TCACTTTGAA CAACATTTGT 60  
 35 TAACGGATTA TTTGGCAATT CGGTTAGTTG TCGAACAATT GCTAGTTGGT GATGAGTTTA 120  
 AGTCAGTCGC TAAAGATTGT GAAAGTAGAT CGGAAAATTG GTTTAAGCAA ACTGTTGCAT 180  
 CATGGTGTTA CTACAGTGGA TATGCCTAGC GATGTATTAC TACAACATGA CGTCAATGAA 240  
 40 ATTCAAACGT TTATTCATTT TGGCAGCAAC TATGGAATAA AAATGTATTT AAAATTTATG 300  
 GCTnAATTGC CnGGGGAAAT GACATACGGG ATCTCAGTTT AAAACAAAAA TTAAAGCAGG 360  
 45 TCATGGAAAG TGTGGCGGGC GCCTTAGGTG TnAACCCAGT 400

## (2) INFORMATION FOR SEQ ID NO: 3922:

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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GTGCGCTCTA ACCAGCTGAG CTATAGGCCC ATTTTTTTGA ATGTTAAATA AACATTCAAA 60  
 ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC 120  
 5 TTAGAAAGGA GGTGATCCAG CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC 180  
 CAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTACTIONACC GGCTTCGGGT 240  
 10 GTTACAACT CTCGTGGTGT GACGGGCGGT GTGTACAAGA CCCGGGAACG TATTCACCGT 300  
 AGCATGCTGT ATCTACGTTT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT TGCAGACTAC 360  
 AATnCGAACT GAGGAACAAC TTTTATGGGG TTTGnTTGn 400

(2) INFORMATION FOR SEQ ID NO: 3923:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3923:

AGTAAGTAAA ATATAGATTT TACCAAGCAA AACCGAGTGA ATAAAGAGTT TTAAATAAGC 60  
 TTGAATTCAT AAGAAATAAT CGCTAGTGTT CGAAGAACTC CACAAGATTA ATAACGCGTT 120  
 25 TCCTGTAGGA TGGAAACATA GATTAAGTTA TTAAGGGCGC ACGGTGGATG CCTTGGCACT 180  
 30 AGAAGCCGAT GAAGGACGTT ACTAACGACG ATATGCTTTG GGGAGCTGTA AGTAAGCTTT 240  
 GATCCAGAGA TTTCCGAATG GGGAAACCCA GCATGAGTTA TGTCATGTTA TCGATATGTG 300  
 35 AATACATAGC ATATCAGAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGAGAAG 360  
 AGAAAGAAAT TCGnTCCCTA GTACCGCGAn CGAAACGGGA 400

(2) INFORMATION FOR SEQ ID NO: 3924:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3924:

ATGCGATACG TAGCACAGCT GCAACAATCC ATGCTAGTAA AATCGGAGAC ATCTCTGTAC 60  
 50 CTTCAAACCTA GCAATTGTAT TTCCGACACC GCCGTCAATT AATACTTGTT TAATGTACCG 120  
 CCACCGCCAA TAATCAATAA CATCATTCGG ATTGGATAAA TCGCATTCGT CACTGATTCC 180

GCTATTAGCA TGGCTGTCCC TGCTGTTCCCT ATCATATAAA TGATAGATTG AAATAGATTT 300  
 GTAGGGTTGT CATGCCAGT TACAAGTTGC GTTGATCGTn GACACTAACA TTAATATGAC 360  
 5 TGGTAATGTT GCTGTTAATA AACTCATACC AantCCGGGC 400

## (2) INFORMATION FOR SEQ ID NO: 3925:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3925:

GGCTGGGCTA GCTGGATTG AACCAACGAG TGACGGAnAn AGGTCCGTTG CCTTACCGCT 60  
 20 TGGCTATAGC CCAATATATA GATGGTGGAG GGGGGCAGAT TCGAACTGCC GAACCCGAAG 120  
 AGCCGGATTT ACAGTCCGCC GCGTTTACCA CTTCGCTACC CCTCCAGCTT ATTCATATAA 180  
 TTTAATAATC AAAATGGTGG AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG 240  
 25 CAGATGCTCT CCCAGCTGAG CTAATTCTCC AAAATAATGA CTCCTACGGG ACTCGAACCC 300  
 GTGTTACCGC CGTGaAAGGG CGTGtgCTTA ACCcTTGGAC CAAGGAGCCA TGGCTCaCAG 360  
 GTAGGACTCG AACCTACGAC CGATCGGTTA AcAGCCGATA GCTCTACCAC TGGAGCTGAC 420  
 30 TGTGGATTAA TATTATGCCT GGCAACGTTT TGAnnCTAGC GGAantGAAT TCGGACTGAC 480  
 CATCGACGCh AAGGAGCTGA ACTTCTGTGT TCGGGCATGG GGAAC 525

## (2) INFORMATION FOR SEQ ID NO: 3926:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3926:

TGTTATTGTT CAAAATCATG ATCAAGATCA GTATATCGTT GCITTATTATG AAGCGATGCA 60  
 TACATTATCA CATAATAAGA TTAAATCACA ATTACGTATG ACCTTACCGG AGTACATGAT 120  
 ACCAGTTAAT TTCATGCATA TTGAGCAAAT TCCTATTACT ATTAATGGGA AATTAGATAA 180  
 50 GAAGGCATTG CCTATCATGG ACTATGTCGA TACGGATGCC TATGTAGCAC CGAGTACAGA 240  
 TACCGnACAC TTGCTATGCC AAATTTTTGC AGATATTTTA CATGTGAATC AAGTAGGTAT 300

TCCGGATAGA GGCATCCACT GGGGAACGGT TACCAATTGG

400

## (2) INFORMATION FOR SEQ ID NO: 3927:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3927:

TATCGATCAA TTTCTATCGA GTTGGACAAT GCCGAACGTG ACAAAGTTTT TACCATGCAT 60  
 GGTTCGATTT AGCGCAACAT GACCATAGTT TTAATAAAGC ACAGCGCGCA AGTGATTAAA 120  
 GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT TAACTCATTT TTCAATAGAT 180  
 CAGGAAGACT ACCAAGCTTA TGTGAAGGA CATCTTTTGG CGTTACCGGG TTGGGCAGGT 240  
 ATGTTGTATT ACCGTTTACA ACAGCATCAC TTTGGAACAA CATTGTGTTAA CGGATTATTT 300  
 GGCAATTCGG TTAGTTGTCG AACAATTGCT AGTTGGTGGG TGAGTTTAAG TCCATCGCTA 360  
 AAGATGTGGA AATAGnCCGG AAAATGGTTT TAAGCAAAC 400

## (2) INFORMATION FOR SEQ ID NO: 3928:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3928:

GTGCACCTAA CGCTGAAATA TCGCCTTCTC GTGTATAGCA GACGGAATCA TTTTGTGTC 60  
 AATTTGTGTTAA ATATAGGCCC TGCAATGAGT GTACTGGAAT GGCAATAATC ATACCATACA 120  
 GTAATACATC TCCAACATTT GCCTTTAATT CTTTTCGAT GACTACCGGT CCTGGATGTG 180  
 GTGGTAAAAA GCCATGTGTC ACTGATAAAG CTGTTACCAT AGGTAGTCCT AGTTTAAACA 240  
 CTGAAACATT TGCGCGTTTT GCTACTGTAA ATACTAATGG AATCAGTAAG ACTAAACCTA 300  
 CTTCAAAGAA CAATGCAATA CCGACGATAA ATGCTGGCAA CAAGCATTGC CCCATTGGTA 360  
 CATGGTTTTT GGACCAAATT TTTGGAATCA ACGTGTCTGG 400

## (2) INFORMATION FOR SEQ ID NO: 3929:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3929:

CTCAAGGTGT TGCCTATACA GCTAAAAAAC TTAATTTAAA CGCTGTTATC TTTATGCCAG 60  
 10 TCACTACACC TTTACAAAAG GTAAATCAAG TAAAGTTCTT TGGAAATAGT AACGTTGAAG 120  
 TTGTACTCAC TGGTGATACA TTTGATCACT GTTTAGCTGA AGCTTTAACT TATACAAGTG 180  
 AACATCAAAT GAACTTTATA GATCCATTCA ATAATGTTCA TACAATTTCT GGACAAGGTA 240  
 15 CGCTTGCTAA AGAAATGCTA GAACAAGCAA nGTCTGACAA TGTTAACTTT GCATTATCTA 300  
 TTTGCCGCAA TTGGTGGTGG CGGTTTAATT TCAGGTATTT CGTACTTACT nTTAAACCT 360  
 ATTCACCTAC CACGnAAATT ATAGGTGTTG AACCCnAGT 400

20

## (2) INFORMATION FOR SEQ ID NO: 3930:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3930:

ATATGATCCT ATGAAGCAAT TTTATGTAGT AAGTGGTTCT AACATGACG CCCTTATGCT 60  
 CTGTGAACAT TTATATGACG AGGTTATGGC TGTTTGCTAA nCCCCAAATGA TACATCGAAT 120  
 35 GGCACATATC ATTCGTCGCA ATATGATTAC TATGATGCAT TTATTAAGCA GCAAGAAAAT 180  
 GTAACATATA TTTCAACCGA TCGTCAGAT GCTAATACAG TGTTATGTCA CTAATTTATA 240  
 AAAAATAAAT GAATAAGTAA GGTTCACACC GAGAGAATAT ATTCGTGTTG AAGCCTTATT 300  
 40 TGTCGTTGTG CCAAATTTGA ACGnTTAGA TGGCAATAAG CATGACCATA CAGATTGTGT 360  
 ATTATTTCCA TGrA 374

45

## (2) INFORMATION FOR SEQ ID NO: 3931:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 387 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3931:

TGCTTCTTTC GCTAGCCTCG TATGGGCATC TTTATCAATA ATATACTCGC CATGACTATC 120  
 TTTCGCTTTT AAGTCAATTT CATCAAACTC TTTCCACCT GTTAACGGTG CACCACTATG 180  
 5 TCGTTTCCGA CCAAATGTAG CCTCTTGTTT TTCCAGCGCA GTACGATCCC ACGTTTCAAT 240  
 GTGTATTTGA ATACGTCTGA CAACGCAATA AGTTCCATGT TTCGCCCATC CGTCATCAAT 300  
 AAACACATAA TCTTTAAGTT GATTATTCTT CCTAGGATTA ATTGTTCCAC TTTAAAATGC 360  
 10 CATTAATAATT CTAGGTGTTT CChTAnC 387

## (2) INFORMATION FOR SEQ ID NO: 3932:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3932:

AAGGTAATAA TCCTGTAGTC GAAAATGTTG TCTCTCTTGA GTGGATCCTG AGTACGACGG 60  
 25 AGCACGTGAA ATTCCGTCGG AATCTGGGAG GACCATCTCC TAAGGCTAAA TACTCTCTAG 120  
 TGACCGATAG TGAACCGTA CCGTGAGGAG AAGGTGAAAA GCACCCCGGA AGGTAGnTGA 180  
 AATAGAACCT GAAACCGTGT GCTTACAAGT AGTCAGAGCC CGTTAATGGG TGATGGCGTG 240  
 30 CCTTTTGTAG AATGAACCGG CGAGTTACGA TTTGATGCAA GGTAAAGCAG TAAATGTGGA 300  
 GCCGTAGCnG AAGnAnGTTT TGAATAGGGC GTTTAGTATT TGGTCGTAGC CGATAACCAG 360  
 GTGATTCTAC CCTTTGGTCA GGTTGAAGTT CAAGTAACAT 400

## (2) INFORMATION FOR SEQ ID NO: 3933:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3933:

GCGATGGTTG AAACATTGAC TTATATTAAA GAGTTTATGA ACCAAGTTGA GTCGCATAGC 60  
 TAGTATGAAA CGTGGTGTGC GCATGGGAAC TATCAAGCTT TGAAGATGTG GTACTACATG 120  
 50 CGTTGAATTA GGGATCGGTA CTTTATATGA AGACGTGCTG CTTCCATTAA ATGAGTGATG 180  
 CGATTTTGGC ATGAAGGTCA CCTTAAATGT ACATTGTTGT AATAAAATTG CCTATAAATT 240

AATTGTAAAA AGAAAACCAT ACGCTATGTG nTGCCAAGGA AAAGGTTCTA CCATTGTCAC 360  
 nAAAAATGCA TCTCTACGTG CTAGGAATAA ATATTGGGTC 400

(2) INFORMATION FOR SEQ ID NO: 3934:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3934:

TTTGACGTTT TAGACATAAA AAAAGAGACC TTGCGGTCCA GATGGGGCTC ATCGCATCCA 60  
 CTTTTTGCCT GGCAACGTTT TACTCTAGCG GAAnTAATCG AACTACCATC GACGCTAAGG 120  
 AGCTTAACTT CTGTGTTCCG CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC 180  
 ATATGAATGT AAATTATACA TTCAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA 240  
 AACATTTATT TTGATTAAGT CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT 300  
 GGCTTCCACC TCGAACCTAT TAACCTCATC ATCTTTGAnG GATCTTATAA CCGAATTGGG 360  
 AAnCTCATCT GAAGGGGGCT CAGCTAGATG CTTCAAnACTT 400

(2) INFORMATION FOR SEQ ID NO: 3935:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 393 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3935:

TGTTCTTTTT GGGCAGTGGG ACACAAATGG ATATTTTCGG CAAAATTTAT TTCGTTCGnT 60  
 CCCACCCCAA CTGGGCACAC TATTGTAAGC TGACTTTTCG CCAGCTTCTG TGTGGGGGCC 120  
 CCGCCAACTT GCCATTGTCT GTAGAAATTG AGGAGCTAAT TTCTCTGTGT CGGGGCTCCA 180  
 CCCCAACTTG CACACTATTG TAAGCTGACT TTCCGCCAGC CTCGTGTGTG GGGCCCCGCC 240  
 AACTTGCACA CTATTGTAAG CTGACTTTCC ACCAGCCTCT GTGTGGGGCC CCGACTATTT 300  
 TTGAAAAGAG CGTGTTACAC GGGCATTGTT TTACAGTCAA CTACTGCTAA AATAAAATTA 360  
 ACGAGCTTAA GGCTTTGGnT TCTGTCCCAA GCC 393

(2) INFORMATION FOR SEQ ID NO: 3936:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3936:

10	AAAAAGAAGA CAACCAAGCC CAATAATGGA CTGGCCGCGT AATAATnGTG GCTCTAAAAG	60
	TTGTATTTTA AAAATAGTTC TTAAATTAT ATACCCACCA CATTTGGTGG AGAACCTAAA	120
	AAAAAGCACT TCCCAAAAAT GGAAAGTGCA AGTAGTGAGC CATAGAGGAT TCGAACCTCT	180
15	GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC	240
	TAGCTGGATT CGAACCAACG AGTGACGGAn TCAAAAGTCC GTTGCCTTAC CGCTTGGCTA	300
	TAGCCCAATA TATAGATGGT GGAAGGGGGC AGATCGAACT GCCGAACCCG AGGAGCGGAT	360
20	TTACAGTCCG CCGCGTTTAG CACTTCGCTA CCCTCCAGCT	400

## (2) INFORMATION FOR SEQ ID NO: 3937:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 609 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3937:

	GGTTTAACAC GCCTGCCTGT CACGCAGGAG ATCGCGGGT CGATTCCCTG TCGAGACCGC	60
35	CATTATTATT ACCATTACGG TTCAGTAGCT CAGTTGGTAG AGCAATGGAT TGAAGCTCCA	120
	TGTGTCGGCA GTTCGACTCT GTCCTGAACC ATTCTTAATT CATGGCGGTT GTGGTGAAgT	180
40	GGTTAACACA TCGGATTGTG GTTCCGACAT TCGAGGGTTC GATCCCCTTC AGCCGCCCCA	240
	TAATCGTTTA CATTAGCGGG TGTAGTTTAA TGGCAAAACC TCAGCCTTCC AAGCTGATGT	300
	TGTGGGTTTCG ATTCCCATCA CCCGCTCCAT TATTTTCTAT TATTCCACAG TAGCTCAGTG	360
45	GTAGAGCTAT CGGCTGTAA CCGATCGGTC GTAGGTTTCA GTCCTACCTG TGGAGCCATG	420
	GCTCyTTGGt CAAGCGGTTA AGACACCGCC CTTTCACGGC GGTAACACGG GTTCGAGTCC	480
	CGTAGaGTyC ATACAAGCAG AAGTGnAAAT ATCGCTTCTG TTTTTTTaTT ACATAwTTAA	540
50	TkGTTGgAGG aAGtTGtCG AgCyGGGCCG AAGGaGCACG CCTGGAAATG TGTAAGCGTT	600
	CACAAGCTT	609

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## (2) INFORMATION FOR SEQ ID NO: 3938:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3938:

10 TAAAGTTGTT CTCAGTTCGG ATTGTAGTCT GCAACTCGAC TACATGAAGC TGGAAATCGCT 60  
 AGTAATCGTA GTCAGCATGC TACGGTGAAT ACGTTCCCGG GTCTTGTAACA CACGCCCCGT 120  
 CACACCACGA GAGTTTGTA CACCCGAAGC CGGTGGAGTA ACCTTTTAGG AGCTAGCCGT 180  
 15 CGAAGTGGGA CAAATGATTG GGGTGAAGTC GTAACAAGGT AGCCGTATCG GAAGGTGCGG 240  
 CTGGATCACC TCCTTTCTAA GGATATATTC GGAACATCTT CTTCAGAAGA GCGGAATAAC 300  
 20 GTGACATATT GTATTCAGTT TTGAATGTTT GTTCATTCAA ATTAATGGGC CTATAGCTCA 360  
 GnGGTTAnAG CGCACCTGA TnAACGTGAA GTCGGTGGTT 400

## (2) INFORMATION FOR SEQ ID NO: 3939:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3939:

AGTTTTGAAT GTATAAATTA CATTCAATG TCTGGTGAAT ATAGCAAGGA GGTCCACCTG 60  
 35 TTCCCATGCC GAACACAGAA GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTT 120  
 CGCTAGAGTA GAACGTTGCC AGGCATAATA TTAATCCACA GTAGCTCAGT GGTAGAGCTA 180  
 TCGGCTGTTA ACCGATCGGT CGTAGGTTTC AGTCCTACCT GTGGAGCCAT GGCTCTTGGT 240  
 40 CAAGCGGTTA AGGACACCGC CCTTTCACGG CGGTAACACG GGTTCGAGTC CCGTAGAGTT 300  
 CATTATTTTG GAGAATTAGC TCAGTAGGGA GAGCATCTGC CTTACAAGCA GAGGGTCGGC 360  
 45 GGTTTCGAAC CCTnCATTTT CCACCATTG GTTATTAAAn 400

## (2) INFORMATION FOR SEQ ID NO: 3940:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

ACACAACAGC TGTTCACAAA ATGATTGGTA CAACTGCTGG TTATGTTGGT TATGATGACA 60  
 ATTCAAATAC GTTAACTGAA AAAGTACGCC GTAATCCATA CTCAGTCATT CTATTTGATG 120  
 5 AAATCGAAAA AGCAAATCCA CAAATTTTAA CATTGTTATT ACAAGTAATG GATGATGGTA 180  
 ATTTGACTGA TGGTCAAGGT AATGTCATCA ACTTTAAAAA TACAATTATT ATTTGTACAT 240  
 CAAATGCTGG CTTTGGCAAT GGCAATGACG CTGAAGAAAA AGATATTATG CACGAAATGA 300  
 10 AAAAAATTCTT CCGCCCTGAA TTCCTTAACC GCTTCAACGG CATCGTGAAT TnCTTACATT 360  
 TAGATAAGGT GCCnTGCAGG TATCGTCCAA CTATTATTAG 400

(2) INFORMATION FOR SEQ ID NO: 3941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3941:

ATACAATTTT AAATCTGTAT GTGTGAATCC AACACATGTT AAATATGCAG CAGAGCGnCT 60  
 AGCTGATTCA GAGGTGCTCG TTTGTACGGT AATAGGATTC CCATTAGGTG CGTCGACAAC 120  
 25 TGCAACGAAA GCATTTGAAA CAGAAGATGC AATTCAAAAT GGTGCAGATG AAATTGACAT 180  
 GGTCAATCAAC ATCGGCGCAT TAAAAGATGG ACGTTTTGAT GATGTACAAC AAGACATTGA 240  
 AGCAGTGGTT AAAGCTGCGA AAGGTCACAC AGTAAAAGTG ATTATTGAGA CGGTATTGTT 300  
 30 GGACCATGAC GAAATTGTAA AAGCGAGTGA TTAACAAAAG CGGCTGGTGC GGACTTCGTT 360  
 AAAAACTTCA GCAGGTTTTG CCAGTGGCnG TGCGACTGCA 400

(2) INFORMATION FOR SEQ ID NO: 3942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3942:

CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA 60  
 TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC 120  
 50 CATTTTTATA AGTCAAACGT TAACATGAAG TTACGTTCTT TTATAAAAAG ATTTAAACGC 180

TATTTAAAAC TCTTTATTCA CTCGGTTTGT CTTGGTAAAA TCTATATTTT ACTTACTnAT 300  
 CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA TCCGAACCCG CTGACCCnAC 360  
 5 CnGCGTGCAA AGCAGGCGCT CTACCCAGCT TGAGCTAAGG 400

## (2) INFORMATION FOR SEQ ID NO: 3943:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3943:

CGCTACACTA CGAGACCATT AGTAAAACGG AGGAAGAGGG ATTCTGAACCC CCGCGAGCCG 60  
 20 TTAAGCCCCCT GTCGGTTTTTC AAGACCGATC CCTTCAGCCG GACTTGGGTA TTCCTCCAAA 120  
 ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG GTTATGGAGC CGTTAGCTCT 180  
 25 GAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TGGCGGTGGA 240  
 GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC 300  
 CGCCTTATAT AGTTTGTAAT TnAnnATGGT GGGAGACTAG CGGGGTTCGA ACCGCTGGAC 360  
 30 CTCCTGCGTG CCAAAGCAGG CGGCTTCTAC CCAGCTGGAG 400

## (2) INFORMATION FOR SEQ ID NO: 3944:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3944:

CCAAAATTGC ACCTTGTCGT TTATTCGGAA AATCAATATn GnTAGGGGGT ATAAGATGCA 60  
 45 CCTACTTTAA CTGTCGCCAA CATCGCCGCA ATCATTTCAA AACTACGTTT TGTAACAAG 120  
 GCAACCCGTT GACCATTGCC CACACCATTT GATAGGAGCA TGTGCGCAAT GGCATCCACA 180  
 TAGTTGCGTA ATGTTTCATA CGTCATTGTC AAATCATTCA TGACTAGCGC AACATGATTA 240  
 50 CCTTGTCGTG AGAAACTTCA TTAAAGTAAC TTATGATAGA TTTATTTCCC GGGACATTAA 300  
 GCATTGATC GTTAACATGC GTATTGACCC AATTTAGAAG TTCCTCCGTG CCGTTTGGA 360  
 TATCACAAT TTGTAGTGTA wCtTGaTGCT TCmAAATATc AATCAn 406

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3945:

CAATGACAAC AGCAACTGAG ACAGTGTCAA ACGCTTAATA ATAATGATGT AGTGTGCAAT	60
AATACCGCAT TAAATGTACC AACTAAAACA AATGAAAATG GTTCAGGAGG ACATCTAACT	120
TTAAAGGAAA TTCAAGAAGA TGTTGTCAT TCTTCAAATA AACCAGAGCT AGTTGCAATT	180
GCTGGAACCA GCATCTGAAT AGACCGAAAA AGAGAAGTTA GACGTGCGGC ACCGGCAGAT	240
CCTGAATGCC AACTCCAGCA GATCCAGCGG CTGCAGCGGT TAGGAAACGG TGGTGACCA	300
GTTGCAATTA CAGCGCCATA TACGCCAACA ACTGATCCTA ATGCCATGAn GCCAGGACAA	360
ATGGCACCTA ACGAnGCTTG TTCATTTGAT GGACAnGGTA	400

(2) INFORMATION FOR SEQ ID NO: 3946:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3946:

CTCGCTGCGA TAAAGTACCA GTTCATAGCA ACGTTTGTnT TAATAGGnTC TGAAACGATA	60
CGTGTTGCCG GTTCTGTAAA TGAATAGACC AAAGCATCTT GCATACCAAC AACTATATTT	120
GCTGCAAATC CTCCAACAGC GGAAnATATG CCATCGTTAG TCCAGCGATA GGGTGATAGC	180
CAATTTTAAT AAAAAGCATT GCTGCAACGG CCGCAAGAT AATTGTCGCA GCATCGCCGG	240
CTGTACTACC TAAATACCA ATTAATATAA TAGTCGGTAA AATTAAGAAA CGTGGTGCGC	300
GATTCAACAAC AGAAATCATT AACTTATCGA AGTATCCTGT TTTCTCTGCA ACACCAATAC	360
CAATCATCAC TGCTAGGTAC TAAGCCTAAT GCTGGGnACT	400

(2) INFORMATION FOR SEQ ID NO: 3947:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3947:

5 GCCGGCCAGA GGACTTGGAA CCCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT 60  
 GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTTCG AACCGCCGAC 120  
 CCTCTGCTTG TAAGGCAGAT GCTCTCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT 180  
 10 GGCAACGTTT TACTCTAGCG GAANTAAATC GNACTACCAT CGACGCTAAG GAGCTTAACT 240  
 TCTGTGTTTCG GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 300  
 TAATTTATAC ATTCAAAAC AGATAGTAAG TAAAGTGAT TTTGCTTCG CAAAACATTT 360  
 15 A 361

## (2) INFORMATION FOR SEQ ID NO: 3948:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 382 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3948:

25 TTCCGTCAGA CCCTGACATG GTTCATGGGT TCATATTGCA TAGGACCGAA ATCTTCAAAC 60  
 30 ACTACGTGCT TTGGGCAGAC TTCGCAAAAA TACGGCCTCA ACAAAGGAAT TAAGCCTCGC 120  
 ATAAAGCGGA TTTCGAGTAC AGGGAACCGC TACCTCCCA CCTAGCACGG CAAGATATAT 180  
 ATTACTATAT TTTAATAGTT AATTGCAAGT ATAAATCATT TATATCATTG TTTACTTTAT 240  
 35 ACGACGTCTT GAGAAGTCAT TAATTTAAAT TCATTTGCAA GATGTTTTGA AATATTATAT 300  
 TGAAACGGCA TTGTATTTTC TAAATACACA TACTTCGAA CTGTTGCnGA ATAGGCCACC 360  
 GATACATCAC CAACAATTGG nA 382

## (2) INFORMATION FOR SEQ ID NO: 3949:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 45 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3949:

50 GCCAAGCCAT TTTCTTTGT GTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGA 60  
 GACCTTGCGG TCTCAATGCG GCTCATCGCA TCCATTTTTT GCCTGGCAAC GTTCTACTCT 120  
 55

TTGCTTCTTT CCTCTTCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG 240  
 CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACTTCG CCAAGCCATT TTTCTTTGTG 300  
 5 TTTGCTTTTT AnTTTGACGT TTTAGACATA AAAAAAGAG ACCTTGCGGn CTCAATGnGG 360  
 GCTCATCGCA TCCAATTTTT GGCCTGGCAA CGGTTCTACT 400

## (2) INFORMATION FOR SEQ ID NO: 3950:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3950:

20 ACTCGGTTTT GCTTGAAAA TCTATATTTA CTTACTTATC TAGTTTTCAA TGTACAATTT 60  
 CTTTTTAGTC AAGCGCTCGC ATACTGCTTT ATTTTCATAA GCAATATCAC TTTAACCAAA 120  
 AAATATTTGA ATGTTAAATA AACATTCAAA ACTGAATACA ATATGTCACG TTATTCCGCA 180  
 25 TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG CCGCACCTTC 240  
 CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCACCTTC GACGGCTAGC 300  
 TCCTAAAAGG nTACnCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT GACGGGCGGT 360  
 30 GTGTACAAGA CCCGGGAACG nATTACCCG 389

## (2) INFORMATION FOR SEQ ID NO: 3951:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3951:

45 AAAGCTCGAC TTGTTTACGA TGTGAAAAA CAAGATTATG TACCTGTATC GCAACCACAA 60  
 TTACCAATTT TAAATGAATT TAATAAGAC TTAGTGATA ACCTTGATAC CATATTCAAT 120  
 GCGCAAGACG AnCGGGACTA TTTTATGGG AGACATTACG TAATAATTTC TATTACTCTG 180  
 50 CTATCAATGT ACCTAAAGCT ACCGATGATT TCCGAGACAT AGACCGTGCG CTTGTCTGGG 240  
 GGTTCAACTG GAAACTTGGT CCATTCCAAT TATGGGATGC AATGGGATAC GAACGTGTTA 300  
 AAACAnTGAT GGGAAGACGA ACTTGGGAGA CTTACCACAA TGGGATTAGT GAnTTAGATG 360

## (2) INFORMATION FOR SEQ ID NO: 3952:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3952:

CAAAGGGCAG CGAAACCGCG AGTCCAGAGC AAATCCCATA AAGTTGTTCT CAGTTCGGAT	60
TGTAGTCTGC AACTCGACTA CATGAAGCTG GAATCGCTAG TAATCGTAGA TCAGCATGCT	120
ACGGTGAATA CGTTCCCGGG TCTTGACAC ACCGCCCGTC ACACCACGAG AGTTTGTAAC	180
ACCCGAAGCC GGTGGAGTAA CCTTTTAGGA GCTAGCCGTC GAAGTGGGAC AAATGATTGG	240
GGTGAAGTCG TAACAAGGTA GCCGTATCGG AAGGTGCGGC TGGGATCACC TCCTTTCTGA	300
AGGATATATT CGGGAACATC TTCTTCAGAA GAGCGGGAAT AACGTGACAT ATTGTATTCA	360
GnTTTGGAAT GTTTnnTTAA CATTnCAAAA AAATGGGGCC	400

## (2) INFORMATION FOR SEQ ID NO: 3953:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3953:

TGATTTTGAC GTTTTAGACA TAAAAAAG AGACCTTGCG GTCTCAAATG CGGCTCATCG	60
CATCCATTTT TGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAATTGGCT ACCATCGACG	120
CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTTCTT CGGCTCTCGC	180
TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG	240
TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTGCTTTT TATTTTGACG TTTTAGACAT	300
AAAAAAAGA GACCTTGCGG TCTCAATGCG GGCTCATCGC ATCCATTTT TGCCTGGCAA	360
CGTTCTACTC nAGCGGGAAG TGAAGnCGGA CTGACCAAGC	400

## (2) INFORMATION FOR SEQ ID NO: 3954:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3954:

AAACTACATA ATGAAAATGC CGTTTTAATC GGTAAATTAA ATATGGATGA GTTTGCAATG 60  
 5 GGTGGTTCAA CAGAAACATC TTATTTCAAA AAAACAGTTA ACCCATTGA CCATAAAGCA 120  
 GTGCCAGGTG GTTCATCAGG TGGATCTGCA GCAGCAGTTG CAGCTGGCTT AGTACCATTT 180  
 AGCTTAGGTT CAGACACAGG TGGTTCAATT AGACAACCGG CTGCATATTG TGGCGTTGTC 240  
 10 GGTATGAAAC CAACATACGG TCGTGTATCT CGATTGGAT TAGTGCTTTG CATCTTCATA 300  
 GACCAAATTG GGCCATGACT CGAATGTAAA GTAATGCCAT CGTATTAGAA GCTATTCTGG 360  
 15 TGCAGATGnT AATGACTCTA CCAGTGCACC AGTGATGAGG 400

## (2) INFORMATION FOR SEQ ID NO: 3955:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3955:

TCGATTGGCA TTTCTCCGCT ACCCTCAGTT CATCCGCTCA CTTTTCAACG TAATCGGTTC 60  
 GGTCCTCCAT TCAGTGTTAC CTGAACTTCA ACCTGACCAA GGGTAGATCA CCTGGTTTCG 120  
 30 GGTCTACGAC AAATACTAAA CGCCCTATTC AGACTCGCTT TCGCTACGGC TCCACATTTA 180  
 CTGCTTAACC TTGCATCAAA TCGTAACTCG CCGGTTTATT CTACAAAAGG CACGCCATCA 240  
 35 CCCATTAACG GGCTCTGACT ACTTGTAAGC ACACGGTTTC AGGTTCTATT TCACTCCCCT 300  
 TCCGGGGGTG CTTTTCACTT TTTCTTCAA GGTATGGGTT CACTATCGGT nACTAGAGAG 360  
 TAATTAGCTT AGGnGATGGT CCTCCCAGAT TCGGAAGGGA 400

## (2) INFORMATION FOR SEQ ID NO: 3956:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3956:

GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG AACCGGTAGT 60

ATAAAAATGG AGCAGAAGAC GGGATTGGA CCCGCGACCC CAACCTTGGC AAGGTTGTAT 180  
 TCTACCGCTG AACTACTTCT GCATATGCGG GTGAAGGGAG TCGAACCCCC ACGCCGTAAG 240  
 5 CTTAGGATCC TAAGTCTAGT GCGTCTGCCA ATTCCGCCAC ACCCGCAAAT GGTGAGCCAT 300  
 AGAGGATTCG AACCTCTGGA CCCTCTGGAT TAAAAGTCAG ATGCTCTACC AACTGGAGCT 360  
 10 AATGGCTCTT TCCATGGTGC CGGGCCAGAG GACTTTGAAN 400

## (2) INFORMATION FOR SEQ ID NO: 3957:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3957:

CAGACATGTG TTATACGGGA AATTGGGCGA ACCGCAACTA TTATACATTG ATTTACACCT 60  
 TATACATGAA GTTACTTCTC CTCAAGCATT TGAAGGACTT AGGCTTCAAA ACAGAAAATT 120  
 25 AAGACGCCCA GATTTAACAT TTGCAACACT CGATCACAAT GTTCCTACTA TTGATATATT 180  
 CAATATTAAA GATGAAATTG CAAACAAACA AATCACAACA TTACAAAAAA ACGCCATAGA 240  
 TTTTGGGGTG CATATTTTGG ATATGGGTTT TGATGAACAA GGTATTGTTC ACATGGTAGG 300  
 30 ACCTGAGACA GGACTTACAC AGCCTGGCnA GACCATCCGT nTGTGGGTGA CTCTCACACA 360  
 GCCACACATG GnGCCTTTT 379

## (2) INFORMATION FOR SEQ ID NO: 3958:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3958:

TGTTAAATA CGGTACATCT AAATTAATGT TAACTGATTT TCAAAAAGAG AATTAAATAA 60  
 ATATATTCAA GGTCAGAAAC AACGCGTGAT ATTTGAAAT GGCCATTTTG TCTAATTGAT 120  
 50 AGTGAATATA ATTAGAGTAA GAGGCTGGGA CATAAATCCC TAAAAACAG CAGTAAGATA 180  
 ATTTTCAATT AGAAAATATC TTAAGTCTGT TCTCTATTTA TACAATACTT CGTATTGAAT 240  
 GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT GCTCCCTCAG 300

AATAAGACAT TTGnCCAAC TGA CACTACC ATTAAAAACT

400

## (2) INFORMATION FOR SEQ ID NO: 3959:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3959:

GAGCCGCAGT GGAATGAGGC CCAAGCGACT GTTTATCAAA AACACAGGTC TCTGCTAAAC 60  
 CGTAAGGATG TGTTATAGGG GCTGACGGCT GCCCGGTGCT GGAAGGTTAA GAGGAGTGGT 120  
 TAGCTTCTGC GACGTACrGA ATCGAAGCCC CAGTAAACGG CGGCCGTAAC TATAACGGTC 180  
 CTAAGGTAGC GAAATTCCTT GTCGGGTAAG TTCCGACCCG CACGAAAGGC GTAACGATTT 240  
 GGGCACTGTC TCAACGAGAG ACTCGGTGAA AATCATAGTA CCTGTGAAGA TGCAGGTTAC 300  
 CCGCGTACAG GACGGAAAGn CCCCTGGAGC TTTACTGTAG CCTGATATTG AAATnCGGCA 360  
 CAGTTTGTAC AGGATAGGTT AGGAGCCTTG GAAACGTGTG 400

## (2) INFORMATION FOR SEQ ID NO: 3960:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3960:

TGGTCCCAAA CCAAGTGCTC TACCAAGCTG AGCTACTTCC CGTATAATTA ACGCGCCCGA 60  
 TAGGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG 120  
 GGCGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTGAnTnC 180  
 ACTCACCGCA GATTTTAAGT CCTGTGCGTC TGCCAGTTCC GCCACCCCGG CACTATAAAA 240  
 ATGGAGCAGA AGACGGGATT CGAACCCGCG ACCCCAACCT TGGCAAGTTG TTATTCTTAC 300  
 CGCTGGAAC TTTCTGGCA TATGCGGGTT GAAGGGGAGT CGAACCCCA CGCCGTAGGC 360  
 TTAAGATTCC TGAAGTCTAG TGCCTCTGGC CAATTTCCGG 400

## (2) INFORMATION FOR SEQ ID NO: 3961:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3961:

	TTTGTATACA TAATCTAAAT TTCTCAAAGC GCCAATAACA GAGGACCATC TCCTAAGGCT	60
10	AAATACTCTC TAGTGACCGA TAGTGAACCA GTACCGTGAG GGAAAGGTGA AAAGCACCCC	120
	GGAAGGGAGT GAAATAGAAC CTGAAACCGT GTGCTTACAA GTAGTCAGAG CCCGTTAATG	180
	GGTGATGGCG TGCCTTTTGT AGAATGAACC GGCGAGTTAC GATTTGATGC AAGGTTAAGC	240
15	AGTAAATGTG GAGCCGTAGC GAAAGCGAGG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA	300
	GACCGGAAAC CAGGTGATCT ACCCTTGGTC AGGTTGAAGT TCAGGTAACA CTGAATGGAG	360
20	GACCGAACCG ACTTACGTTG AAAAGTGAGC GGATGAACTG	400

(2) INFORMATION FOR SEQ ID NO: 3962:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 361 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3962:

	TAATAATTAC AGTATATCGG GAAGACAGGA TTCCAACCTn CGACCCCTTG GTCCCAAACC	60
	AAGTGCTCTA CCAAGCTGAG CTAATTCCCG TATAnTTAAC GCGCCCGATA GGAGTCGAAC	120
35	CCATAACCTC TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTG	180
	TTTATTGAAA ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA	240
40	TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAnAAAT GGATCAGAAG	300
	ACGGGATTCTG AACCCGCGAC CCAACCTTG GCAAGGTTGT ATTCTACCGC TGAACACTT	360
	C	361

45

(2) INFORMATION FOR SEQ ID NO: 3963:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 375 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3963:

AAGTGTCTTA TTTTTTTAAA GTATTTCAAA GTAAAATTAC ATGTTAATAC GTAGATTAAT 120  
 GCGGAGACTC CTGAGGGAGC AGTGCCAGTC GAAGCCGTAG GCTGAGACGG CACCCTAGGA 180  
 5 AAGCGAACCA TTCAATACGA AGAThThATh AAATAGAGAA CAGCAGTAAG ATATTTTCTA 240  
 ATTGAAAATT ATCTTACTGC TGTTTTTTAG GGATTTATGT CCCAGCCTCT TACTCTAATT 300  
 ATATTCATA TCAATTAGAC AAAATGGCCA TTTTCAAATA TCACGCGTTG GTTTCTGACC 360  
 10 TTGGAATATA TTTAT 375

## (2) INFORMATION FOR SEQ ID NO: 3964:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3964:

AAAATGGCCT TGATAGACTT GCTCAATGCA GGGTTGCCAC AAACCAATGA TGCACTTACA 60  
 25 ATTTTAAATA GATTTTAAAG ACCTTGTTGG TTTGTACAA TTAATGTGAC ATGACTAGGT 120  
 CTGCACGTT TATATGCATC TTCATTACTG AGTTTTTTGT TGATTTTCGTT ATGATTTAAT 180  
 30 ACGCCTAATT CTTTCATTTG TTGAACCATT TTTATGAAAA TGTAAGCTGT TGCTTCTGTA 240  
 TCATAAATGG CACGGTGATG TTGCGTTAAT TCTACGCCAT ATTTTTTTAGC CAAGAAATTC 300  
 AAACCATGTT TACCATATTC AGTATTAATC GTACGAGGAT AATTCTAAAG TATCGATAAC 360  
 35 ACCATTCGTT GGATGGTCCA AACCCAAGAC GTTCATATCC 400

## (2) INFORMATION FOR SEQ ID NO: 3965:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3965:

ACTTTTAATT TTGTCATGAT GTGCCTCCTT ACCGTATGAT GTTATTCAA GTAAATTGCT 60  
 50 TTGCCTGATT TTGCAGACTG ATAAATCGCT TCAAGAATTT TTGTAAC TAC CATGCTTGT 120  
 TCCGGTTTCA CAACTGGTTC AGTATCATTT ACAACTGCAT CAATCCAAGC TTTTGCTTCT 180  
 55 TCTTCAGCTT CATCCACTTC ATTACCTTCA TAAAAGTCGA CGCCTTTGTT TTCCAATTCA 240

TCAGCACCTG CTTTAGGTTT CTGATAATGA ACATTTTGGC CTCATCCACT TCTAAAnGAA 360  
TTAATCGCCC AAGnGGGATT CCAAAAAGGA n 391

(2) INFORMATION FOR SEQ ID NO: 3966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3966:

CGCTATCAGG TATTGTTTCA ACAATTTTCAT TAACATATCG TGAAATATCA TTTGAGGGA 60  
TTCTAACAGA AGTTTCTATT GGTAGTGTAG TTGGGGCATG TTATAATTTT TATACATAAG 120  
GCACCTCGTT AATTTAGTTT AGTGGTATTT ATTAAATTAT AAGAAGGGAC CCAACACAGA 180  
AAATTCATTT TATTGAATTT TACATTTATG TGCAAGTTGG GCAAAGTGTC TTATTTTTTA 240  
AAAGTATTTT AAAGTAAAT TACATGTTAA TACGTATaTa ATGGcGAGAC TCCTGAGGGA 300  
GCAGTGCCAG TCGAAGcCAA GGCTGAGACG GCACCCtAGG AAAGCGAcnC ATTcAATACG 360  
AAGATTGTAT AAATAGAGAA CAGCAGTAAG ATATTTTC 398

(2) INFORMATION FOR SEQ ID NO: 3967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3967:

GCTATAGAAA AAATAAAATC ACAAGTTACG ATTAGCGTAC TTGATGGGGA GTGAAAATAA 60  
TGAGAGTAAC AGAGTTATTA ACAAAGATA CAATAGCAAT GGATTTAATG GCAAATGACA 120  
AAAATGGTGT TATTGATGAG TTAGTAAATC AATTAGACAA AGCAGGTAAA TTAAGTGATG 180  
TCGCGTCATT TAAGGAAGCG ATTCACAATC GAGAATCACA AAGTACAAC TGTATCGGCG 240  
AGGTATTGCC ATTCCACATG CCAAAGTGGC CGCAGTTGAA GTCACCAGCT ATTGCGTTTG 300  
GTAAATCTAA AGCAGGCGTG GATTATCAAn TTTGGnTATG CAACCAGCAC ACTTnTTCTT 360  
TGTGGTTGGC AGCG 374

(2) INFORMATION FOR SEQ ID NO: 3968:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3968:

```

10  ACCCCGGCAC TATAAAATG GAGCAGAAGA CGGGATTGGA ACCCGCGACC CCAACCTTGG      60
    CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA GTCGAACCCC      120
    CACGCCGTAA nCTGAGGATC CTAAGTCTAG TGGCTCTGCC AATTCGCGCA CACCCGCAAA      180
15  TGGTGAGCCA TAGAGGATTC GAACCTCTGG ACCCTCTGAT TAAAAGTCAG ATGCTCTACC      240
    AACTGAGCTG AATGGCTCTT CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTGACT      300
    GGATTACAAG TCAGTTGCTC TACCAATTGA GCTAAGGCCG GGCAATATGT AAGAATAAAT      360
20  GGTGGAGAAT GACGGGTTTC GAAnCGCCGA CCCTCTGCTT      400
  
```

## (2) INFORMATION FOR SEQ ID NO: 3969:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3969:

```

35  GCGAGTTGGG GTGTGGGCCC CAACATAGAG AAATTGGATT CCAATTTCT ACAGACAATG      60
    CAAGTTGGCG GGGCCCCAAC ACAGAAGCTG ACGAAAAGTC ATTAnCAATA ATGTGCAAGT      120
    TGGCGGGGCC CCAACACAGA AGCTGACGAA AAGTCATTAn CAATAATGTG CAAGTTGGCG      180
40  GGGCCCCAAC ACAGAAGCTG GCGGAAAGTC AGCTTACAAT AATGTGCAAG TTGGGGTGGG      240
    ACAACGATAA AGTAATACTT TTTCTATAGA AATTAGTATT TCTTATGCAT GAGTTTACT      300
    CATGTATTCC TATTTTAAAG TACACATTAG CTGTGGCTAA TGTTTAAGAC CCACTACATA      360
45  ATAAATCATT AGTGGCTCTn TATCATTTCT GTCCCACTCC      400
  
```

## (2) INFORMATION FOR SEQ ID NO: 3970:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 419 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GATAAGATCA GCCGAAAATG GATGGTGTGA AGAGCGTTAC TTGGTTTGGC GGTATGCTTA 60  
 TTTTAAATGG CATTGTGTAC GACACCATTa CAGTTTGTAC TTGTGAGGTT ATTGCAGGGA 120  
 CTATTTGGTG GTGTTGTTGA TGCATCAAGT GCGTTTCCGA GTGCAGAGGC GCCACTGAKa 180  
 GATCGTGGAA AGtATTAGGA gACTGCAAAT TCAGTCAGCG CAGGtCTCTT GTGGGGCCAT 240  
 TAATTGGCGG TGTTACAGCT TCGATATTAG GTTTTAGTGC GTTACTGATG AGTATTGCCG 300  
 TTATTACTTT TATTGTCTGT ATTTTCGGTG CATTAAAATg ATTGAAACGA CACATATGCC 360  
 AAaATCACAA ACACCAAATA TTAATAAAGG TnTTCGCCGT TCCAnTTnCA ATGTCTAAT 419

(2) INFORMATION FOR SEQ ID NO: 3971:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 381 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3971:

AAACTTGGGA GACTTCAATA ACAGATTTAG GTTTATCTAA AAATCAGGCA TATAATTTCT 60  
 TAATTACATC TAGTCAAAGA TGGGGCCTTA ATCAAGGGAT AAATGCAAAT GGCTGGATGA 120  
 GAACTGACTT GAAAGGTTCA GAGTTTACTT TTACACCAGA AGCGCCAAA ACAATAACAG 180  
 AATTAGAAAA AAAAGTTGAA GAGATTCCAT TCAAGAAAGA ACGTAAATTT AATCCGGATT 240  
 TAGCACCAGG GACAGAAAAA GTAACAAGAG AAGGACAAAA AGGTGAGAAG ACAATAACGA 300  
 CACCAACACT AAAAAATCCA TTAAGTGGAG TAATTATTAG TAAAGGTGAA CCnnAAGGAG 360  
 GGGTTTCCAn AGTCCGTTAT G 381

(2) INFORMATION FOR SEQ ID NO: 3972:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3972:

GGGTTTCAGAA CGTCGTGAGA CAGTTCGGTC CCTATCCGTC GTGGGCGTAG GAAATTTGAG 60  
 AGGAGCTGTC CTTAGTACGA GAGGACCGGG ATGGACATAC CTCTGGTGTA CCAGTTGTCG 120  
 TGCCAACGGC ATAGCTGGGT AGCTATGTGT GGACGGGATA AGTGCTGAAA GCATCTAAGC 180

GAnGTTAATA GGTTTCGAGGT GGAAGCATGG TGACATGTGG AGCTGACGAA TACTAATCGn 300  
 TCGAnGACTT AATCAAAATA AATGTTTTGC GACCAAATCA CTTTACTTAC TATCTAGTTT 360  
 5 GAATGATAAA TACATCATAT GCTGGnGCCA TACCAAGGGG 400

## (2) INFORMATION FOR SEQ ID NO: 3973:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3973:

TCTTTTAATT ACGTAATGGC TTACCAGTTT TTAACATATG TGCAATTCTT TCATATGATT 60  
 20 TTTTAGATTT TAGTAAGTCA ATAAAGCCAA TTTTCTCCAA CGATTGAATG TAACGTTGAT 120  
 TGATAAATGT ATTTCTTGGT AAATCACCAC CCGCTAAAAT TGTGGCGATA TTTAAGGCAA 180  
 25 TATGATAATC ATGGTCGCTA ATAAATGAC CCCGTCTTTG CGCATCTAAT TGTCCTTGGA 240  
 TCAATGCTTT GAAGTCTTCA CCTAAAGCGA TATATTGATG TCTAGGATTC GGAATATAGT 300  
 TTGTTTCTGC TTCATATTTT GCACGTGTGA GCGCAACTTC GACACGnTGG TGCCTGGATT 360  
 30 nGAAAATAAA CCGGAnCCnG GGATCCACGG GAAATAACCC 400

## (2) INFORMATION FOR SEQ ID NO: 3974:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3974:

TGCCATGTTT ACCTTGTTTA AAATCAAGGT TTGTAATGTT TCCTTGTGTC ACGATAATAG 60  
 45 GCGTAATATC ACTCTTTGCA TGATTGCGGA TGTAGTCTAA ATCAAAGTTG ATTAATAAAT 120  
 CACCTTGTTT AACTTCTTGA CCTTCCTCAA CATGTAAAGT AAAGCCTTCT CCGTTTAATT 180  
 TAACAGTGTC TAAACCGATG TGGATTAATA GTTCTAAACC ACTATCTGAA TACAAGACCA 240  
 50 ATTGCATGTT TTGTTGGGAA AATCATTTGT TACTTTACCG TTGAAATGGT GCACGAAACT 300  
 TCACCTTGTG AnGTTTTTGG ATAGCGATAC CGTCACCCCA TCCATTTTTT TTCGCTGAAA 360  
 55 CACTTGGATC AnGGCACTTC TGAATAAATG GTGGTTAACT 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 372 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: lin ar

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3975:

CCTTTGCAGC GCCTCCGTTA CTTTTTAGGA GCGACCGCC CCAGTCAAAC TGCCCGCCTG 60  
 ACACTGTCTC CCACCACGAT AAGnCGGGn GTTTAGAAAG CCAACACAGC TAGGGTAGTA 120  
 TCCCACCAGC GCCTCCACGT AAGCTAGCGC TCACGTTTCA AAGGCTCCTA CCTATCCTGT 180  
 ACAAGCTGTG CCGAATTTCA ATATCAGGCT ACAGTAAAGC TCCACGGGGT CTTTCCGTCC 240  
 TGTCGCGGGT AACCTGCATC TTCACAGGTA CTATGATTTC ACCGAGTCTC TCGTTGAGAC 300  
 AGTGCCCAA TCGTTAACGC CTTTCGTGCG GGTCGGAAC TACCCGACAA GGATTTTCGC 360  
 TAACTTAGGA CC 372

## (2) INFORMATION FOR SEQ ID NO: 3976:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 395 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3976:

AGGGAATCGA ATTTCTTTC TCTTCCTnCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT 60  
 GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC 120  
 CCCATTCGGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTIA 180  
 GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AAATAACTTA 240  
 ATCTATGTTT CCACCATTTT TATAAGTCAA ACGCTCACAT ACGGCTTCGT TTTCATTATT 300  
 TTAAAGCTCA TTTACATAAG TAAACTCTGC TTAAATGAT TTAACTCATT GTCTGCTAAA 360  
 ACGGTTTnTT TTATGAAAAG GTTTGAAACG GGTn 395

## (2) INFORMATION FOR SEQ ID NO: 3977:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3977:

TTGGTCCCAA ACCAAGTGCT CTACCAAGCT GAGCTACTTC CCGTATAATT AACGCGCCCCG 60  
 ATAGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG 120  
 GCGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTnnTTCA 180  
 CTCACGCAGA TTTTAAGTCC TGTGCGTCTG CCAGTTCGCG CACCCCGGCA CTATAAAAAT 240  
 GGAGCAGAAG ACGGGATTG AAGCCGCGAC CCCAACCTTG GCAAGTTGTT ATTCTACCGC 300  
 TGAAGTACTT CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA GGCTTAGATC 360  
 CTTAAGTCTA AGTGCGTCTG GCCAATTTCC GCCAnACCCG 400

## (2) INFORMATION FOR SEQ ID NO: 3978:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3978:

AAGTGTTAA ATATTATAGA AACATCAAA GGATGTTAAG AAATACAATT TATTACCCAG 60  
 CATTTAATAA TGGTGCTATA GAAGGAATTA ATAATAAGAT AAAATTAATC AAGTGAATTT 120  
 CTTTGGTTA CAGAAATTC AACAACTTTA AAGCACGTAT AATGATGATT TTCAGCTTGT 180  
 ACAAAGGAGA AAAAAAGAAG ACAACCAAGC CCAATAATGG ACTGGCCGCC TAATAATAAA 240  
 AGCTCTAAAA GTTGTATTTT AAAAATAGTT CTTTAAATTA TATACCCACC ACATTTGGTG 300  
 GAGGAACCTA AAAAAAGCA CTTCCCAAAA ATGGGAAAGT GCAGTnAGTG GAGCCATAGA 360  
 GGATTCCGAA CCTCGGACCC TCnGAnT 387

## (2) INFORMATION FOR SEQ ID NO: 3979:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3979:

TGGAGCAGAA GACGGGATTC GAACCCGCGA CCCCAACCTT GGCAAGGTTG TATTCTACCG 60  
 CTGAACTACT TCTGCATATG CGGGTGAAGG GAGTCGAACC CCCACGCCGT AAnTTAGCAT 120

CGAACCTCTG GACCCCTCTGA TTAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTT 240  
 CCATGGTGCC GGCCAGAGGA CTGAACCCC CAACCTACTG ATTACAAGTT CAGTTGCTCT 300  
 5 ACCAATTGAG CTAGGCCGGn CAATATGTAA GAATAAATGG TGGAGAATGA CGGGTTTCGA 360  
 ACCGCCGAAC CCTCTGCTTG TnAAGGGCAG ATGGCTCnTC 400

(2) INFORMATION FOR SEQ ID NO: 3980:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3980:

20 TTACCACGTA TTTAGGTTTC TTGGTGGCT CTAGATTTGT CCCTATTGTC ACAGCATTTG 60  
 CCGCAATCTT TTTAGGTGTA TTGATGTTTT TCATTGGGCC AAGCATACAA GCCGGCATT 120  
 ATCATGTTGG TGGATTTGTA ACGAAAACAG GTGCCATCGG TACTTTTGTT TATGGCTTCA 180  
 25 TCTTAAGATT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TACTTACCG TTTTGGCAGA 240  
 CGGCACTTGG TGGTACTTTA GAACTCAAAG GGCACITAGT TCAAGGTACG CAGAACATCT 300  
 TCTTTGCTCA ACTTGGTGAT CCAGATGTGA CGAnTATTAT TCCAGGTGTG TCACGCTTTA 360  
 30 nGTCAGCCGT TTTAATACGA GGATGTTCCG CTAnGTGGTG 400

(2) INFORMATION FOR SEQ ID NO: 3981:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3981:

45 CGACATACGC TGATAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTTACAC 60  
 GTCGCAATAA TACGAGTCCA TGGGTGAAAG AAGCATCTGC AGCAACTGTA GCAGGTATTG 120  
 CTGGAATAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GATACAATTC 180  
 50 AAGTTGTTGC AACGCAAGGG AAGCGGAGAG ACAGTGTAGT GGATGGAGCA ACGTATAGTT 240  
 GGATTTTACA GTTGTCGCAC CACAACCGAA CCAAGCGACT GACTGAAGAT TTGGCAAAT 300  
 GGnCATATTG ATATCACGCC TAATGAnTCC ATTcAGGACA TTTAATTAAT CCAACTCAAG 360

## (2) INFORMATION FOR SEQ ID NO: 3982:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3982:

```

TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTATAG ATCCATTCAA      60
TAATGTTCAT ACAATTTCTG GACAAGGTAC GCTTGCTAAA GAAATGCTAG AACAGCAAA      120
GTCTGACAAT GTTAACTTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTTC      180
AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG AAAATTATAG GTGTTGAACC      240
TTCAGTGCAA GTAGTATGTA TGAATCTGTT GTGGTAAATA ATCAGGTAGT CACATTGCCT      300
AATATCGATA AATTTGTGGG ACGGTGCATC TGTAGCTAGA GTTGCGGATA TTACATTGGA      360
AATTGCCAAA GAAAAGTAGA GGATTACGTT CCAGTAGAGn      400

```

## (2) INFORMATION FOR SEQ ID NO: 3983:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3983:

```

CCACCATTAT TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT TTACCAAGCA      60
AAACCGAGTG AATAAAGAGT TTAAATAAG CTTGAATTCA TAAGAAATAA TCGCTAGTGT      120
TCGAAAGACG CGACAAGATT AATAACGCGT TTAAATCTTT TTATAAAAGA AAACGTTTAG      180
CAGACAATGA GTTAAATTAT TTAAAGCAG AGTTTACTTA TGTAATGAG CATTTAAAT      240
AATGAAAACG AGGCCGTATG TGGAGCGTTT GACTTATnAA AAATGGTGGG AAACATAGAT      300
TCAAGTTATT GAAGGGCGCA CGGTGGGATG CCTTGGGCAC TAGnAAGCCG nTGGAAGGAC      360
GTTACTAACG ACGATATGCC TTGGGGGAGC      390

```

## (2) INFORMATION FOR SEQ ID NO: 3984:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3984:

5 GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTTGC CTTGTATCTG CAAATGTTTT 60  
 GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTTGACC ACAAATTCAA ATGTATCAGG 120  
 10 CGTTTCTTTT ATCCATTTCA ATATATTTCT TTCCGGTTGT ATCGCATAGT ATGTCGCATC 180  
 TAATTCGACA ACCGGAAAAT GTCCAGCATA TGTTTTAAGT TTATCGGTTT GCGGTTCTAA 240  
 ATCTTCATAT AATGAATAGT GATCACCCCA ACCTGTTAAT CCGATGTTTT ATCATATATA 300  
 15 TCACCAATGT CATCATACCA TATAACTTTT ATCATnATCA TTTCAGCGAA CTTTAGGTTT 360  
 GnAGGTTTTT TGGCCTGGAT TAAAnATCTT TCGGGCGGAT 400

## (2) INFORMATION FOR SEQ ID NO: 3985:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3985:

30 GCATTTGCTT ATATCTTTAA AAAAGATTTT GAAGATATTG AAAGAAAAAC TAAAGAAATT 60  
 ATTTCTGATA TTGAAAGTAA AAATAACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT 120  
 AAAAAACAGC AGTAAGATAA TTTCAATTA GAAAATATCT TACTGCTGTT CTCTATTTAT 180  
 35 ACAATACTTC GTATTGAAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTTGGTCTTC 240  
 GACTGGCACT GCTCCCTCAG GAGTCTCGCC ATTGAATACT ACGTATTAAC ATGTnAATTT 300  
 TACTTTGGAA ATACTTTTAA AAAATAAGAC ACTTTGCCCA ACTTGGCACA TAAATGTTAA 360  
 40 AATnCAATGA AATGAATTTT CTGTGTTGGG TCCCCTnCTA 400

## (2) INFORMATION FOR SEQ ID NO: 3986:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3986:

55 TTCGTTCAAA GTCATCTAGG TCACATTATT CTATTTGGGA TTCTTAGTGC TGTTCATT 60

ATGACAATAC AAAACGTAAA AAAGTCGCAG TGATCGGTAG TATTTTAGTA TTTATCATT 180  
 GTATTCCAGC AACCTTATCT TTTGGTATCT TAAAAGATGT AAGATTCCGT GCGGGAACGA 240  
 5 TTTTGGATAA TATGGATTTC ATCGTTTCGA ATGTATTGAT GCCATTAGGC GCATTAGGTA 300  
 CTACGCTTGT CGTAGGnCAA TTATTAGnTA AAAAATTATT ACAnCAATAT TTTGGTAAAG 360  
 AnCGATTTAG GATTATTCAG TGGTTGGTAT TACTTAATTA 400

## (2) INFORMATION FOR SEQ ID NO: 3987:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3987:

GGATTCGAAC CCCC GCGAGC CGTTAAGCCC CTGTCGGTTT TCAAGACCGA TCCCTTCAGC 60  
 CGGACTTGGG TATTCCTCCA AAATTATATG GACCTTGCAG GACTCGAACC TGCGACCGAA 120  
 25 CGGTTATGAG CCGTTAGCTC TAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC 180  
 TAATAAATAG TGGCGGTGGA GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC 240  
 TCTAGCCAGC TGAGCTACAC CGCCTTATAT AGTTTGTAAA TAATATGGTG GGGACTAnCG 300  
 GGATCGGAAC CGCTGGACCT CCTGCGTGGC AAAGCAGGCC GCTCTCCCAG CTGGAGCTAA 360  
 GnCCCCCATA ATAATnACAG TATATChGGG AAGACAGGAT 400

## (2) INFORMATION FOR SEQ ID NO: 3988:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3988:

CAGCTGATAA ACAAGTTGAT CTGGTCCCGA TTTGTTGGGT AAACGGTTGA TTAATGnAAA 60  
 ATGTTGCGCG AAGGATTCAT AATCCGAGAG GTCTAATTCA ACGTATCATT AATCAAGATG 120  
 50 CGCCTATTTA TCAATCTGAA ACAAATTATC ATTCGAAAGA TCGCGGTAAG TCTAAAAATG 180  
 GTATTCAAAT GGTGTATCAA CATTTAATGA ACGGTGTATC GTTTATGGnT CCTTTTATCG 240  
 TAGTTGGTGG ACTCCTTATC GCCATCGCGC TGA CTCTAG GCGGTGAACG ACCATCCAAA 300

CCTTTAAATT AATGGTCCCA TACCAGnCGG GATAAACGCT

400

## (2) INFORMATION FOR SEQ ID NO: 3989:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3989:

15	CCAGAGATTT CCGAATGGGG GAAACCCAGC CATGAGTTAT GTCATGTTAT CGATATGTGA	60
	ATACATAGCA TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC CCGGAGAAGA	120
	GAAAGAAAAT TCGATTCCCT TAGTAGCGGC GAGCAAACGG GAAGAGCCCA AACCAACAAG	180
20	CTTGCTTnGn GGTnTG TAGG ACACTCTATA CGGATTACAA AGGACGACAT TAGACGAATC	240
	ATCTGGAAAG ATGAATCAAA GAAGGTAATA ATCCTGTAGT CGAAAATGTT GTCTCTCTTG	300
	AGTGGATCCT GAGTACGACG GAGCACGTGG AAATTCCGTC GGAATCTGGG AGGACCATCT	360
25	CCT	363

## (2) INFORMATION FOR SEQ ID NO: 3990:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3990:

40	TTTCCAAGAA CATGAGCCTG TACAGTTAAC ACCATGTnTG nTTCTTACTT CTTTATCGTG	60
	GCTCCAACGT TCTCTGTACA TTTTTCCTCA TTCTCTACTT TTACTTTCTA GGATCGACCA	120
	ATTCCCATTA AATTTTCTG TTGGCTTAAA GAAATTC AAT CCAAATTTTC CCATATTTAT	180
45	ATCCTCCTAC GTATAAAAAT ACGATGTGTA GATGTCGTGT TTTTAAATAC TTTAAATGC	240
	CCAAGACTAT TGCTTTAATT AGATTGTACA TTTTTCACA AACATAAAAT ATTAGGGAAT	300
	CACCTAATTA CTTAAGGnAT TCCCTATCAA TAACGGGATT TCATTGAAAT AATACACAAT	360
50	CAGTAnGGTC AGCCTAATGC CAGGCTAAAT CGTTCAAATT	400

## (2) INFORMATION FOR SEQ ID NO: 3991:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3991:

AAAGTGGTTA AATATTATAG AAAACATCAA AGGATGTTAA GAAATACAAT TTATTACCCA	60
GCATTTAATA ATGGTGCTAT AGAAGGAATT AATAATAAGA TAAAATTAAT CAAGTGAATT	120
TCTTTTGGTT ACAGAAATTT CAACAACCTT AAAGCANGTA TAATGATGAT TTTCAGCTTG	180
TACAAAGGAG AAAAAAAGAA GACAACCAAG CCCAATAATG GACTGGCCGC CTAATAATnn	240
GAGCTCTAAA AGTTGTATTT TAAAAATAGT TCTTTAAATT ATATACCCAC CACATTGGT	300
GGAGAACCTA AAAAAAGCA CTTCCCAAAA ATGGAAAGTG CAAGTAGTGA GCCATAGAGG	360
ATTGGAACCT CTGACCCTCT GATTAAAAGT CAGATGCTCT	400

(2) INFORMATION FOR SEQ ID NO: 3992:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3992:

AGTGTATGGT TATCAAAGAT TTGATACGAC GGTCAATTATT ATTACCGTTA TTGTATTAGT	60
CATTATTGTC CAAGTGATTC AAACGCTAGG GAATGTTCTA GCTAGATTCA TACGTnGACA	120
TTAATGATAT ATAGTGAAGA TTTTGAAAGG AATTGATAGA ATGAAAAGAT TGATTGGGTT	180
AGTTATCGTA GCACTTGTAT TAATTAGCAG CGTGTGGTGG TAACAATGAT AAAAAAGTAA	240
CAATTGGTGT CGCATCAAT GACACTAAGG CTTGGGGAGA AGGTTAAAAG AATTAGCTAA	300
AAAAAGATGG ATnTTGATGT GGGAGATTAA GCACTTCCTC nGGATTACAA TTTACCGGAT	360
TAAAGCCTn AAATGGATGG TGATATTGAT AATGAATGCC	400

(2) INFORMATION FOR SEQ ID NO: 3993:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 383 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3993:

TTATCAGAAG AACAAATTCGA CATTCTTACTG AATCATCCAT TAATCGATGA AGAAGTAGCC 120  
 AATAGTTTAA TTGAAAATGT CATCGCGCAA GGnGCATTAC CCGTTGGATT ATTACCGAAT 180  
 ATCATTGTGG ACGATAAGGC ATATGTTGTA CCTATGATGG TGGAAGAGCC TTCAGTTGTC 240  
 GCTGCAGCTA GTTATGGTGC AAAGCTAGTG AATCAGACTG GCGGATTTAA AACGGTATCT 300  
 TCTGAACGTA TTATGATAGG TCAAATCGTC TTTGATGGCG TTGACGATAC TGAAAAnTnT 360  
 CCGCCGGCAT TGAGAGCCTT AGA 383

## (2) INFORMATION FOR SEQ ID NO: 3994:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 366 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3994:

GGTACTATGA TTTCACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGCCTTTCGT 60  
 GCGGGTCGGA ACTTACCCGA CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC 120  
 GCCTTTACTG GGGCTTCGAT TCGTAGCTTC GCAGnnAAAC CnACTCCTCT TAACCTTCCA 180  
 GCACCGGGCA GCGGTCACCC TGATACATCA CCTTACGGTT TAGCAGAGAC CTGTGTTTTT 240  
 GATAAACAGT CGCTTGGGCC TATTCACTGC GGCTCTTCTG GCGGTTAACC CTGAAAGAGC 300  
 ACCCCTTCTC CCGAATTACG GGGTCATTG CCGATTCTT AACGAGATTG GCTCGCTCAC 360  
 CTTAGA 366

## (2) INFORMATION FOR SEQ ID NO: 3995:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 359 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3995:

AGATATTTTA CATGTGAATC AAGTAGGTAT TCATGATAAT TTCTTTGAAT TAGGTGGCCA 60  
 TTCATTAAAA GCAACGTTAT GntGAATCGG ATAGAGGCAT CTACTGGGAA ACGATTACAA 120  
 ATTGGTGATT TATTACAAAA GCCAACTGTA TTTGAACTAG CACAAGCGAT TGCTAAGGTT 180  
 CAAGAACAAA ACTATGAAGT GATTCCAGAA ACTATAGTTA AAGATGATTG TGTGCTGAGC 240

GTACCTTTT TATGGCGGTT ATnCATCAGA ACTTAATGTA GCTCAnTGCG ACAAGCATG

359

(2) INFORMATION FOR SEQ ID NO: 3996:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3996:

CAATTATTGG TATTCAACTT AAAGATCATG ATGATTTAAT ACAACTCAAA CAACGTTnAA	60
ATCATTTCGA TCCTTCCAAT ATTTATATTA ATGAAAATAA GATGTTATAT TCATTGTTAA	120
TTTAACACAT AGTAAGAAAA ACAGTCATAA ATTGATTTCT AATTGAAATC ATCTTATGAC	180
TGCTTTTTAT TATACTTTAC ATTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA	240
AGCCATCTTT CTTTGTGTTT GCTTTTATTT TGACGTTTTA GACATAAAAA AAGAGACCTT	300
GCGGTCTCAA ATGCGGCTCA TCGCATCCAC TTTTGCCTG GGCAACGTTT TACTCTAGGC	360
GGAAngTAAG TGGGACTTAC CATCGACGn TAAGGGGCTT	400

(2) INFORMATION FOR SEQ ID NO: 3997:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3997:

GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC TTATCGTGGT GGGAGACAGT	60
GTCAnGCGGG CAGTTTGA CT GGGGCGGTCG CTCCTAAAAG GTAACGGAGG CGCTCAAAGG	120
TTCCCTCAGA TGGTTGAAA TCATTCATAG AGTGTAAGG CATAAGGGAG CTTGACTGCG	180
AGACCTACAA GTCGAGCAGG GTCGAAAnCG GACTTAGTGA TCCGGTGGTT CCGCATTGAA	240
GGGCCATCGC TCAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG	300
TTACACGAC GGGGAGGTTT GGCACCTCGA TGTCGnCTCA TCGCATCCTG GGGCTGTA	358

(2) INFORMATION FOR SEQ ID NO: 3998:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3998:

5	TAGGAGGAAT TTATATGACA TTTGAAAAAG AAACGGTCTT AAAACATTA TTTCCTGAAG	60
	ATGTACTTAG TATTGCTAAA GGTTTAACAG ACGGTGAAGT CGAATTTTAA CAACAAGTAG	120
	ATTCAATTGCT AGAAAGTAAG TACCGTGAAA ATATTAATCA ACATTGGATA GACGCTACTG	180
10	TACCCGAGGA CTATTTTAAA GATCTGGGAG AATTAAATTA TTTTAACAT CCATTACTTT	240
	ACAAGGATCG TCCAAACGCC AAAATGCCTA GTCAACTATT TCAGTTTTTC ATGTCTTACC	300
	TACTCGCGCG ATTTGATATT TCCTTAGCTA CCCTACTCGG TGTTACACAA GGTTAGGGCA	360
15	TAACACTTTC TATTTGGGAG GTAGCAAAGA CAAATTGCCA	400

## (2) INFORMATION FOR SEQ ID NO: 3999:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3999:

	CGCCCCCTTAG TGCTGCACTA ACGCATTAAG CACTCCGCT GGGGAGTACG ACCGCAAGTG	60
30	AAACTCAAAG GAATTGACGG GGACCCGCAC AAGnGTGGAG CATGTGGTTT AATTGAGGC	120
	AACGGTAGAA CCTTACCAA TCTTGACATC CTTTGACAAC TCTAGAGATA GAGCTTTCCC	180
	CTTCGGGGAC CAAAGTGACA GGTGGTGCAT GGTTGTCGTC AGCTCGTGTC GTGAGATGTT	240
35	GGGTAAAGTC CCGCAACGAG CGCAACCCCTT AAGCTTAGTT GCCATCATT AATTGGGCAC	300
	TCTAAGTTGA CTGCCGGTGA CAAACCCAGG AAGTTGGGG ATGACGTCAA ATCATCATGC	360
40	CCCTTATGGn TTTGGGTTAC ACAAGTGGTT ACAATGGG	398

## (2) INFORMATION FOR SEQ ID NO: 4000:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4000:

	TGTTCTTGCA ACGCTATTTA GTATCAGGTT TAACAACAGG TCGACAAAA GGTTAGTTTG	60
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GACGTTATGA TGACGATTAA AGTTGGAATC ATTGGGTGTG GTGGTATTGC GAATGGCAAG 180  
CACATGCCAA GTTTACAAAA AGTTGAAAAT GTTGAAATGA TCGCATTTTG TGACGTAGAC 240  
5 ATTCGAAAG CAGCGaGTGC GGCAGAAGCA TACGGAACTG ACAATGsCAA aGtTTATGAT 300  
GATTACmAAG CaTTGTtAAA AGATGACACG ATTGATGTTA TCCATGTTTT GTACCCCCAA 360  
TGGACCCCGC ATTGTGG 377

## (2) INFORMATION FOR SEQ ID NO: 4001:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4001:

TCGGGTTCTC AAATCATCGA ACATAACAAA AGAAGCTAAG CAACATGTAG GCCGTTGTCA 60  
CTTAACTTCT TGTTTTCCG ATGACAGCTT CTATTAGAG AATGTCATGA TTATTTTATA 120  
25 TTCACTTCAA TGTTATCAAT ATTAGTGCCA TCTATGACAT CTGCCATGCG ATTTTCTTGT 180  
AATTTTTTGT GCAATTCAAA CGTGTACTTT CCACCGTTTT TCATTTTAAT AACAAATTTA 240  
CCTGAACCAA CGTTACCGTA CAGATTATTT TTTTCAATAA GTGTTTTCTC AATTTAAAAT 300  
30 CAAGTTCTTT CAAGGAAATC TGTTCTTTAG TAATCTTGAA TTCTGAAACA TCATGGGnGA 360  
TTGTACCGTA TnATCTTnCC TAGTAAT 387

## (2) INFORMATION FOR SEQ ID NO: 4002:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4002:

CTATTACGAT TGCTGCGAAA GAAGGTATTA AAAATATACA AATAGGCATG GCTCACCGTG 60  
GACGTTTAAA CGTTTTAACG CATGTCTTAG AAAAACCGTA CGAAATGATG ATTTCAGAAT 120  
45 TTATGCATAC AGATCCAATG AAATTCCTTAC CTGAAGATGG TAGCTTGcAG TTAACtGCTG 180  
GATGGACTGG TGATGTGAAA TATCACTTGG TGGGCATTAA AACTACTGAT TCATACGGTA 240  
CAATGCAGCG TATTGCACTG GCTAACAATC CAAGTCACCTT GGAAATTGTT GCACCTGTTG 300

TCCATCATAA AnGCAATGnC CATTGTTGAT ACATGGCGAT

400

## (2) INFORMATION FOR SEQ ID NO: 4003:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4003:

AGAAATATAT GCATTTGCGA TATCATGGTA AAGAGAATGG ATTAAGCGGT AAATCACGTG	60
ATGAAGTGCG AGCGAAATGA AACAAAATTT AGATGTCATG CGAGACGATA ATCAAAGGGA	120
CGACAGGTGA TGGGGTTGAA AGTGTAACGn GCTACACTGG TCATGATGCT GCTAAACTAC	180
GTGATTATAA TGAAACACAT CATGCTTTGT CTGGATATGA AATGATTGAC GCAGCAAAGG	240
TGCCATTGCA ACAAATGAAG TCAATGCTGC GATGGGTATT ATTTGTGCAC GCCAACAGCT	300
GGTTCCTCGG GTACCATTCG CCGTGCACTT TTTAAATTAG GAAAAACAC ATGATTTAAC	360
AGAAGAGCAA ATGATTGAT TTCTTATTCA CTTCAGCATT	400

## (2) INFORMATION FOR SEQ ID NO: 4004:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4004:

TGAAATAGAA CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCGTTAAT GGGTGATGGC	60
GTGCCTTTTG TAGAATGAAC CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT	120
GGAGCCGTAG CGAAAGCGAG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA GACCGAAACC	180
AGGTGATCTA CCCTTGGTCA GGTGGAAGTT CAGGTAACAC TGAATGGAGG ACCGAACCGA	240
CTTACGTTGA AAAAGTGAGC GGATGAACTG AGGGTAGCGG AGAAATTCCA ATCGACCTGG	300
AGGATAnTGG TTCTCTCCGA ATAGTTTtagG GCTAGCCTCA AGTGTGATTA TTGAGGTAGA	360
nACTGTTTGA CGAGGGGCCC TCTCGGGTAC CGAATTCAGG	400

## (2) INFORMATION FOR SEQ ID NO: 4005:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 415 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4005:

ATACTAAGGC GTTATTAGAC GaTTAGACAA TGGTGTGATT AAAGGTGCAG CACTTGATAC	60
GTATGAATTT GAACGCAAAC TTTTCCCAAG TGATCAAAGG GGCAAAACAC TGAACGATCC	120
ATTGTTAGAA TCGTTGATTG ACAGGGAAGA TGTCATATTA ACACCACATA TTGCGTTTTA	180
TACTGAAGCT GCAGTTAAAA ATCTAATTGT CGATGCATTA GATGCAACAT TAGATGTATT	240
GGCAGACTGG AGATACTAGG TTACGAGTAA ATTAAAAATC GAACTGATGA GATAATTGG	300
ATTGTTGGGG ATTCTGCATC CAGTTCGATT TTTTAAATTT GGTGTTGGAT GACGTTGnAA	360
TGTTGCCTAA TTAAACGAC ATCGTAAACC nTGGATCCTC CAATGGCGTC CTnnc	415

(2) INFORMATION FOR SEQ ID NO: 4006:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 444 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4006:

CTAACAGAAG CTAGTATAGG AAATCGGTAC TCGTTAAGGC TGATCTGTGA TGGGGAGAAG	60
ACATTGTGTC TTCGAGTCGT TGATTTTACA CTGCCGAGAA AAGCCTCTAG ATAGAAAATA	120
GGTGCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG	180
AACTCTCGTT AAGGAACTCG GCAAAATGAC CCCGTAACTT CGGGAGAAGG GGTGCTCTTT	240
AGGGTTAACG CCCAGAAGAG CCGCAGTGAA TAGGCCCAAG CGACTGTTTA TCAAAAACAC	300
AGGTCTCTGC TAAACCCGTA AGTGATGTAT AGGGGCTGAC GCTGCCCGGT GCTGGAAAGT	360
TAAAGAGAGT GGGTTACTTC TTGCGACTTA nCGAAATCGA GnCCCCAGTA AACGGCGGGC	420
CGTAACTATA ACnGTCCTAA GGTA	444

(2) INFORMATION FOR SEQ ID NO: 4007:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

TTTGAACTCT ATCAAAGCAT CAGCAATCAA AACATACGTA TCTTTACAAC AGTAATCATG 60  
 CATTCTATGA TGCTTCTAAC TGAATTAAAG CATCGAACAA TCGGAAGCAT ATTTCTAAAT 120  
 TATTTATTCA TTATAGTCTT AACATAACA TGACCTAATA TATTACTAAC CTATTAAAAT 180  
 AAACCACGCA CATCTAAGTG ATATACGACA ATCACAGCAA TAATAATTGC TTTAGAAAGT 240  
 CGTGCCGAAC TGGAACCTAC AAGTCTAGTT CGAACACACA CTGATGTGAG TGGTTTTCTT 300  
 TATTTTAAAC ATGAACAATC AGATAAGTTA CTAGCATTAG CAAATATTAT TAAATCAAGG 360  
 GCTTCGnTTC ATAAATTTAA AACATGTAA ATTAGACGTG 400

(2) INFORMATION FOR SEQ ID NO: 4008:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4008:

TATACTTGTT TTTACAAACC AAAAAAGCT CTAAACATTA GTTTAAACCA ATGCTTAGAG 60  
 CTTTCTAATT ATTTTATGCT TTAAAGATA CTGTGTTATC TACGATGACC TTACCGTCTT 120  
 TAATAACTTT TTCTGCGTGA TTGATACCAA AATGATATGG AATATATTCA TGATTTGGTG 180  
 CATCCCAAAT TACTAAATTA GCCTTATCAC CTGTGTTAAT TGTACCCGCG TTAATGTCTA 240  
 TTGCTTTAGA GCCATTGACC GTAACAGCAT TCCAACTTC ATTAGGTGAT AGCTTTAATT 300  
 TCAAGGCTGC AATCGCCATA ACAAGTTGTA AGTTGTTTGT GGACACTACT ACCAGGGTTA 360  
 TAATCAGTTG GCTAATGCCA TCGGCACCGG TTAATGGTCC 400

(2) INFORMATION FOR SEQ ID NO: 4009:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4009:

ACAAACATTG AAATTAGAGG TATATAAAAA ATGCTTCTGC AATAGATGCA ATAAACATGC 60  
 AATACAATAT GGAGGCGAAG TAAATGAAAA GTATTACGTT TGAAGAACAT TATGTCATTG 120  
 AAGATATTCA AAAAGAAACG ATGAATGCGA TATCAGCAGA TCCTAAAGGT GTACCGATGA 180

ATCATGATGA ACGTATCCAA TTTATGAATA ATCAAGACGT TCAAATTCAA GTCTTATCTT 300  
 ATGGAAATGG TTCTGCTTCA AATTTGGTTG GTCAGAAAGC CATTGAATTA TGTCAAAAG 360  
 5 GCAAATGATC CATTGGGCAA ACTATATTGC ACCATATCCC 400

## (2) INFORMATION FOR SEQ ID NO: 4010:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4010:

ACTAGAGAAG GTATGTTACG TGACAATGAA TTAATAAATG GTATTTATTC ATCGAGTTAC 60  
 20 ATCTATAGTT TATTAAAATC AGAATACGAC CAAAATGAC AAATTAGACT TACAAAAGAG 120  
 TGATGACATT TAAATGGCA GCGCTCTTTT ATTTAATTTT TGAAAATAAA AGGTTGTTGA 180  
 CAGTATTATT TTATAACAAT ATAATGATT TGATAATTAT TATCAACTAG ATGATGTTTA 240  
 25 TGGGAGGATG CTTTAAAACA GCCGTTTTAA GTGTAATGTA TTATTTTAGC GTGTAGGGAT 300  
 GCGAAAATAT ATTTATAGGA CACATCTTGG GGATAATnGA TTTCTATAAT GAGGTGTCAA 360  
 30 ATGGAAAAGT TACCACGCTA TTATTAGCCn CCACGTTATT 400

## (2) INFORMATION FOR SEQ ID NO: 4011:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4011:

TnTCAATTAG AAAATATCTT ACCGCTGnCT CTATTTATAC AATCCTCGTA TTGAATGGnT 60  
 CGCTTTCCTA GGGTGCCGTC TCAGCATCGG CTTGACTGG CACTGCTCCC TCAGGAGTCT 120  
 45 CGCCATTAAT ACTACGTATT AACATGTAAT TTTACTTTGA AATACTTTAA AAAAATAAGA 180  
 CACTTTGCCC AACTTACACT ACCAATAAAA ACTTCTGTGA GAATTCCTCA AAATGATATT 240  
 50 TCGCGACATG TTAATGAAAT TGTTGAAACG ATACCTGATA GCAAATTCGA TGAATTCAGA 300  
 CATCATCGTG GCGCAACATC CTATCATCCA AAGATGATGT TAAAAATCAT CTTATATGCA 360  
 TATACTCAAT CTGTATTTTC TGGTCGTAGA ATAGAGAAAT TACTTCATGA CAGTATTCGA 420

GAATCCnAAT ACTG

494

## (2) INFORMATION FOR SEQ ID NO: 4012:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4012:

TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGACATA 60  
 AAAAAAGAGA CCTCACGGTC CAACTTGCCT GGCAACGTC TACTCTAGCG GAAGTAATTG 120  
 GCTACCATCG TCGCTAAAGA CCTTTCTTGA CTGTGACAA TCGCTTGCTT CTTTCCTCTC 180  
 CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGGCTCTTT TCTCGTTTCG 240  
 TCAGATTCAA ACGTTTTTCAC TTCGCCAAGC CATTTTTCTT TGTGTTTACT TTTTATTTTG 300  
 ACGTTTTAGG CATAAAAAA AGAGACCTTG CGGTCCCAAT GCGGGCTCAT CGCATCCATT 360  
 TTTTGGCCTG GGCAACGTC TnATnCCAGC GGAAnTnAAT 400

## (2) INFORMATION FOR SEQ ID NO: 4013:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4013:

CGAACTGCCG AACC CGAAGA GCGGATTTAC AGTCCGCCGC GTTTACCACT TCGCTACCCC 60  
 TCCAGCTTAT TCATATAATT TAATAATCAA AATGGTGGAG AATGACGGGT TCGAACCGCC 120  
 GACCCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGACT 180  
 CCTACGGGAC TCGAACCCGT GTTACCGCCG TGAAAGGGCG GTGTCTTAAC CGCTTGACCA 240  
 AGGAGCCATG GCTCCACAGG TAGGACTCGA ACCTACGACC GATCGGTAA CAGCCGATAG 300  
 CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTTA CTCTnAGCGG 360  
 AACGTGAATT CGACTTACCA TCGACGnTAA GGAGCTTnAC 400

## (2) INFORMATION FOR SEQ ID NO: 4014:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4014:

ATTAGGACCT CAAGACGATA TTAATAAATT TGAATACTTA AAAAAATCTT CTCAAAATAC	60
AGGTACTTCA TTATTGGTAT TCAACTTAAA GATCATGATG ATTTAATACA ACTCAAACAA	120
CGTGTGAAAT CATTTGATC CTTCCAATAT TTATATTAAT GAAAATAAGA TGTTATATTC	180
ATTGTTAATT TAACACATAG TAAGAnAAAC AGTCATAAAT TGATTCTCTAA TTGAAATCAT	240
CTTATGACTG CTTTACATT ATACTTTACA TTTCTCGTTT CGTCAGATTC AAACGTTTTTC	300
ACTTCGCCAA GCCATCTTTC TTTGTGTTTG CTTTATTTT GACGTTTTAG ACATAAAAAA	360
nGnGACCTGC GGTCTCAATG CGGCTTCATC GCATCCACTT	400

(2) INFORMATION FOR SEQ ID NO: 4015:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 377 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4015:

GAATGAAAAG CTCTAAAAGT TGTATTTTAA AAATAGTTCT TTAAATTATA TACCCACCAC	60
ATTTGGGGAG GAACCTAAAA AAAAGCACTT CCCAAAAATG GAAAGTGCAA GTAGTGAGCC	120
ATAGAGGATT CGAACCTCTG ACCCTCTGGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT	180
AATGGCTCTG AATGGCTGGG CTAGCTGGAT TCGAACCAAC GAGTGACGGA GnAAAGGTCC	240
GTTGCCTTAC CGCTTGGCTA TAGCCCAATA TATAGATGGT GGAGGGGGGC AGATTCGAAC	300
TGCCGAACCC GAGGAGGCGG ATTTACAGTC CGCCGCGTTT AGCCCACTTC GnTACCCCTG	360
CCAGnTTATT CATATGA	377

45

(2) INFORMATION FOR SEQ ID NO: 4016:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4016:

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ATGACGCACC TGACATCCTC TCGGTTTCATA TTCAGGCATA TCCGGACCAC AACTTGGATA 120  
 GTCAGTTTGT TGATTTTCCC AGGTAATCAC ACCATTTTTC ACAAATACTT TCCAAGAACA 180  
 5 TGAGCCTGTA CAGTTAACAC CATGTGTTGT TTCTTACTTC TTTATCGTGG CTCCAACGTT 240  
 CTCGTACAT TTTTCCCAT TCTCTACTTT TACTTTCTAG GATCGACCAA TTCCCATTTGA 300  
 10 AATTTTTCTG TTGGCTTAAA GAAATCAATC CAAATTTCCC ATATTATATAT CCTCCTACGG 360  
 GTGAAAAATA CGGTGTGTAG AnGTCGTGGT TTTTnAAATA 400

## (2) INFORMATION FOR SEQ ID NO: 4017:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4017:

CTTTGAGCGC CTCCGTTACC TTTTAGGAGG CGACCGTCCC AGTCAAACCTG CCCGnCTGAC 60  
 25 ACTGnCTCCC ACCACGATAA GGGCGTGGGT TAGAAAGCCA ACACAGCTAG GGTAGTATCC 120  
 CACCAGCGnC TCCACGTAAG CTAGCGCTCA CGTTTCAAAG GTCCTACCT ATCCTGTACA 180  
 30 AGCTGTGCCG AATTTCATA TCAGGCTACA GTAAAGCTCC ACGGGGTCTT TCCGTCCTGT 240  
 CGCGGGTAAC CTGCATCTTC ACAGGTACTA TGATTTACAC GAGTCTCTCG TTGAGACAGT 300  
 GCCCAAATCG TTACGTCTTT CGTTGCGGGT CGGAACCTAC CCGACAAGGA ATTTGTTAC 360  
 35 CTTAGGACCT TATAGTTACG GCCGnCTTTA ATTGGGGTTT 400

## (2) INFORMATION FOR SEQ ID NO: 4018:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4018:

TGTCGATTTA AGAGGCATGC TACGAGGAAT GATTGGTCAT CCGAAAAAAG ATCGAGCGGC 60  
 50 ATATGAGGCA CGCCAAGCGA TTCCAACAT TAATGAAAAC AGTCCGCCAA TATTAATTGT 120  
 ACATGGAGGG AAAGACCAGC AAGTTGGTAT TCATCATGCG TATTATTAG CGGACCAACT 180  
 AGAGTTAAAA GGTGCCACGC ATGnAAACAT TTTATCAAAT GGCAGAAGGA CATGTGCCAA 240

CGCATAGCTT AGTTATGGAA ACGTGGTGTG CGCATGGGGA ACTATTCAAG CTTTGGAGGA 360  
TGTGGTACTT ACATGCGTTG GAATTAGGGG TCCGGTTACT 400

(2) INFORMATION FOR SEQ ID NO: 4019:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4019:

GGAGGTTTGG CACCTCGATG TCGGCTCATC GCATCCTGGG GCTGTAGTCG GTCCCAAGGG 60  
TTGGGCTGTT CGCCCATTAAG ACGGTTACCA AGCTGGGTTT AGAACGTCGT GAGACAGTTC 120  
GGTCCCTATC CGTCGTGGGC GTAGGAAATT TGAGAGGAGC TGTCTTAGT ACGAGAGGAC 180  
CGGGATGGAC ATACCTCTGG TGTACCAATT GTCGTGCCAA CGGCATTAGC TGGGTAGCTA 240  
TGTGTGGACG GGATAAGTGC TTGAAACATC TTAAGCATGA AGCCCCCTC CAAGATGGAG 300  
ATTTCCCAAC TTCGGTTTnT AAGATCCCTC CAAAGnTGAT GGAGGTTTAA TAGGTTTCGA 360  
GGTGGGAAGC AnGGTGGACA GTTGGGAGCT GGACGAnTAC 400

(2) INFORMATION FOR SEQ ID NO: 4020:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4020:

GAAGATGTTT GTCATTCTTC AAATAAACCA GAGCTAGTTG CAATTGCTGA ACCAGCATCT 60  
AATAGACCGA AAAAGAGAAG TAGACGTGCG GCACCGGCAG ATCCTAATGC AACTCCAGCA 120  
GATCCAGCGG CTGCAGCGGT AGGAAACGGT GGTGCACCAG TTGCAATTAC AGCGCCATAT 180  
ACGCCAACAA CTGATCCTAA TGCCAATAAT GCAGGACAAA ATGCACCTAA CCGAnTnTTG 240  
TCATTTTGAT GACAATGGTA TTAGACCAAG TACCAACCGT TCTGTGCCAA CAGTTAAACG 300  
TTTGTTAATA ACTTGCCGGG CTTCACTA ATCAATGGTG GGCAAAGTAn GGGTGTtTAG 360  
TCATGCAATG GGTAAAGACG AGCATGTTTG GATTTACGGG 400

(2) INFORMATION FOR SEQ ID NO: 4021:

(A) LENGTH: 396 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4021:

10	CTAAGTCATG AATGGGAAGT GGCTCGCGTT GAAGAAGGAC TGACTACTGC TGCCACACAG	60
	CTTGCTAAAC AATTATCAGA ATTAGATTTA GCGTCACATC CTTTGTGAT GTCAGAGCAG	120
	TTTGCAAGTn TAAAAGATCG TCCATTTCAT CCATTAGCTA AAGAAAAAAG AGGATTAAGA	180
15	GAAGCGGATT ATCAAGTGTA TCAAGCTGAA TTAATCAAT CATTTCTTT AATGGTTGCA	240
	GCAGTTAAAA AGACACATAT GATTCATGGC GATACTGCAA ATATCGATGA ATTAGAAAAT	300
	TTGACAGTAC CTATAAAGA ACAAGCGACA GACATGTAA AATGATCCAA GGTATCAnT	360
20	AGATGACTAT GTACCATTCC GGTACnTCCT GGCCAT	396

## (2) INFORMATION FOR SEQ ID NO: 4022:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 376 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4022:

	GATTGGTCTG nAAGAAGAAT TAATGGAAAA GCTACGTGAA AAATTAGAAG CGGCATTTGA	60
35	TACGATTTAC GAATTGTCTC AAAACCGAAA AATAGATATG AGACTTGCAG CATATATCAT	120
	AGGTATTAAA CGTACAGCAG AAGCAGCTAG ATATCGTGGT TGGGCATAAT TAATTATCAT	180
	ATGTGATTTA ACGAGCTTGG GACAGAAAAC AAAGCCCTAA GTCGTTAAT TTTATTTTAG	240
40	CAGTAGTTGA CTGTAAACA ATGCCCGTGT AAACGCTCTT TTCAAAAATA GTCGGGGCCC	300
	CAACACAGAG GCTGGTGGGA AAGTCAGCCT ACAATAGnGT GCAAGTTGGC nGGGGCCCCA	360
45	ACACAGAGGC TGGCGG	376

## (2) INFORMATION FOR SEQ ID NO: 4023:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 381 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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CAAATGGTGG AGCCATAGGA GGATTGGAAC CTCTGACCCT CTGATTAAAA GTCAGATGCT 60  
 CTACCAACTG AGCTAATGGC TCTTCCATGG nGcngGCCAG AGGACTTGAA CCCCCAACCT 120  
 5 ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC GGCAATATGT AAGAATAAAT 180  
 GGTGGAGAGT GACGGGTTCG AACCGCCGAC CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG 240  
 10 CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTT TACTCTAGCG GAAnTAATTC 300  
 GGACTACCAT CGACGCTAAA GGAGCTTAAC TTCTGTGTTC CGGCATGGGA ACAGGTGTGA 360  
 CTCCTTGCTA TATCACCAGA C 381

(2) INFORMATION FOR SEQ ID NO: 4024:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4024:

25 GCCCCTTATG ATTTGGGCTA CACACGTGCT ACAATGGACA ATACAAAGGG CAGCGAAACC 60  
 GCGAGTCGAA GCAAATCCCA TAAAGTTGTT CTCAGTTCGG ATTGTAGTCT GCAACTCGAC 120  
 TACATGAAGC TGGAATCGCT AGTAATCGTA GATCAGCATG CTACGGTGGG ATACGTTCCC 180  
 30 GGGTCTTGTA CACACCGCCC GTCACACCAC GAGAGTTTGT AACACCCGAA GCCGGTGGGA 240  
 GTAACCTTTT AAGGAGCTAG CCGTCGAAGG TGGGGACAAA TGGATTGGGG TGAAGTCGTG 300  
 35 AACAGGTAG CCGTGATCGG AAGGTGCGGC TGGGATCACC TCCTTTGCTG AAGGATGATG 360  
 ATTTCCGnAA CATCnTTCTT CCAGAAGATG CCGGTAATAA 400

(2) INFORMATION FOR SEQ ID NO: 4025:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 352 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4025:

50 CTTAGAAGTG AGAATGCCGG TGTGAGTAGC GAAAGACGGG TGAGAATCCC GTCCACCGAT 60  
 TGCTAAGGTT TCCAGAGGAA GGCTCGTCCG CTCTGGGTTA GTCGGGTCCT AAGCTGAGGC 120  
 CGACAnGTAn GGCGATGGAT AACAGGTTGA TATTCCTGTA CCACCTATAA TCGTTTTAAT 180

GCTGAGTATT AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT 300

GTGTCTTCGA GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AA 352

(2) INFORMATION FOR SEQ ID NO: 4026:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4026:

TGGGGCTCTT CCCGTTTCGC TCGCCGCTAC TAAGGGAATC GAATTTTCTT TCTCTTCCTC 60

CGGGTACTAA GATGTTTCAG TTCTCCGGGT GTGCCTTCTG ATATGCTATG TATTCACATA 120

TCGATAACAT GACATAACTC ATGCTGGGTT TCCCCATTCG GAAATCTCTG GATCAAAGCT 180

TACTTACAGC TCCCCAAAGC ATATCGTCGT TAGTAACGTC CTTTCATCGGC TTCTAGTGCC 240

AAGGCATCAC CGTGCGCCCT TAATAACTTA ATCTATGTTT CCACCATTTT TATAAGTCAA 300

ANGTTAACAT GAAGTTAGGT TCTTTTATAA AAGGATTAAA nGGGTTATTA ATCTTGtGnG 360

TGTTCTTTTCG 370

(2) INFORMATION FOR SEQ ID NO: 4027:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4027:

TCAIGTTTTG CTIGGTTTAA TGCTGTTAAT GCGTTATCGA CACGATGTTT TTCATCTGAA 60

ATTGTTGTG CAGTTCATC GCCATGTCA ATAACACGTT GAGCTGCAGT TATTTCAAGT 120

TCTGCTTCCG CTTCTTCGCA TTATAGTTAT CAATACTTTG TTGCGTCATA CCAGCAGTTG 180

ATGGTACTTG GTTCACAGAA CTTTGTAAGT TATTTTTAGA CGTTACTAAT TGGCTATTAT 240

CTTCTTTATT TTGAAGTAAT GCTTACTTG GATCAATCTT AGTTTGTGCG CACGAACTTT 300

AGTTAGTGCG TGCAGAAACT TGTGTGGTG TTGCACGCTC ATThATGAAG CACTGTTGGT 360

GCCTCCGTTT TCGCATAnTG GATIGTTGTT GCGCATGAGG 400

(2) INFORMATION FOR SEQ ID NO: 4028:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4028:

CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC 60  
 CATCGTCGCT AAAGACCTTT CTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG 120  
 GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTGCGC TCTTTCTCG TTTGTCGAGA 180  
 TTCAAACGTT TCACTTCGC CAAGCCATTT TTCTTTGTGT TTACTTTTAA TTTTGACGTT 240  
 TTAGACATAA AAAAAAGAGA CCTTGCGGTC TCAATGCGGC TCATCGCATC CATTTTTTGC 300  
 CTGGGCAACG TTCTACTCTA GCGGGAACGn AAGTTGGGCT TACCATCGAC GCTAAGAACC 360  
 TTTCTTGGAC TTGGTGGACA AACGGnGTGG CTGCTTTTCC 400

## (2) INFORMATION FOR SEQ ID NO: 4029:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4029:

AGGACTTGAA CCCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC 60  
 GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTTCG AACCGCCGAC CCTCTGCTTG 120  
 TAAGGCAGAT GCTCTCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTT 180  
 TACTCTAGCG GAATTAATTC GGACTACCAT CGACGCTAAG GAGCTTAACT TCTGTGTTTCG 240  
 GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG TAATTGATA 300  
 CATTCAAAAC TAGATAGTnA AGTGAAAAGT GATTTTGGnT TCGCAAAACC ATTTGATTTT 360  
 GATTGAAGTC CTTGATCGA TTGAGTGATT CGTGCAGCTn 400

## (2) INFORMATION FOR SEQ ID NO: 4030:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 390 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GATGATAAAT CATGTTTTTC ATACCAAGTC GCTGCCGGCA AAACAATGTC AGAATATAAC 60  
 GGTGTTGCCG TCATTCTGAA GTCTAAAGAG ACCACTAAAT CTAACCTACC TGTTGTTTCT 120  
 5 TCACGCCACG TAATTTCTTC TGGCTTTTCA TCTTCATTG GTGTAGCTAA TAACCCTGAT 180  
 TTTGTGCCAA GTAAATGCTT CATAAAGTAT TCTTGACCTT TTGCAGAACT TGAAATTAAG 240  
 10 TTTGAACGCC ATATAAATAA TGATTTTGGG TGATTCTTTT CAAATCAGGA TCTTCTATTG 300  
 CAAATTGTGG TTTGTnTTGG ATTTCAChTC ATCAATTGCA CGTTGCAAAA TCGCTTCATG 360  
 TGAATCTATA CCCTGCATCT TGTAGChTCC 390

(2) INFORMATION FOR SEQ ID NO: 4031:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4031:

25 TGGTTGCAAT CCAGCTAGCC CAGTTATTGG CGGCATAGCA AGTGGAAGG CAGAGGTCTG 60  
 CAAAACCTTT ATCACC GGTT CAAATCCGGT TGCCGCCTCC AGGTTTATGC GGGAGTAGTT 120  
 30 CAACTTTTAG AACACGTTCC TTCCCGGAAn GAGGTATAGG TGCAAATCCT ATCTTCCGCT 180  
 CCATAATTTA ATAATAATGC GGGAGTATTT CAACTCTTAG AATACATTCC TTCCTGGAAT 240  
 GAGGTATAGG TGTAATCCT ATCTTCCGCT CCATAATTTA ATATTGCGG GGAGTAGTTC 300  
 35 CAACTTTTAG AACACGTTCC TTCCCGGGAA GGAGGTATAn GTGTATCCTA TCTTCCGChC 360  
 CATAATGCCT TCCAAAGGGG AATTTTTTGG TTTnACCATT 400

(2) INFORMATION FOR SEQ ID NO: 4032:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4032:

50 GTATCGATGA GTTCTTTCGG TGCCTCTTCG ACAGCCATTT TGACTTCGAC AAAATGCATC 60  
 ACATCGGGAT GACCATTAAAT TGCATTAAAC GTGTCTTGTA AATCTTTTGA TGATTCAACG 120  
 TCATGAATTT CAACATTTTT ACCACCAAAT ACAGCTGGTA AAGCTTTATA ATCCACATG 180

TTATTAATCA CCAATAATAC CGGGTTAATA TGCTGTCTAA TCATAGTTGG AAATAGCTTG 300  
 AACAGTTAGT TGGCCATGAG CCATCACCCA TTTAATAATA AGTTACGACG GATCTTTGGT 360  
 5 CTGCCAATTG GGGGAnCnCA ATGTTGCAGG GnAATGGTAT 400

(2) INFORMATION FOR SEQ ID NO: 4033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4033:

CACGACGTTT TGAACCCAGC TCGCGTACCG CTTTAATGGG CGAACAGCCC AACCCTTgGG 60  
 20 ACCGACTACA GCCCCcAGGA TCGGATGAGC CGACATCGAG GTGCCAAAct CCCCCTCGAT 120  
 GTGAACTCTT GGGGGAGATA AGCCTGTTAT CCCCggggTA GCTTTTATCC GTTGAGCGAT 180  
 GGCCCTTCCA TCGGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG CTCGACTTGT 240  
 25 AGGTCTCGCA GTCAAGCTCC CTTATGCCCTT TACACTCTAT GAATGATTCC AACCATTCTG 300  
 AGGGAACTTT GAAGCGCTCC GTACCTTTTA AGAnGGCGAC CGGCCcAGTC AAACCTGGCCG 360  
 30 CTGACACTGT CTTCCAACAC GATAAGTGGT GCGGGTTAGA 400

(2) INFORMATION FOR SEQ ID NO: 4034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4034:

AATTCcATGT GTACGGTTGA AATGCGCAGA GATATGGAGG AACACCAGTG nCGAAGCGAC 60  
 45 TTTCTGGTCT GTAACtGACG CTGATGTGCG AAACGTGGGG ATCAAACAGG ATTAGATACC 120  
 CTGGTAGTCC ACGCCGTAAa CGATGAGTGC TAAGTGTtAG GGGGTTTCCG CCCCTTAGTG 180  
 CTGCAGCTAA CGCATTAAAGC ACTCCGCCTG GGGAGTACGA CCGCAAGTTG GAAACTCAAA 240  
 50 GGAATTGACG GGGACCCGCA CAAGCGTGGn AGCATGTGGT TTAnTTcGAA CAACGCAGAG 300  
 AACCTTACCA AATCTTGACA TCCTTTGACA ACTCTAGAGA TAAAGCCTCC CCTTCGGGGA 360  
 CAAATGACAG TGGTGCAngT TGTcCTCACT CGTGTcGTGA 400

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4035:

TTCGCTTTGC CCGTCTGTCA CATTACTGTA AAATTCTATA AATAGAATTT TTGATGACGG 60  
 GTCCCTTCCT AGGGTGCCGT CTCAGCCACC CCAACCGGCA CATTGTTGTA AGCTGACTAT 120  
 ATGTCACTTC TGTGTTGGGG CCCCTGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC 180  
 CATTAACTAC ACGTATTAAC ATGTAATTTT ACTTTGAAAT ACATTAAAGC CCAAATTAAT 240  
 CAAAAGCTTT CTGAACCAGA AACGAAAAAA ATCTATAGTC ATAGAAAAAT TTATGTAGAG 300  
 CCTGTTTTTG GATTTATGAA GGCTATTTGG GGTTCACCTG AATGTCAGTT CGAGGAATAA 360  
 TNAAGTnAAC GAGAGCCAGG TTTGTAATTA TGGCACTnAT 400

## (2) INFORMATION FOR SEQ ID NO: 4036:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4036:

TAAATGTTGA AAAAGCACGA TTAGATAGAA TTTTGAATAA CAATGAAATT CGTCAAATGA 60  
 TCACAGCATT TGGTACAGGA ATCGGTGGCG ACTTTGATCT AGCGAAAGCA AGATATCACA 120  
 AAATCGTCAT TATGACTGAT GCCGATGTGG ATGGAGCGCA TATTAGAACA TTGTTATTAA 180  
 CATTCTTCTA TCGATTATG AGACCGTTAA TTGAAGCAGG CTATGTGTAT ATTGCACAGC 240  
 CACCGTTGTA TAAACTGACA CAAGGTAAAC AAAAGTATTA TGTATACAAT GATAGGGGAC 300  
 TTGATAAACT TAAATCTGAA TTGAATCCAA CACCAAAATG GCTATTGCAC GTACAAAGGC 360  
 TTGGAGAATG AATGCAGTCC ATTTGGGAAC ACATGACCTG 400

## (2) INFORMATION FOR SEQ ID NO: 4037:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4037:

TCGTCGCTAA AGACCTTTCT TGACTTGTA CAATCGCTTG CTTCTTTCTT CTCCTTCGGC 60  
 5 TCTCGCTTAC TCATTTAGCT CTAATAAAGT CGTTGCGCTC TTTTCTCGTT TCGTCAGATT 120  
 CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT TTGACGTTTT 180  
 AGACATAAAA AAAAGAGACC TTGCGGTCTC AATGCGGCTC ATCGCATCCA TTTTTTGCCT 240  
 10 GGCAACGTTT TACTCTAGCG GAATTAATTT GGGCTACCAT CGACGCTAAG AACCTTTCTT 300  
 GACTTGTGAC AATCGCTTGC TTCTTTCTCT TTCTTCGGCT CTCGCTTACn CATTTAGCTC 360  
 15 TACnAAACTC GTTGGCGCTCT T 381

## (2) INFORMATION FOR SEQ ID NO: 4038:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 360 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4038:

CTGTTTGTCA TACTTCATAA ATCCTTTAAA TTCACCCATC GTATCTCCCC CTTTCCTTAA 60  
 TACACAACGG CTGGTTTATG TTTAGCATCG ATTGTTTTAC TGTCATCGTA AAATGCAGCT 120  
 30 AACATCGCTT CATCTTCATT GTCATGTAAT GATTTGTGCA AATGAATTTT TTGCATCATT 180  
 AATTGATAAT CTTTAGGAAT AACTTTAAGC ACGACATCTT CAATGCGATC AAAATGTTTT 240  
 35 AACACATGAA TCGCTCTCGT ACTATTCGTG TGTGACACAT GTnCTTCCAG CATTTGCTTA 300  
 ATGAATGCTT TnCTTCTTG GTGTTTAATC TTTGTAAACG AAAGCGTATC TAGTGATAnG 360

## (2) INFORMATION FOR SEQ ID NO: 4039:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4039:

AGTGCGAACC CATAACCTCT TGATCCGTAG TCAAACGCTC TATCCAATTG AGCTACGGGC 60  
 50 GCATATGTTT TTATTGAAAA TGGTGCCGAG GACCGGAATC GAACCGGTAG TGAnTGCACT 120  
 CACCGCAGAT TTTAAGTCCT GTGCGTCTGC CAGTTCCGCC ACCCCGGCAC TATAAAAATG 180

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GAAGTACTTC TGCATATGCG GGTGAAGGGA GTCGAACCCC CACGCCGTAA GCTnAGGATC 300  
 CTAAGTCTAG TGGCTCTGCC AATTCGCGCA CACCCGCAAA TGGTGAGCCA TAGAGGATTC 360  
 5 GAACCTCTGG ACCCTCTGGA TAAAAAGTC AGATGCTCTA 400

## (2) INFORMATION FOR SEQ ID NO: 4040:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4040:

CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCTCTCC TTCGGCTCTC GCTTACTCAT 60  
 20 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 120  
 TCGCCAAGCC ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTGTAGAC ATAAAAAAG 180  
 AGACCTCAGC GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA 240  
 25 CCATCGTCGC TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC 300  
 GGCTCTCGCn TACTCATTTA GCTCnACTAA ACTCGTTGCG CTCTTGTTCT CGTTTCGGGC 360  
 30 AGATTCAAAC GntTGTCa 378

## (2) INFORMATION FOR SEQ ID NO: 4041:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4041:

GTACCTTAAC AATATCTCGA AATGGACGAA CTAAATTATG AACCGCATGA AAGGATACTT 60  
 45 GCGAATCATT TGAGCATGCT TGAATCATAA TATCACCATC GCTGTAATCG TCTATTAAC 120  
 GATCATTTCG AAAATGCGGT AAATCTTTAA AGGCATCGGG AATTTTACTA GATAACCCAA 180  
 TTTTCTTCAT CAAAGACTTA CTAATCCCAA AGGTAATCGT TAACTTGCTT GCACCTAATC 240  
 50 CTATCGATTC ACCGGTATCT ACTGGTGGGC ATTAAAGGAT TGTTACTCGG GCTTGGCCAA 300  
 CTGTATCACC ATCCATCATA CGATTCAGCC ATAACGGTCC ACTTTTTTAA ACATTGGCTT 360  
 TATTGGCACC CnAACCTTTG GACTTCnAAT CTAACGGCCA 400

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4042:

GACTTGCAAA CGTTGTGATG ACGGTCAAGA AAAGTGGTAA CACACCAGAC GGACGTAAAG 60  
 CTGGCGAACC ATTTGCTCCA GGTGCAACC CAATGCATGG CCGTGACCAA AAAGGTGCAT 120  
 TATCTTCATT AAGTTCTGTA GCTAAGATCC CTTACGATTG CTGTAAAGAT GGTATTTCAA 180  
 ATACATTGAG TATCGTACCA AAATCATTAG GTAAAGAACC AGAAGATCAA AACCGTAACT 240  
 TAACTAGTAT GTTAGATGGT TACGCAATGC AATGTGGTCA CCACTTAAAT ATTAACGTAT 300  
 TTAACCGTGA AACATTAATA GATGCAATGG AACATCCAGA AGGAATATCC ACAGTTAACA 360  
 ATCCGTGTAT CTGGTTACGC TGTTAACTTC ATTAAATTAA 400

## (2) INFORMATION FOR SEQ ID NO: 4043:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4043:

CTATTTTATC TAAAGTTAAA CCTGACCCAC CTAGAATTGA CGCAAATCT GTGACATATA 60  
 AAGCAGGTCT TACAAACCAA GAAATTAAAG TTAATAACGT ATTAAATAAC TCGTCAGTAA 120  
 AATTATTTAA AGCAGATAAT ACACCATTAA ATGTCACAAA TATTACTCAT GGTAGCGGTT 180  
 TTAGTTCGGT TGTGACAGTA AGTGACGCGT TACCAAATGG CGGAATTAAA GCAAAATCTT 240  
 CAATTTCAAT GAACAATGTG ACGTATACGA CGCAAGACGA ACATGGTCAA GTTGTTACAG 300  
 TAACAAGAAA TGAATCTGTT GATTCAAATG ACAGTGCACA GTGAACAGTG GACACCACAA 360  
 TTGACAAGCC AACTACTGAA GGCGCnGTGn TTATTAAAG 400

## (2) INFORMATION FOR SEQ ID NO: 4044:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4044:

5 AAAATGGCTT GATTTGAAAA ACGACCAGCA TCGCTACTG GnATAATAGC GAGGCTACCA 60  
 TGTGTGTTTCA TCGTAGnCGC ATGTTAGTTA ATCCAGGGAT ACAAGCATCA TGATCAATAT 120  
 TAAAGCCATA TTCAAACAAT TGACCATAAG GTTCAATGTA AGCAGCGCCG GTGCACTTGC 180  
 10 ATTCCAGCTG AATTAGAGCG ACGTGCAGCA TAAGCCAAGT CTTCTTTTGT AATATAGCCT 240  
 TCTTTTGTG ATGTGTTTAC GGTCCATTGG GTGGATAATA CAAAGCGATT CGAAATTTTG 300  
 ATGCCATTAG GTAAGTGGAT TGATTGTAAA AGTGGTTTGT ATCGGTACAT ACTATGATTC 360  
 15 CnTTTCCATT GCAAT 375

## (2) INFORMATION FOR SEQ ID NO: 4045:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4045:

25 GTTCCAATGA AGATAGCTAG AAATGATATC CAAAACACAT GATGCATCAC TGGTGATGCT 60  
 30 CGACTAATTG TATTCCATGA TGCATTAATA ATAATGACCA ATACACATAA AATAAGCAGC 120  
 CATTATCGT TTATTTTAAA AATATAATGC AGCAAAAATC CCAAATGAT TAATTGCACA 180  
 ACTGCTCGTA ATGTCGCAAC AATTAAATCT TTAATAATAT GTAAACCTTC TTTATATGAA 240  
 35 ATGATAATCG GAATGACTAA AAGCAATGCC GTCAATCCAA GTGCCGTATT ACTCATGTnG 300  
 ATTCAACTCC TCTGTATTAG AAATTTGACC ATCAACAATT GTTATACGCT TTTTGnAAGT 360  
 GGTCGCATAC TTTGGGGCAT CGCTGTGGGG TAGGGGGnCh 400

## (2) INFORMATION FOR SEQ ID NO: 4046:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 375 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4046:

50 CGAGTCTGAG TCGCTGTCTG AATCTGAATC GCTGTCTGAG TCGGAATCGC TATCTGAATC 60  
 TGAGTCGCTG TCTGAGTCTG AATCGCTATC TGAATCTGAG TCGCTATCTG AGTCTGAGTC 120

TGAGTCTGAG TCGCTATCTG AGTCTGAGTC GCTGTCTGAA TCTGGAGTCG CTGTCTGAAT 240  
 CTGGAATCGC TGTCTGGAGT CTGAATCGCT ATCTGAGTCT GGAATCGCTA TCTGAGTCTG 300  
 AATCACTGGT CTGGAGTCCG AGTCACTGTC TGAATCTGAC TGCACnACn GGATTCTGAG 360  
 TCGCTAACnG GAATC 375

(2) INFORMATION FOR SEQ ID NO: 4047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4047:

ATGGGTAAAA AGGCATTAGA GTCAATCATT GATAACGCTG ATGAAACAAC TCAAGAGCGT 60  
 TTACGTTTAC GATATGAAGA TGCTGTAGAT TATAACCGTT ATGTCGGTAA TATTTATACT 120  
 GGATCATTAT ATTTAAGCCT AATATCATT CTTGAAAATC GAGATTTACA AGCTGGTGAA 180  
 ACAATCGGTT TATTCAGTTA TGGCTCAGGT TCAGTTGGTG AATTTTATAG TCGGACATTA 240  
 GTTGAAGGCT ACAAAGATCA TTTAGATCAA GCTGCACATA AAGCATTATT AAATAACCGT 300  
 ACTGAGTAT CTGTTGGATG GCATATGGAA ACATTCTTCC AAACGTTTTG GATGACGGTG 360  
 GAATTTGACG GnGGACCAAG ATGChTGTTC CAGGAGGTCC 400

(2) INFORMATION FOR SEQ ID NO: 4048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4048:

CAAACCATCT GACATAATAT ACACTTGGAT GTTAGATAAG GGTTTGCCAA TTGGAATCGT 60  
 CTCAGGTATC AATCACCACA ATGATGTGAC CAATACGATG TGATGACTGT TGAATCAGAT 120  
 GGTCATAGG CATTGAAATA CGTGCCACAA TGCTTCTCAA TATATTAAAC AAAGGATGCC 180  
 GTACTAGTTG CCCCCTGT AATCAACTTT TCAATATAAA AGTCTTCCAT AACACTACAC 240  
 ATCTGTAACG GAATCGACGC AACCGTCACA CGATGCTTAT TAATGAGTTG TTGTAAGTGT 300  
 TCTGGATTAA CACGnTCCTC TCTATCTGGA nTCACAAGCG TATGACCATT AACAAACAAC 360

## (2) INFORMATION FOR SEQ ID NO: 4049:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4049:

TCTGCATGTT	CTCGAGATCC	ACCAAATGTT	AAATGGGTAT	GTGCATCTAC	TAATGCTGGG	60
GACACTACCT	TCCCACTAGC	ATCAATCGTC	TCAGTCGCAT	CGTAGTCATC	TGTATGTGTT	120
CCAGCATATA	CAATTTTGGC	CATCTTTAAT	GACAACGTGA	CCATTTTTC	CAACATTTGA	180
ATTCATCTAA	TTCTTACCC	TTCAAAGGTT	TATCTGTTGA	TCTCGGTAAA	ATTAATTGCT	240
GCTATATGAT	TAAATATAAA	TCATTCATTA	CTATCACCTG	CTTATCAATC	ATGGAATAGA	300
ATACCTTTTC	ATTAGCGTTT	GAATAGCGAG	TCATAGCCAG	CATCAACATG	TCGGGCAACA	360
CCCATACCGG	GGTCATCGTC	CAATACACGT	TCCAATCTn			400

## (2) INFORMATION FOR SEQ ID NO: 4050:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4050:

ATCACCCATG	TTCTGACTCC	CAAGTTAAAT	TAATTGGCAT	TCGGAGTTTG	TCTGAATTCG	60
GTAACCCGAG	AGGGGCCCT	CGTCCAAACA	GTGCTCTACC	TCCAATAATC	ATCACTTGAG	120
GCTAGCCCTA	AAGCTATTTC	GGAGAGAACC	AGCTATTTC	AGGTTGATT	GGAATTTCTC	180
CGCTACCCTC	AGTTCATCCG	CTCACTTTTC	AACGTAAGTC	GGTTCGGTCC	TCCATTTCAGT	240
GTTACCTGAA	CTTCAACCTG	ACCAAGGGTA	GATCACCTGG	TTTCGGGTCT	ACGACAAATA	300
CTAAACGCCT	ATTGAGCTCG	ATTTCGTACGG	CTCCACATTT	ACTGCTAAn	TTGCATCAAT	360
CGTACTCGCG	GTCAATCTAC	AAAAGnACGC	ATCACCAnTA			400

## (2) INFORMATION FOR SEQ ID NO: 4051:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4051:

5 AGTGAAAATG ACTTTATCGG GCTGTTTCAGC GATATGGATT TGAGTTCAAC GCGACTAGGT 60  
 AACAAATGTCA AAGAACGTAC TGCTTTAATC TCTAAAGTCA TGGTTAATCT TGACGACTTA 120  
 10 CCATTCGTTT ACAGTGACAT GGAAATTGAT ATGTTAGGTG ATGCATATGA ATTCCCTAATC 180  
 GGGCGCTTTG CGGCGACAGC GGGTAAAAAA GCAGGCGAGT TCTATACACC ACAACAAGTA 240  
 TCTAAGATAC TGGCGAAGTT GTCACAGACG GTAAAGATnA ATTACGTCAC GTGTAACGAC 300  
 15 CCAACATGTG GgnTCCGGTT CATGTGTGTA ACGTGTGGT AAAGAACGCA AGTGATATCGT 360  
 TAATTCGGAC nAAGAACGTA ACAATACTAC nTACGACTTA 400

## (2) INFORMATION FOR SEQ ID NO: 4052:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 390 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4052:

30 TCCTACAACC CCAACAAGCA AGCTTGTGGT GTTGGGCTCT TCCCGTTTCG CTCGCCGCTA 60  
 CTAAGGGAAT CGAATTTTCT TTCTCTTCCT CCGGGTACTA AGATGTTTCA GTTCTCCGGG 120  
 TGTGCCTTCT GATATGCTAT GTATTCACAT ATCGATAACA TGACATAACT CATGCTGGGT 180  
 35 TTCCCCATTC GGAAATCTCT GGATCAAAGC TTAATTACAG CTCCCCAAAG CATATCGTCG 240  
 TTAGTAACGT CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGGC CCTTAATAAC 300  
 TTAATCnATG TTTTCCACCA TTTTnTATAA GTnCAAAGGC TTCACATACG GCTTCGGTTT 360  
 40 TTCATTAATT TTAAATGGCn CAATTTAACA 390

## (2) INFORMATION FOR SEQ ID NO: 4053:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4053:

55 AACATACCGA TGTATATAAT CTATACACAA AGGATAATTA CTTATGCAA GGCGGAGGAA 60

GTCGATTGCG AATGATTTAA GAGGGAACAT GGATGCGAGT GAATTCCGTA ATTACATTTT 180  
 AGGCTTGATT TTCTATCGCT TCTTATCTGA AAAAGCCGAA CAAGAATATG CAGATGCCTT 240  
 5 GTCAGGTGAA GACATCACGT ATCAAGAAGC ATGGGCAGAT GAAGAATATC GTGAAGACTT 300  
 AAAAGCAGAA TTAATTGATC AAAGTCGGTT ACTTCATTGA GCCACAAGAT TTATTCAGTG 360  
 10 CGATGATCGT GAAATTGANA CGCANGATTT CCGATATAGA 400

## (2) INFORMATION FOR SEQ ID NO: 4054:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4054:

GTAAGACCAT CGTACTTGAG TCTTCAAGTG TTCTTGATAA AACGGAACGA GAGACTTGGT 60  
 ATTTTTCGAA CAAATCTTTC ATTAACACAC CGACCATAAT AATTACAATC GAAGCAACAC 120  
 25 CTGCAGCGAA TACAAGCGCA ATACAACAAA TAACAGTAAT ACATATTAAA CTTCTACAG 180  
 AATGGATGCC TTTAGAAATA GTAGTTAATA AGACTTCTAA ACATCCTGCT TTTCTACAA 240  
 30 TACCTGCAA TGCATATCCG CAAAATATCG TTACTAATAT TTGGGnCATA CTCATCATAC 300  
 CACCCTGTTT TAACAAGCTT TCACACTGGA TGAATATGAG nTGATGTATC ATTGATCGTT 360  
 AAACCCTAAT GTGCTTTGAA CCATCGTCAT TTGAATGTGA 400

## (2) INFORMATION FOR SEQ ID NO: 4055:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4055:

CGTCTACAAG TTCAAATTC AAGTCTTCCA TAATTGGTTT AACATCACT TCTACTTGTT 60  
 CTGTAATTTT ACTCATACAG GCCTCCCTTT TTGGCAAATA GAAAGAGCG GGAATCTCCC 120  
 50 ACTCTTCTGC CTGAGTTCAC TAATTTTTAA GCAACTTAAT TATAGCATAA GTTTATGCTT 180  
 GAAACAAATG ACTTCACTAT TAATCAGAGA TTCTTGTAAG AGTTTGTTCC TTTATTTTAC 240  
 CATTACATTT GAATAGACTC GTAAGACATT GAAAAGAAAT ACGGGCATAA TTTTGTGTCC 300

TCATTTTACA TATCAAATAT CGGAAGTTGA GCTTTATCTG

400

## (2) INFORMATION FOR SEQ ID NO: 4056:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4056:

ATTTTGGTTT ACTTCATGTT GAGTTTTAGA CATTTTAACC ATCTCCAATA TAAAAATAAA 60  
 TTAAATTAAA TTCTCAGGGA CTTCATGAC GCCACCTGTA TTTGCGCTAG TTACTAGGGC 120  
 AGTATAACGA GCTAGATAAC CTGTTTTTAC TTTCGCTTTA AATGGTGTTA AAGATTCTCG 180  
 GCGACGCGCT AGAACATCTT CAGGCTGGTT TACGTTTAAT GTACGATTTG TTAAATCAAT 240  
 AGTAATCTCA TCACCATCTT CAATTAAGGc AATTGGTCCA CCAGATGCAG CTTCAGGGGA 300  
 AATATGACCA ACTGcAATAC CTCTTGTTGg ACCGGtAAAA ACGCCCATCA GTKAATTAAT 360  
 GCaACATCTT TACCTAAGCC GCGaCCAACA ATAGAGGAAG TAGGTGCTAA CATTTTCAGG 420  
 nCATACCTGG GTCCACCTTT TAGGTGCCTT TCantATCTn ATGGACAACG ACGTGGGCCT 480  
 G 481

## (2) INFORMATION FOR SEQ ID NO: 4057:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4057:

TTTTTGCTG GCAACGTTCT ACTCTAGCGG AACGTAAGTT GGCTACCATC GTCGCTAAAG 60  
 ACCTTTCTTG ACTTGTGACA ATCGCTTGCT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC 120  
 ATTTAGCTCT ACTAAACTCG TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA 180  
 CTTGCCAAG CCATTTTTCT TTGTGTTTAC TTTTATTTT GGACGTTTTA GACATAAAAA 240  
 AAAGAGACCT TCGGGTCTCA ATCGGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT 300  
 ACTCTAGCGG AAGTAAATTG GGCTACCAnc GACGCTAAGA ACCTTTCTTG GACTGTGACA 360  
 ATCGGCTGcn TCTGTnCCT 379

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4058:

CTGCATCACT GCCATAAAAA CTACCGTCAG CAGCGATAGn CGGCCAATCA TACCAGGAAC 60  
 AAGACCGGGC TTGTCAGCGA TACTAACAGC GATATATCCA GCTAGTATTG GAACCATAAA 120  
 TTTAAAGGCT AACTACCAA TGTTTTCAAT GGATTTCCTAA AATGAATCAT CTGGGATGAC 180  
 TAATCCTTTT GATGTCGTTT CACCGCCTAG AGTCAGCGCG ATGGCGATAA GGAGTCCACC 240  
 AACTACGATA AAAGGAACCA TAAACGATAC ACCGTTTCATT AAATGTTGAT ACACCATTG 300  
 AATACCATTG TAGACTnACC GCGATCTTTC GAATGATAAT TTGTTTCAGA TGGTTAAATA 360  
 GGCGCATTTG ATTTAATGAT ACGTGGATTT GGACCCTCGG 400

## (2) INFORMATION FOR SEQ ID NO: 4059:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4059:

TTAAAAAACT GCCTGGCAAC GTTCTACTCT AGCGGAACTA AGTnGAnCTA CCATCGACGC 60  
 TAAGGAGCTT AACTTCCTGTG TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC 120  
 CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG TAAGTAAAAG TGATTTTGCT 180  
 TCGCAAAACA TTTATTTTGG ATTAAGTCTT CGATCGATTA GTATTGTCGA GCTCCACATG 240  
 TCACCATGCT TCCACCTCGG AACCTATTAA CCTCATCATC TTTGGAGGGA TCTTATAAAC 300  
 CGAAATTGGG GAAATCTCAT CTTGAGGGGG GCTTnCATGC TTAGATGCTT TCCAGCACTT 360  
 ATCCCGT 367

## (2) INFORMATION FOR SEQ ID NO: 4060:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4060:

5 TTCCGnACTC ACATAGCGAC TCAGGATTCA GACAGCGCAT TCAGATTGAG ACACCGCATT 60  
 CAGATTGAGC ATAGCGATTG AGCATTCCGC ACAGTGACTC AGnATTCCGA CAGTGACTCG 120  
 GATTGAGATA GCGATTGAGA TTCCGACAGT GACTGAGATT CCGACAGTGA CTCGACTCA 180  
 10 GACAGTGATT CGGATTGAGC GAGTGATTG GATTGAGATA GTGATTCCGA CTCCGACAGT 240  
 GACTCGGATT CAGATAGCGA CTCGACTCG GATAGCGACT CGGATTGAGA TAGCGATTG 300  
 GACTGAGATA GCGATTGAGA ATCAGACAGC GATTGAGATT CAGACAGCGA CTCGACAGT 360  
 15 GACTGAGATT CAGA 374

## (2) INFORMATION FOR SEQ ID NO: 4061:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 432 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4061:

25 AAAATCATAA TATTTGGCAA TTTTTTCAAC TTGACTCTGG TCCTTCTGCA TAACTGCCGT 60  
 30 AAATAATTCA CCTTCATCAC ACGCTGTACC TACCAATAAT CCCTCAGGAT ATTCATCTAA 120  
 CAATGAACGT GGAAATTCGAG GTGTACGGTA GAAATACTTC ACCAATGATG CACTTACAAT 180  
 TTAAATAGA TTTTAAGAC CTTGTTGGTT TTGTACAATT AATGTGACAT GACTAGGTCT 240  
 35 TGCACGTTTA TATGCATCTT CATTACTGAG TTTTTrGTtG ATTTCGTTAT GATTTAATAC 300  
 GCCTAAWTCy TTCATTGTG GAACCATTTT TATGAAAATG TAAGCTGTTG CTTCTGTATC 360  
 ATAAATGGCA CGGTGATGTT GCGTTAATTC TACGCCATAT TTTTAGCCA AGAAATTCAA 420  
 40 ACCATGTTTA CC 432

## (2) INFORMATION FOR SEQ ID NO: 4062:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4062:

55 TATCTTCGTT CTCAATAGAA TGATTTAAAC CTTCGATTTC TTTATCTAAA TGACTIONCAA 60

TTTTTCTTC AACTAAGTCA CGATATAATG TTTTGAATT TTCGTTCAAT TTCGATTTCGT 180  
 GATTTTGAAT ACTTTTCTTC CACACAAATG TATACCTATT GGCATTAGCT TCTACTTTTG 240  
 5 TACCATCAAT AAGATTTTGC TTAAACATT GACTATGAAA CTGGGATAAA TAAAGANTCA 300  
 ATTAACGCAT CAGTATTAGG GANTCACTCT AATACGATTA ATAGTTTTTA TAAGAAGGTG 360  
 nTTGGATTG GAGCTAACCA CATCCA 386

## (2) INFORMATION FOR SEQ ID NO: 4063:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4063:

TAGGAGAGCG TTCTAAGGGC GTAGCATGAT CGTAAGGACA TGTGGAGCGC TTAGGAGAAT 60  
 GCCGGTGTGA GTAGCGAAAG ACGGGTGAGA ATCCCGTCCA CCGATTGACT AAGGTTTCCA 120  
 25 GAGGAAGGCT CGTCCGCTCT GGGTTAGTCG GGTCTAAGC TGAGGCCGAC ACGTAGGGCG 180  
 ATGGATAACA GGTGATATT CCTGTACCAC CTATGAATCG TTTTAATCGA TGGGGGACG 240  
 CATAGGTATA GGCGAGGTGA CGATTGGGAT TGCACGCTT AAGCAGTAAG GCTGAGTATT 300  
 30 AGGCAAATCC GGTACTCGTT nAAGGCTTGA GCTGTGGATG GGGAGAAGAC ATnGAGTCTT 360  
 CGAGTTCGTT GnnTTTCACA ATGGCC 386

## (2) INFORMATION FOR SEQ ID NO: 4064:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4064:

TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTT 60  
 TACTCTAGCG GAACGTAAGT TGGAGCTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT 120  
 50 CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT 180  
 ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTTGCTTC GCAAACATTT ATTTTGATTA 240  
 AGTCTTCGAT CGAnTAGTAT TCGTCAGCTC CACATGTCAC CATGCTTCCA CCTCGAACCT 300

AGGGGGGGCT TCATGCCTTT AGAATG

386

## (2) INFORMATION FOR SEQ ID NO: 4065:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4065:

AATTCTTTTCG CTAATTGAAT GACAACACTT TGTTTTACGC CTGAAATGGC TTCTTGCCAA 60  
 GCAGGTGTAT ATTTTGATTG TGCATCGTCG TATCCTTTTG ATTCTAATTT ATGATCAAAA 120  
 CGACGCACGC CATATTGACT TGCCATTAAAG TCAAAAATTG TAGCAATACG GACTTTGTCA 180  
 CCATTTGCTA AAGTGACTTG TCGAGTTGGA ATTGGACGAT TGAATATCCC ATCTCCATCA 240  
 CTATCAAAGT ATGGGAATTG AATTGTTTCT AATTCGTATC CACCTTCTGT CATTGATAAT 300  
 GTAGGGTTAA TTTTAGAACC ATCTTCTGTT TCTAGTTTAA AGTTCCACTT CTTACCTTCT 360  
 TCCCAACGTG GACCCATGGT GCCATTAnGn ACTACTAAAC 400

## (2) INFORMATION FOR SEQ ID NO: 4066:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4066:

ATTTTGAAAT TGAGAAAACA ACTTATTGAA AAACATAATC TTTACGGTAA CATGGGTTCA 60  
 GGAACAATCG TTATTAAAT GAAAAACGGT GGGAAATATA CGTTTGAATT ACACAAAAAA 120  
 CTGCAGAGCA TCGTATGGCA GACGTCATAG ATGGCACTAA TATTGATAAC ATTGAAGTGA 180  
 ATATAAAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA TCGGAAAAC AAGAAGTTAA 240  
 GTGACAACGG TTTACATGTT GCTTAGCTTC TTTTATTATG CGTAATGATG TAAAAAGACG 300  
 NATATTCATT TGTTTGTAAG AGTGGCATTG TATGTCTTAA AGTGACGnAA CTTCCAATGT 360  
 GCCCAGTGTT TGATTCACAT CAAATCCATT TTTATTTAAC 400

## (2) INFORMATION FOR SEQ ID NO: 4067:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4067:

	CCTCATTCCA GGAAGGAATG TATTCTAAGA GTTGAAATAC TCCCGCATTG TTATTAAATT	60
10	ATGGAGCGGA AGATAGGATT TGCACCTATA CCTCGTTCCG GGAAGGAACG TGTTCTAAAA	120
	GTTGAACTAC TCCCGCATAA ACCTGGAGGC GGCAACCGGA TTTGAACCGG TGATAAAGGT	180
	TTTGCAGACC TCTGCCTTAC CACTTGGCTA TGCCGCCAAT AACTGGGCTA GCTGGATTCTG	240
15	AACCAACGAG TGACGGAGTC AAAGTCCGTT GCCTTACCGC TTGGCTATAG CCCATTAATA	300
	ATAAGGGCGG CTGAAGGGGA TCGAACCTC GAATGTCGGA ACCACAATCC GATGTGTTAA	360
20	CCACTTCACC ACAGCCGCCA TGGCAGGGGC AGTAGGAATC	400

(2) INFORMATION FOR SEQ ID NO: 4068:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
25	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4068:

	TATCTAATAG TTTTACTTTA AGTCCAGCAT TCACAAAAG TGCTGCCAGT TGAGCGCCCA	60
	TTGTGCCTGC GCCAAGAACG GTTACTTTAT TAATTGTCAT AGTGATTCCT CCAATTTAGT	120
35	TGAGGATAAG ATAACCATTA AGATAATTGG AATAACGTTG CTATTTTATA AAATTAATTA	180
	AGTATCTTTG ACAGTCATCT TAGCCTCTTA TTTAAGGAAA AAGCTTTATG CTTAAAATAA	240
	GTCTTTTTTA GTGAAATTAA TGCATCTCAT ATAATTATTT GCTATTTATA CGAAAGCAGA	300
40	ATCTCCAGTC AAAGCGCGTC CANTACTAAG GCATTAATTT CATGTGTACC TCGTACGTGT	360
	AAATCGnTTC TGCATCAGnG AGGAAACGTG CAATATCATA	400

45

(2) INFORMATION FOR SEQ ID NO: 4069:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 356 base pairs
	(B) TYPE: nucleic acid
50	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4069:

AAAAAGAAGA ATTGAAACGC CATATAAAGT AACGTTAAAT AATAACGAAA AAAGGGCACT 120  
 ATTCAAACAA TTAGCGTATG TTGAAGGGTT TGAAAAATAT CTTCATAAAA ACTTCGTTGG 180  
 5 TGCAAAGCGT TTTTCAATTC nCGGGGTAGA CGCACTTGTA CCGATGTTAC AACGTACTAT 240  
 TACGATTGCT GCGAAAGAAG GTATTAAAAA TATACAAATA GGCATGGCTC ACCGTGGGAC 300  
 10 GTTTAAACGT TTTTAAACGCA TGTnCTTAGA AAAAACCgTA CGAAATGATG ATTTCh 356

## (2) INFORMATION FOR SEQ ID NO: 4070:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4070:

AAACGTTTtag GGAAAATTAT CACACAGATA CAACAATACA CAGATATTGA TTACCCGATA 60  
 GCGATTGTCT TTCAAGCATC GTGTTTTAAC GAGTTTGTG TTAAGGGGCG TTTAAGTAAT 120  
 25 ATTATTTCAA AATTGCAACA CTATTCAATT GAGGCGAAAC CAGGTATATG TATTATAGGG 180  
 GAAGTTGTTG ATTATACTGA AAACACTCCT AAATCATATG ATCCTATGAA GCAATTTTAT 240  
 30 GTAGTAAGTG GTTCTAAACA TGACGCCCTT ATGCTCTGTG AACATTATAT GACGAAGGTT 300  
 ATGGCTGTTG CTAAACCCCA ATGATACATC GAATGGGCAC CATTATCCAn TCGTCGCAAT 360  
 AATGGATTAC CCAAGGATGC CATTtAnTTA AGCCnGCCAn 400

## (2) INFORMATION FOR SEQ ID NO: 4071:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4071:

CCTCTGGAAG CCTTAGTCAA TCGGTGGACG GGATTCTCAC CCGTCTTTTCG CTA CTCACAC 60  
 CGGCATTCTC ACTTCTAAGC GCTCCACATG TCCTTACGAT CATGCTTCAA CGCCCTTAGA 120  
 50 ACGCTCTCCT ACCATTGTCC AAAGGnATnC CCACAGCTTC GGTAATATGT TTAGCCCCGG 180  
 TACATTTTCG GCGCATGTGC ACTCGACTAG TGAGCTATTA CGCACTCTTT AAATGGATGG 240  
 CTGCTTCTAA GCCAACATCC TAGTTGTCTG GGNAAAGCCA CATCCTTTTC CACTTAACAT 300

T

361

## (2) INFORMATION FOR SEQ ID NO: 4072:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4072:

ATGGTGACAA AAACATCGCA TTATTACTAG GTGTCGGCAC AGGCGTTTGT GGTGCTGCTG 60  
 CTATTGCCGC AGTCGCTCCA ATATTCAAAT CACGTGAAAA GGATACAGCT ATTAGTATCG 120  
 GTATCATCGC ATTGATTGGT ACGATATTTT CACTTATATA TACAGCTATC TACGCTATCT 180  
 TTTCAATGAC GACAAATGTT TATGGCGCTT GGTCTGGTGT TAGTCTTCAT GAAATTGnCA 240  
 CACGTTGTCT TAGCTGGTGG CTTTGGTGGT AGTGATGCAC TTAAAATTGC ACTTCTTGGT 300  
 AAAC TTGGTA GGAGTATTCT TACTGGATTC CCATTAACCA TCGTACTTAA TTTTAAATAT 360  
 GCGGTTnCCG TnCATCAGG AnTCATCTAG GCAAGGGGTC 400

## (2) INFORMATION FOR SEQ ID NO: 4073:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4073:

GCGACGATCA TTTTAGAATC CGCTGGGCG ATTAATTCTT TAGAAGTGGA TGAGGCAAAA 60  
 TGTTCAATTAT CAGGAACTAA AGCAGGTGCT GATATGAAAG ATGGTCTACG TATTCATGGT 120  
 GAAGACATGG GTACACTTTA TACCAAACAC GTTGAATTGG AAAACAAAGG CGTCGACTTT 180  
 TATGAAGGTA ATGAAGTGGA TGAAGCTGAA GAAGAAGCAA AAGCTTGGAT TGATGCAGTT 240  
 GTAAATGATA CTGAACCACT TGTGAACCGG AACAAGCAAT GGTAGTTACC AnAATTCTTG 300  
 AAGCGATTTA TCCGTCTGCC AAATCCAGGC CAAAGCCATT TACTTTGGAA TAACATChTA 360  
 CCGGTAAGGG GGCnCATCCT GGACCAAATT TAAAAGTTGG 400

## (2) INFORMATION FOR SEQ ID NO: 4074:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: lin ar

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4074:

TCTTCCTAAT	ACCTTTCCAC	GATCTTCAGC	TGGCGCCTCT	GCACTCGCAA	ACGCACTTGA	60
TGCATCAACA	ACACCACCAA	ATAGTCCCTG	CAATAACCTC	ACAAGTACAA	ACTGTAATGG	120
TGTCGTACAC	AATGCCATTA	AAAATAAGCA	TACCGCCAAA	CCAAGTAACG	CTCTTAACAC	180
CATCCATTTT	CGGCTGATCT	TATCACCTAG	CTTCCCCCAT	ATCGGCGGAG	TTATGCATCG	240
TCGTTACAGC	TGGAGCAGCA	ATCGCTATAC	CACTCCACAn	CTGTATTTCT	ACGGACTGAT	300
AGGATTTTGT	AGTGATGnCC	ATGATGAAAT	GGGCAATAAT	GGGCACAAGT	ACTGTTTCAGT	360
CCAGCCAATC	GTTATGAAAC	TGGACTGGGG	CCATnAAATG			400

(2) INFORMATION FOR SEQ ID NO: 4075:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4075:

GGTTCAGAAC	GTCGTATGnA	GTTCGnTCCC	TATCCGTCGT	GGGCGTAGGA	AATTTGAGAG	60
GAGCTGTCCT	TAGTACGAGA	GGACCGGGAT	GGACATACCT	CTGGTGTACC	AGTTGTCGTG	120
CCAACGCATA	GCTGGGTAGC	TATGTGTGGA	CGGGATAAGT	GCTGAAACTC	TAAGCATGAA	180
GCCCCCTCA	AGATGAGATT	TCCCAACTTC	GGTTATAAGA	TCCCTCAAAG	ATGATGAGGT	240
TAATAGGTTT	CGAGGTGGAA	GCATGGTGAC	ATnTGGAGCT	GACGAATACT	AATCGATCGA	300
AGACTTAATC	AAAATAAATG	TTTTGCGACA	AATCCACTTT	TACTTACTAT	CTAGTTTGAA	360
TGATAAATTA	CATCCATATG					380

(2) INFORMATION FOR SEQ ID NO: 4076:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4076:

TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA CGTGCAATCC AATCGCACGC TTCGCCTATC 120  
 CTACTGCGTC CCCCCATCGA TTA AACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA 180  
 5 TCCATCGCCT ACGCCTGTCTG GCCTCAGCTT AGGACCCGAC TAACCCAGAG CGGACGAGCC 240  
 TTCCTCTGGA AACCTTAGTC AATCGGTGGA CGGGATTCTC AnCCGTCTTT CGCTACTCAC 300  
 10 AnCGGCATTG TCACTTCTAA GCGGTCCACA TGTCTTACGA TCATGCTTnA AGGCCTTAGG 360  
 AAGGTTCTTA CCATGGTCAA 380

## (2) INFORMATION FOR SEQ ID NO: 4077:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4077:

GCAGGTCTGA CTCTAGAGGA TnCCACGCG CGCAAGATT AAATCGAAGA AACCAGCAAC 60  
 25 AGATTCTCTCA AAATAGCGCG GCGAACACG AAACATCAAA TAGTGACCT GCAGCTGGTA 120  
 ATGGTGTAGC ATCAACGCCA CCAAGTGCAC CAAGTGGCGA TACTGCACCA AATAATAATG 180  
 30 TTACGCAAAA TACCGCACCA AATAGTAATA ATGCGCCTGT ATCGACTACA CCACAAAGTA 240  
 CAAGGCGGGA AnAAAGATGG TCAAAGTTTT GTAGATATAA CAACAACACA AGTCAGCACA 300  
 GCTAACGAGA ACACACAAAA CATTACAGAT AAAGATGTTA AATCAATGGA AGCGGCATTA 360  
 35 ACGGGCTCTT 370

## (2) INFORMATION FOR SEQ ID NO: 4078:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4078:

AAACATTTTA TCAAATGGCA GAAGGACATG TGCCAAGACC ACCAGCGATG GTTGAAACAT 60  
 50 TGAATTATAT TAAAGAGTTT ATGAACCAAG TTGAGTCGCA TAGCTAGTAT GAAACGTGGT 120  
 GTGCGCATGG GAACTATCAA GCTTTGAAGA TGTGGTACTA CATGCGTTGG AATTAGGGAT 180  
 CGGTACTTTA TATGAAGACG TGCTGCTTCC ATTAAATGAG TGATGCGATT TTGGCATGAA 240

TAAGAGGGGC CAACCATTGT TAGAATAAC AACGGTTGGC TCTTTAATG T

351

(2) INFORMATION FOR SEQ ID NO: 4079:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4079:

15	TTGAAGTAAC TAAATTAATA TTATGTTGTT CAATTAAAAG CTTCATACAA ACCTAATCTA	60
	TTTGCACTCC ACCGCTAACA CGAACAATT GTCCGGTTGT ATAACCTGAT TCTTCTGACG	120
	CTAATAGCAC ATAAGTTCCA CATAACTCAA CAGGTTGACC TGCACGACCT AAAGGTGTTT	180
20	TTTGACCAAA TGTGGGATT TACTTTGAG GTTGTCCACC AGAAATTGT AATGGTGACC	240
	AGAATGGACC AGGCGCTACA CAGTTCACCT TAATTCCTTT TGGTCCTAAT TCTTCTGAAA	300
	AACTTTTAGT TAATGAAATA ATTGCTGCCT TTTGAAGGGG CATAATCCAT GAAGAATAG	360
25	GCCAGGGAGT AAAACCCCTGG ACNAAAGAAG CCGTGGAAT	400

(2) INFORMATION FOR SEQ ID NO: 4080:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4080:

	TCGTTGGACA CAATCTGAAA AATAAATAGA TATAAATTCG CGAGATATAT TCGTATTTAT	60
40	AGTAAAATTA AATAAGAGA TTATATAACA CGAGGAGTAG TAAGTATGAA ATTTGAGAAA	120
	TATATAGATC ACACTTTATT GAAGCCTGAG TCAACACGTA CGCAAATCGA TCAAATCATC	180
	GATGAAGCGA AACATTACAA TTTTAAATCT GTATGTGTGA ATCCAACACA TGTAAATAT	240
45	GCAGCAGAGC GACTAGCTGA TTCAGAGGTG CTCGTTTGTG CGGTAATAGG ATTCCCATA	300
	GGTGCGTCGA CAACTGGCAA CGAAAGCATT TGAAACAGAA GATGCAATTC AAAATGGTGC	360
50	AGATGAATTG GACATGGTCA TCCACATCGG CGCATTAAAA	400

(2) INFORMATION FOR SEQ ID NO: 4081:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 359 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4081:

	CGACTAGTGA GCTATTACGC ACTCTTTAAA TGATGGCTGC TTCTAAGCCA ACATCCTAGT	60
10	TGTCTGGGCA ACGCACATCC TTTTCCACTT AACATATATT TTGGGACCTT AGCTGGTGGT	120
	CTGGGCTGTT TCCCTnChCG AACACGGACC TTATCACCCA TGTTCTGACT CCCAAGTTAA	180
	ATTAATTGGC ATTTCGGAGTT TGTCTGAATT CGGTAACCCG AGAGGGACCC CTCGTACCAA	240
15	ACAGTGCTCT ACCTCCAATA ATCATCACTT GGAGGCTAGC CCTAAAGCTA TTTACGGAGA	300
	GAACCAGCTA TCTCCAGGTT CGATTGGAAT TTCTCCGChA CCCTCAGTTC ATCCGCTCA	359

(2) INFORMATION FOR SEQ ID NO: 4082:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 379 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4082:

30	TTTGACATTT AGTGTAAGCG TnTTACAAAT AAAGCGTGT TTTTTTGAAT TAAATGCATT	60
	TCACATTAGT ATTCATATTA TTTTtaggag GAATTTATAT GACATTTGAA AAAGAAACGG	120
	TCTTAAAAAC ATTATTTTCT GAAGATGTAC TTAGTATTGC TAAAGGTTTA ACAGACGGTG	180
35	AAGTCGAATT TTTACAACAA GTAGATTCAT TGGCTAGAAA GTAAGTACCG TGGAAAATAT	240
	TAATCAACAT TGGATAGACG CTACTGTACC CGAGGACTAT TTAAAGATC TGGGGAGAAT	300
	TAAATTATTT TAACAATCCA TTACTTTACA AGGGATCGTC CAAACGCCAA AnGGCCTAGT	360
40	CCAACTATTT nCAGTTTTT	379

(2) INFORMATION FOR SEQ ID NO: 4083:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4083:

	TTGAAACAGC CAGAGGTGTT TTATACCCAG GTGTTTCAGA TATGTATGAT GCGAAACAAT	60
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TTGGAACATA TGGTCCTAAC AAAGATGTTG TAGGCATATC TACTCGTCTT ATTAGAGTGA 180  
 CATATGATAA TAGACAAACA GAAGATTAA CTATTTTATC TAAAGTTAAA CCTGACCCAC 240  
 5 CTAGAATTGA CGCAAACCTCT GTGACATATA AAGCAGGTCT TACAAACCAA GAAATTAAAG 300  
 TTAATAACGT ATTAATTAAC TCGTCCGTGA AATTATTTAA GCCGATAATA CACCATTAAA 360  
 TGTnCAAT ATTACCCnGG GTAGCGGGTT TTAGTTCGG 400

(2) INFORMATION FOR SEQ ID NO: 4084:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4084:

AGCATATCGT CGTTAGTAAC GTCCTTCATC GGCTTCTAGT GCCnAGGCAT CCACCGTGCG 60  
 CCCTTAATAA CTTAATCTAT GTTTCATCC TACAGGAAAC GCGTTAGTAA TCTTGTGAGT 120  
 25 GTTCTTTCGA ACATAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC 180  
 ACTCGGTTTT GCTTGGTAAA ATCTATATTT TACTTACTTA TCTAGTTTTC AATGTACAAT 240  
 TTCTTTTITAG TCAAGCGCTC GCATAAGCAA TATCATTTA ACCAAAAAAT ATTTGAATGT 300  
 30 TAAATAACA TTCAAAACTG AATACAATAT GTCACATTAT TCCGCCATCT nCTGAAGAAG 360  
 ATGTnCCGA ATATnATCCT TAGAAAGGAG GTGGATCCCA 400

(2) INFORMATION FOR SEQ ID NO: 4085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4085:

TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGAGAC TAGCGGGATC GAACCGCTGA 60  
 CCTCCTGCGT GCAAAGCAGG CGCTCTCCCA GCTGAGCTAA GCCCCCAAAT AGGTATTAAA 120  
 TTAATGGTGG GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCGCTCT 180  
 50 GAACCAGCTG GAGCTATAGG CCCATTAAAT TGGAATGAAC AAACATTCAA AACTGGAATA 240  
 CAATATGTCA CGTTATTCCG CATCTTCTGG AAGAAGATGT TTCCGAATAn ATCCTTAnGA 300

AAGCATTGTG TCCACCTTC GACGGCTGAG CTCCTAAAAG

400

(2) INFORMATION FOR SEQ ID NO: 4086:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4086:

GTCATTGGAA ACTGGAGnAC TTGAGTGCAG AAGAGGAAAG TGGAAATCCA TGTGTAGCGG 60  
 TGAAATGCGC AGAGATATGG AGGAACACCA GTGGCGAAGC GACTTTCTGG TCTGTAAGTG 120  
 ACGCTGATGT GCGAAACGTG GGGATCAAAC AGGATTAGAT ACCCTGGTAG TCCACGCCGT 180  
 AAACGATGAG TGCTAAGTGT TAGGGGGTTT CCGCCCCCTTA GTGCTGCAGC TAACGCATTA 240  
 AGCACTCCGC CTGGGGAGTA CGACCGCAAG TTGnAACTC CAAAGGAATT GACGGGCGCA 300  
 CAAGCGTGGG AGCATGTGGT TTAATTCGAA CCAACGnATA GAACCTTACC AAATCTTGGA 360  
 C 361

(2) INFORMATION FOR SEQ ID NO: 4087:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4087:

GACCTTGCAG GACTCGAACC TGCACCGAA CGGTTATGAG CCGTTAGCTC TAACCAACTG 60  
 AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TGGCGGTGGA GGGGATCGAA 120  
 CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC CGCCTTATAT 180  
 AGTTTGTAAG TAATATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC TGCGTGCAAA 240  
 GCAGnCGCTC TCCCAGCTGA GCTAAAGCCC CCATAAATAA TTACAGTATA TCGGGAAGAC 300  
 AGGATTCGAA CCTGCGACCC CTTTCCCCAAA CCAAGTGCTT TTACCAAGTT GGTACTTCCn 360  
 GTATAATTTA ACGGGCCCCGA TAGGAGTTTCG GAACCCCTAA 400

(2) INFORMATION FOR SEQ ID NO: 4088:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4088:

	AGCTATTATT TTTGACAGAT TCCATATCGT TCAACATTTA AATAGAGAAC TTAATAAGTA	60
10	TCGTGTACAA GTTATGAATG AATACCGTAA TAAAAAAGGA CCTGATTATA CAATTTTTAA	120
	GAATAACTGG AAAGTCCTAT TGATGGATAC TAGTAAAACC ATATTTAGTA AATACAGATG	180
	GAATAAATCT TTTAAGGCTT ATAAACGCTC ATCTGACATT GTAGGAATTC ATGCTTTCAA	240
15	AAGACGATAT ACTACGACAC TCCTACGAAC TTGTCCCAAG GGATTACGGA AAAGGCCCTA	300
	AGGGTTATGT TAATTGGCCC TAAATTTATT AAATGCGTTT GAAATTCAGT TAGTTAAAAA	360
	GTCTGTGAGT GAnGGGTGTA TGGGAAAGTG GTTAAATAT	400

20

(2) INFORMATION FOR SEQ ID NO: 4089:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 374 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4089:

	ATCGTTTTAG ATAAGACGGG TACATTACAA ATGGTCGTCC AGTCGTGACA GATTATCATG	60
	GTGACAATCA AACGCTACAA CTACTTGCTA CTGCTGAAAA AGATTCTGAA CACCCATTGG	120
35	CAGAAGCCAT TGTCAATTAT GCAAAAGAAA AGCAATTAAT ATTAAC TGAG ACAACAACAT	180
	TTAAAGCAGT ACCTGGGCCA TGGTATTGAA GCAACGATTG GATCATCACC ATATATTGGT	240
	TGGTAACCGT GAAATTAATG GCTGACAATG GATATTAGCT TGCCTAAGCA TATTTnnGGA	300
40	TGGATTTAAC ACATTATGAA CGAGATGGTA AACTGCTAG CTCATTGCTG TTGAATTATT	360
	nCATAACGGT ATCA	374

45

(2) INFORMATION FOR SEQ ID NO: 4090:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 367 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4090:

TTAATAACGT ATTAAATAAC TCGTCAGTAA AATTATTTAA AGCAGATAAT ACACCATTAA 120  
 ATGTCACAAA TATTACTCAT GGTAGCTGTT TTTGTTGGT TGTGACAGTA AGTGACGCGT 180  
 5 TACCAAATGG CGGAGTTAAA GCAAATCTT CAATTTCAAT GAACAATGTG ACGTATACGA 240  
 CGCAAGACGA ACATGGTCAA GTTGTTACAG TAACAAGAAA TGAATCTGTT GATTCAAATG 300  
 10 ACAGTGCACC AGTAACAGTG ACACCACANT TACAAGCAAC TACTGAAGGC GCTGTATTTA 360  
 TTAAGTT 367

## (2) INFORMATION FOR SEQ ID NO: 4091:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4091:

TAATATTATA TTGCTAGTAG TTGACTGAAT GAAATGCGC TTGCAACAAG CTTTTTTTCAA 60  
 25 CTCTAGTCAG GGGCCCCAAC ACAGAGAATT TCGAAAAGAA ATTCTACAGG CAATGCGAGT 120  
 TGGGGTGTGG GCCCCAACAC AGAGAATTTT GAAAAGAAAT TCTACAGGCA ATGCGAGTTG 180  
 GGGTGTGGGC CCCAACACAG AGAATTTTGA AAAGAAATTC TACAGGGCAA TGCGAGTTGG 240  
 30 GGTGTGGGCC CCAACATGAG AGAAATTGGA TTCCCAATTT CTGACAGACA ATGCAAGTTG 300  
 GCGGGGGCCC CAACACAGAA GCTGGACGAA AATCCTTGAA CGAATGAATG TGGCAATTGG 360  
 35 CGGGGGCCCCA ACACAGAAGn TGACGAAAAT nCTnGAACCA 400

## (2) INFORMATION FOR SEQ ID NO: 4092:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4092:

GCATTTCTCA TAACACAAGG AATTTCAACA AGTCCGGCTA CTGGATCACA AACTAAACCT 60  
 AATAAATTAC TTATCGCTAA TGCCATAGCG TGCCCGGATG CTTCTGGTGA TCCTCCGAAT 120  
 50 ATAGCTACTG CTGCAGCTGC GGCCATTGCA GATGCTGAAC CAACTTCAGC TTGGCAGCCA 180  
 CCTGTTGCAC CAGCTACACT TGCATTGTTT GCTACGACAC GCCCAAACAA TGCTGAAGTG 240

CCGGGAATGG TAnCCGAGGG AAnCAGCTGT GGGCGTTGCA CAAATAATAC CCCATCGCAG 360  
 CATTTGACCT TCATTGGTT GCAATGGGAA CCTTTGACTG 400

(2) INFORMATION FOR SEQ ID NO: 4093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4093:

TGACTTACGT ACTGTTCAAC CAATCGATGT TGACACAATT GTAGCTTCAG TTGAAAAAAC 60  
 TGGTCGTGCA GTTGTAGTTC AAGAAGCACA ACGTCAAGCT GGTGTTGGTG CAGCAGTTGT 120  
 AGCTGAATTA AGTGAACGTG CAATCCTTTC ATTAGAAGCA CCTATTGGAA GAGTTGCAGC 180  
 AGCAGATACA ATTTATCCAT TCACTCAAGC TGAAAATGTT TGGTTACCAA ACAAAAATGA 240  
 CATCATCGAA AAAGCAAAAG AAACTTTAGA ATTTTAATAC ATTTTAAAAG TTAACGAATT 300  
 AGCGTATTTT AGTCTCATTG ATTAAnATGA AATGnGnTAA TTTACGGAAT CCTA 354

(2) INFORMATION FOR SEQ ID NO: 4094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4094:

CGTTAACATG AAGTTACGTT CTTTATAAA AAGATTTAAA CGCGTTATTA ATCTTGTGAG 60  
 TGTTCTTTCG AACACTAGCG ATTATTTCTT ATGAATTCAA GCTTATTTAA AACTCTTTAT 120  
 TCACTCGGTT TTGCTTGGA AAATCTATAT nTTACTTACT TATCnAGTTT TCAATGTACA 180  
 AATAATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC TCGGTGCAAA GCAGGCGCTC 240  
 TCCCAGCTGA GCTAAGCCCC CAAATAGGnA TTAAATTAAT GGTGGGCCTA AGTGGACTCG 300  
 AACCACCGAC CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT A 351

(2) INFORMATION FOR SEQ ID NO: 4095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4095:

5 ATTGTTGCGA CTGGCACACC CGAAGATATT GCTCAGACAA AGTCATCATA TACAGGAAAG 60  
 TATTTAAAAG AAGTACTTGA ACGAGATAAA CAAAATACTG AAGATAAATA AGATTAAAAG 120  
 AAGTGAAGGA TGTATAATT TATCCTTCGC TTCTTTTAT TAATTAGTA ATGAATAGTA 180  
 10 GAAAGAAAAG ATGCGTAAAA AGAATTATGT TAAGATAGGG TCAATCTAGA GTAGTTAAAC 240  
 ATAAATCGAA CTnGGAGTGG GACAGAAATG ATAAAGAATC ACTAATGATT TATTATGTAG 300  
 TGGTTCTTTG TCATTAGCCA CAGCTATTG TGTACTTAAA AnTAGGTATG CCAGTGTGCA 360  
 15 CTCCTTGAGA GGAAATACTn ATTT 384

## (2) INFORMATION FOR SEQ ID NO: 4096:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 387 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4096:

CTGCATCTTC ACAGGTACTA TGATTTCACC GAGTCTCTCG TTGAGACAGT GCCCAAATCG 60  
 30 TTACGCCTTT CGTGCGGGTC GGAACCTACC CGACAAGGAA TTTCGCTACC TTAGGACCGT 120  
 TATAGTTACG GCCGCCGTTT ACTGGGGCTT CGATTCTAG CTTCGCAGAA AGAGCCGACT 180  
 CCTCTGAAC CTTCCAGCAC CGGGCAGGCG TCACCCTGAT GACATCACCT TACGGTTTAG 240  
 35 CAGAGACCTG TGTTTTTGAT AAACAGTCGC TTGGGCCTAT TCACTGCGGC TCTTCTGGGC 300  
 GTTAACCCTn AAAGAGCACC CTTCTCCCG AAATnACGG GGTCAATTTG GCCGAGTTCC 360  
 TTAACGAGnA TTCGCTCGGT GCAACTT 387

## (2) INFORMATION FOR SEQ ID NO: 4097:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4097:

50 CCACTCACAT TCACACATCG ATTCACACAC CGCACTCAGC ACTCAGnATA CCGCATTACG 60

TCAGATAGCG ACTCAGATTC GGATAGCGAC TCAGACTCAG ATAGCGATTG AGATTTCAGAT 180  
 AGCGATTTCGG ACTCAGACAG TGATTTCAGAT TCAGACTCAG ATAGCGACTC AGATTTCGAC 240  
 5 AGCGATTTCAG ACTCAGACAG CGACTCAGAC TCAGACAGTG ATTCAGATTC AGACAGCGAC 300  
 TCAGATTTCAG ATnGCGACTC AGACTCAGAT AGCGACTCAG ATTCAGATAG CGATTTCGGAC 360  
 TCAGACAACG ACTCAGATTC AGATAGCGAT TCAGATTTCAG 400

(2) INFORMATION FOR SEQ ID NO: 4098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4098:

TCGTACCTGA ACTACTTTGT ATTAAAATAG TTACAACGAT ACCTGCAATA ACACCTAATA 60  
 CTGGATTGTA TGTAATTTG TTTAAAATAT CTCGTAGCCT GTCTCCTGCT GATGCTTGAA 120  
 25 GCCCGTCTCC CATGATTTTT AAGCCGTAAA GGAAAATACC TAAACCACCT AAAAAGGAGA 180  
 AAATGACTTC TGTAACCGAC ATTTCCATTA TTTCACCTCA AATAAGCTTT ATATTTAGAT 240  
 TATCGCTTAT AATTGTAAAT TTAATGTTAA GATTAGGTAA AATTATTTAA CAATATATGT 300  
 30 TATTTGTATA TGACTTGTA AATATCGTCA CTTATTATGT AAATTTTCAG TGGTGGnAAT 360  
 GGCCAGTTTG CCAAGCACTG GTTTGACCAn ATGGnGGCAn 400

(2) INFORMATION FOR SEQ ID NO: 4099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4099:

ATCCTTTTCC ACTTAACATA TATTTTGGGA CCTTACCTGG TGGTCTGGGC TGTTTCCGGA 60  
 CCGAACACGG nACCTTATCA CCCATGTTCT GACTCCCAAG TTAAATTAAT TGGCATTTCG 120  
 AGTTTGTCTG AATTCGGTAA CCCGAGAGGG CCCCTCGTCC AAACAGGGCT CTACCTCCAA 180  
 50 TAATCATCAC TTGAGGCTAG CCCTAAAGCT ATTTCCGAGA GAACCAGCTA TCTCCAGGTT 240  
 CGATTGGAAT TTCTCCGCTA CCCTCAGTTC ATCCGCTCAC TTTCAACGTA ATCGGTTTCG 300

## (2) INFORMATION FOR SEQ ID NO: 4100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4100:

TAGAACTTGT	TGCCAAACAG	CATGCTTAAT	TTCAATATCT	TCTTTGACTG	CTTCGATATA	60
TAAATCAGCA	TCATCATTTA	CCAAGTCATC	ATCAAAATTA	CCATATGTTA	AATGACTCGC	120
TAGATTTAAG	TCGAATAGTA	GCGGCCGTTT	CTTATCTGTA	ATTTTATCGT	AAGATTTTTT	180
CGCAATGAGA	TTTGATCGT	TTTGTCCAC	TACAATATCT	AATAGTTTTA	CTTTAAGTCC	240
AGCATTCA	AAAAGTGCTG	CCAGTTGGAG	CGCCCATTTG	GCCTGCGCCA	AGAACGGnTA	300
CTTTATTAAT	TGGTCATAGT	GAnTCCnCCC	ATTAGTTGA	GGGATAAGAT	AACCATT	357

## (2) INFORMATION FOR SEQ ID NO: 4101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4101:

TAACTCAGGC	TGGGGACATA	AATCAATATT	CTATGCTCTA	CGAATTATAT	TGGCAGTAGT	60
TGACTGGnCG	AAAATGCGCT	TGTAACAAGC	TTTTTTCAAT	TCTAGTCAGG	GGCCCCAACA	120
CAGAGAATTT	CGAAAAGAAA	TTCTACAGGC	AATGCGAGTT	GGGGTGAGGG	CCCCAACACA	180
GAAGCTGACG	AAAAGTCAGC	TTACAATAAT	GTGCAAGTTG	GGGATGGGCC	CCAACAAAGA	240
GAAATTGGAT	TCCCAATTTT	TACAGACAAT	GCAAGTnGGG	GTGGGACGAC	GnGATAAAATT	300
TTGCGAAAAT	ATCATTCTG	TCCCACTCCC	ATCAAAAGAA	TGACAT		346

## (2) INFORMATION FOR SEQ ID NO: 4102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AATGATGAAA ATCAATTAGA CAAAGCAGGT AAATTAAGTG ATGTCGCGTC ATTTAAGGAA 60  
 GCGATTACA ATCGAGAATC ACAAAGTACA ACTGGTATCG GCGAAGGTAT TGCCATTCCA 120  
 5 CATGCCAAAG TGGCCGCAGT TAAGTCACCA GCTATTGCGT TTGGTAAATC TAAAGCAGGC 180  
 GTAGATTATC AAAGTTTGGG ATATGCAACC AGCACACTTA TTCTTTATGA TTGCAGCGCC 240  
 AGAAGGTGGC CCCAAACACA TTCTAGATGC TTTACTAAAG TTGnCTGGTA TTTTAATGGG 300  
 10 ATGAAAATGT ACGTGAGGAA ATTNttACAT GGCTTCATCA nCTGAAGAAG TACTAGCGAT 360  
 CAT 363

(2) INFORMATION FOR SEQ ID NO: 4103:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4103:

25 GAGTGCAGCG GATAACATTA AACCGACGAC AnCTTTTTTIA TGttCAGGTT TAGCTGTGTG 60  
 ATAAATTGCA AGTGCGGCAC CACATAAGCC GAACATCATC GTAATAAAAC GGCCTGACAT 120  
 AAAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGGA TCACCAAGTT GAGCAAAGAA 180  
 30 GATGTTCTGC GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC CAAGTGCCGT 240  
 CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT GGACCTAACA ATCTTAAGAT 300  
 GAAGCCATAA rCAAAAGTAC CsGTTGGcAC CTGTTtTCGT TACAAATCCA CCAACATGtK 360  
 35 AaTGCCGGTT TGTATGGTTG GCCCAAnTGA nAACATCATA 400

(2) INFORMATION FOR SEQ ID NO: 4104:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4104:

50 AATTGAGAAT TTGTCGCTAT TTGTAAATTG TATCCTGGCT TAAGTTGGCC AAAGTGTCTT 60  
 ATTTTTTTAA AGTATTTAAA AGTAAATTA CATGTTAATA CGTATATTAA TTGGCGAGAC 120  
 TCCTGAGGGA GCAAGTCCAG TCGAAGCAGG GGCCCCAACA CAGAAGCTGA CATATAGTCA 180

CAAAAATTCT ATTTATAGAA TTTTACAGTA ATGTGCCAGA TGGGCATAGC GACCCATTCA 300  
 ATACGAnTAT nTGAnTAAAT AGAGAACAGC AGTAAGATAT TTTCTAATTG AAAATTAT 358

(2) INFORMATION FOR SEQ ID NO: 4105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4105:

GACGCGTTAC CAAATGGCGG AATTAAAGCA AAATCTTCAA TTTCAATGAA CAATGTGACG 60  
 TATACGACGC AAGACGAACA TGGTCAAGTT GTTACAGTAA CAAGAAATGA ATCTGTTGAT 120  
 TCAAATGACA GTGCAACAGT AACAGTGACA CCACAATTAC AAGCAACTAC TGAAGGCGCT 180  
 GTATTTATTA AAGGTGGCGA CGGTTTTGAT TTCGGACACG TGGAAAGATT TATTCAAAC 240  
 CCGCCACATG GGGCAACGGT TGCATGGCAT GATAGTCCAG ATACATGGAA GGAnTACAGT 300  
 CGGTAACACT TCATAAAACT GCGGTTTGt ACCATTACCT AATnGTCAAG GGTACGGCGT 360  
 TAATGTTGA AGGTTCCCGT TCCAAGGTTT TTTCCCGTTT 400

(2) INFORMATION FOR SEQ ID NO: 4106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4106:

GAAGTTAAGC TCCTTAGCGT CGATGGTAGT CGAACTTACG TnCCGCTAGA GTAGAACGTn 60  
 TGCCAGGCAG TTTTTTAATC AAATTTTGGT TAAAAAATAA AATGGACAAG ATAAAAAAG 120  
 TTATTGACTT AAATGTTAAT AAAATGTATA ATTAATTCTT GTCGGTAAGA AAAATGAACA 180  
 TTGAAAAC TG AATGACAATA TGTCAACGTT AATTCCAAAA AACGTAAC TAAGTTACAA 240  
 ACATTATTTA GTATTTATGA GCTAATCAAA CATCATAATT TTTTATGGGA GAGTTTGGAT 300  
 CCTGGGCTCA GGATGGAACG CTGGGCGGCG TGCCCTAATA CATGGCAAGT CnGAGCGAAC 360  
 GGGACGAGAA GGCTTTGCTT CTCCTGGATG TTAACCGGcn 400

(2) INFORMATION FOR SEQ ID NO: 4107:

(A) LENGTH: 343 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4107:

10 GATTGTGCCA CGCTTTTAAC CGAAATACAA CATCATCATT GACAATTTGT TGATTGAAA 60  
 AATCTTTCTC TTCAATAAAT ACATACGTTT GCATCGTAGT TGCTTTCATG TAACTCAATA 120  
 TTGGTTTTAA ATGCATTTCA GGAATTAAAT AATGTTTACT AGAACCTGCT GTCGCTACAA 180  
 15 GTCCTATTAC CTTGTACGGA AACGCATTGA CTGGAAGTAG ATCAAACACA TTTnnCAAAG 240  
 CACCAGGGAT GGAAAGCTTG AAAAATTGGA AAACCAATAA AAATCACATC AGCCTGCATT 300  
 AACGACGTCG TTAATTTATA TACATCTCCT GTAGTATCTA Gnt 343

20

(2) INFORMATION FOR SEQ ID NO: 4108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4108:

30

ATACAAAACA CCAGGTCGTG AAGATAAACA ATCACAAGCG GCTACTGCTT CAGCAACTGA 60  
 ATTACCATAT GCAGTATTAG AAGCTATGGG TGGCAAAGCA AACATTAAAC ATTTAGACGC 120  
 35 TTGTATCACA CGTCTACGGT TGAAGTTAAC GACAAATCTA AAGTTGATGT TCCTGGTTTG 180  
 AnAGATTTAG GCGCATCTGG TGTATTAGAA GTCGGCAATA ATATGCAAGC AATTTTGGT 240  
 CCTAAATCTG ACCAAATCAA ACATGAAATG CAACAGATTA TGantGGTCA AGTAGTAGAA 300  
 40 AATCCTACTA CTATGGAAGA CGATnaAGAC GAACTGTTG TGGGTTGGCA G 351

40

(2) INFORMATION FOR SEQ ID NO: 4109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4109:

CCTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT 60

55

CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT AGCGACGnAT CACACCTTCT 180  
 GCGGCACCAC GGAATAATAC ACCATGTGGG AGTACGACTG CnATGGTACC TTCATCGTCT 240  
 5 AAGGTAATGT ACCCTGTGGT TGAATAAAGG CAAAATCTGC TTTGGGATTT TGGCGCAACT 300  
 TTGCCCGTAA CCACTGAATC GTTCATCATT TTCAAATTTT TGAATCnGCT GGTCCATTCTG 360  
 CACTGTA 367

(2) INFORMATION FOR SEQ ID NO: 4110:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 15 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4110:

GTCGTCCGAT-TGAAGGATGG-AGTACTGTCTG-CATTTCGAA-AGACTGGCAA-GGACCACCAC 60  
 GTTTGCAAAA CGGAACAAGT TGGTTCATT TTGCAACAGA CCAATGGAAA TATGAAGAGT 120  
 25 CAAATGTAGA TCGTTTAAAA TCTCCATTAG CTAAACAGA GGAGTTAAAG CATCAACATC 180  
 CAGCTGATTA TAATGTTTTA GCAGCTAGAC TTGGTTGGTT ACCATCATAT CCACAATTTA 240  
 ATAAAAATAG TTTGTTGTTT GCAGAAGAAG CTAAAGATGA AGGTATAGAT TCAAATGAAG 300  
 30 CGATTTTGCC ACGTGCAATT GATGAAGTGA ATCAAACCA AACACCATT GCCATAnGAA 360  
 AATCCTGATT TGGAAAAGGA TCCTnCCAAA ATCCAnnATT 400

(2) INFORMATION FOR SEQ ID NO: 4111:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4111:

TCAGATGAAG CTAAAAAGTAA AGGTATTACA TGTGCAAGTG CAGGTAATCA TGCTCAAGGT 60  
 GTTGCCTATA CAGCTAAAAA ACTTAATTTA AACGCTGTTA TCTTTATGCC AGTCACTACA 120  
 CCTTTACAAA AGGTAAATCA AGTAAAGTTC TTTGGAAATA GTAACGTTGA AGTTGTACTC 180  
 50 ACTGGTGATA CATTGATCA CTGTTTAGCT GAAGCTTTAA CTTATACAAG TGAACATCAA 240  
 ATGAACTTTA TAGATCCATT CAATAATGTT CATACAATTT CTGGACAAGG TACGCTTGCT 300

AATTGGTGGT GCGGGTTTAA TTTCCAGTAT TAGTACTAAC

400

(2) INFORMATION FOR SEQ ID NO: 4112:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 362 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4112:

GCCCTTAATA ACTTAATCTA TGTTTCACC ATTTTATAA GTCAAACGCT CACATACGGC 60  
 TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA 120  
 ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT AAACGCGTTA TTAATCTTGT 180  
 GAGTGTTCTT TCGAACACTA GCGATTATTT CTTATGAATT CAAGCTTATT TAAAACTCTT 240  
 TATTCACCTG GnTTTGCTTG GGAAAATCTA TATTTTACnT ACTTATCTAG TnTTCAATGT 300  
 ACAAATAATG GTGGGCCCAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGGCGTGC 360  
 GG 362

(2) INFORMATION FOR SEQ ID NO: 4113:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 363 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4113:

CAGGTGGTTT TCGGAAAAGT GAAGTATGGC GTCAAATGAT GTCAGATATA TTTGACACAG 60  
 AGTTAGTGGT TCCTGAAAGT TATGAAAGTT CATGCTTAGG TGCTGCGTG CTCGGACTTA 120  
 AAGCTGTAGG TGACATTGAA GATTTTTCATC TCGTTTCATC GATGGTCGGT GCCACAAACA 180  
 ATCATACGCC GATTGAAGAA AATGTCACCTG TTTACCAAGA GATCGTATCC ATTTTATCA 240  
 ATTTAAGTCG TTCTTTAACA GAGAATTATG ACAAATTGCA GATTTCAACG CCACATATCG 300  
 CTGAAATAAA ACnCCATAAA TACGnCACTC AAGCATCTTA GATAAAGTTG TnGGCCATGC 360  
 TAC 363

(2) INFORMATION FOR SEQ ID NO: 4114:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 394 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4114:

	GGTCTGGGCT TGGTTCCGGT TCTGGGTCTG GACTTGGTTC TGGATCTGGC GTTGGTTCTG	60
10	GTTCCTGGGTC TGGACTTGGT TCTGGGTCAA CCGGCGGCCC TGGAGTTGGG TCTTTCGGAT	120
	TTACTGCTGA ATCACCATCA GCACCTCCAC CACCATAACG TACAACATTC TCATTATTCC	180
	AACCGAAAAT ACTGTAGTCT CTATTTGTTA CAGGATCAAC ATTTTCTTGA ATAACCTGAG	240
15	TTTTTAAGTT CTTACCTGTA TTGTCGTAAT GCCCTTCTAC TAATACTACA TATGTTTTAG	300
	TAATATCACC AAATTAATAC TAGCTACATT GGATGCnCAT AATAGATCTA TTTTAAATGG	360
20	nCTGTACTCC TTAAGGTAGA GCATTGGACT GCAn	394

(2) INFORMATION FOR SEQ ID NO: 4115:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
25	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4115:

	GGCGATTATA TTAAAAAGCC AATTACAGAA TG TAGTGGTA ATGAAATATG CCAAGAATGG	60
	CTGTATCACT TAGGTGTATC AACTGACAAA ATTGAAGACT TAGCAAACA TGCATCTAAT	120
35	ACGATTCTCG TTTATATGCC ATATATCACA TCTTATTTC A TGACGCGTGC TATCGGCGAC	180
	AGACCTTTAG TCGTCCCGCA TCAATCTCAG AACTTAGCAT TTATTGGTAA CTTTGCCAGA	240
	AACAGAGCGA GACACTGTAT TTACAACAGA ATATTCGGTT CGTACTGCCA GGAAGCTGT	300
40	TTATCAATTA CTAAATATAG ATCGTGGTAT TCCAGAAGTC ATCAATAAGT CCATTGGATC	360
	TTnCGCGTn TTAATGGGAT GGCCATATAC GAACTGGATG	400

45

(2) INFORMATION FOR SEQ ID NO: 4116:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
50	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4116:

55

TTAAAGGGCG AAATAGAAGT GCCGGGCGAT AAGTCAATGA CACACCGTGC AATCATGTTG 120  
 GCGTCGCTAG CTGAAGGTGT ATCTACTATA TATAAGCCAC TACTTGGCGA ATGTCGTCGT 180  
 5 ACGATGGACA TTTTCCGACT GTTAGGTGTA GAAATCAAAG AAGATGATGA AAAATTAGTT 240  
 GTGACTTCCC CAGGATATCA ATCCTTTAAC ACGCCACATC AAGTATTGTA TACAGGnAAA 300  
 TTCnGGGTAC GACAACACGA TTATAGGTTG TTAAGTGGGT TAGGTATTGA AAGTGGTTTG 360  
 10 GTCnGGGCGA ATGTTTTCCA ATTGGGTAAA AGGCCCATGG 400

## (2) INFORMATION FOR SEQ ID NO: 4117:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4117:

AATAAAAAGG AACAAAACGA TGGCTATTGA TATGGACACA AATCATAAAT AGCTGCTTTG 60  
 25 TTCCCTTTTTT AATTTATATA TTTAnAATAC ACATATTCAA GAGCCTCGAG ATATAAGTCA 120  
 ATGTACTAGG CCACACAATT TAATATTGAC AGTAATTACC CGAACGAAAA TGCGCCCCGG 180  
 30 GGCCCCAACA TGGGGAATTT CGAAAAGAAA TTCTACAGAC AATGCAAGTT GGCGGGGCCC 240  
 CAACATAGAA GCTGGCCAAT AGTTAGCTTT CAATAATGTG CCAGTTGGGG TAAGGGCCCC 300  
 AACACAGAAG CTGGCCAATA GTCAGCTTTC AATAATGTGC CAAGTTGGGG TAAGGGCCCC 360  
 35 CCACCACAGG GAATTTGAA AGAAATnCT 389

## (2) INFORMATION FOR SEQ ID NO: 4118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4118:

AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 60  
 50 TGTGGATTAA TATTATGCCT GGCAACGTTT TACTCTAGCG GAAntAAGTT GACTACCATC 120  
 GACGCTAAGG AGCTTAACTT CTGTGTTCCG CATGGGAACA GGTGTGACCT CTTGCTATA 180  
 55 GTCACCAGAC ATATGAATGT AATTTATACA TTCAAACTA GATAGTAAGT AAAAGTGATT 240

ACATGTCACC ATGCTTCCCA CCTCGAACCT ATTAAACCTC AnCATCTTTG AAGGGGATCT 360  
TATTAACCGA A 371

(2) INFORMATION FOR SEQ ID NO: 4119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4119:

GCACTATTAG CCCAGTTAGA GAAAGATTGA CCTAATCTAT CCAACCAATC AGCCGACCAT 60  
TGAAACAGTG GTGCTAATTG CGGTGAATAC ATTGACTAAT CCGTCACCAA AACCACCTGC 120  
AGCACTTAAT AGCTTGTTAA ATACCGAAAC ACCCGTTGTA TTCATCATAT TAAAGAATCT 180  
TGAAGCTACA CTGCTATTTT CAGCCCATTh AAGCAGCCTT TGAGACGCTT CTTCCATTCC 240  
TCTTGAAATA CCACTAAAAA ACGGnTGTA GCTCTGCATT GCAGTTTTAA CAGTATTTAA 300  
ACCAATTTGCA AGAGTTGTGA AGnTAGCGGA TTGATTTTGC T 341

(2) INFORMATION FOR SEQ ID NO: 4120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4120:

GGTTGAGAAA AGCCAACACA GCTAGGGTAG TATCCACCA GCGCCTCCAC GTAAGCTAGC 60  
GCTCACGTTT CAAAGGCTCC TACCTATCCT GTACAAGCTG TGCCGAATTT CAATATCAGG 120  
CTACAGTAAA GCTCCACGGG GTCTTTCCGT CCTGTGCGGG GTAACCTGCA TCTTCACAGG 180  
TACTATGATT TCACCGAGTC TCTCGTTGAG ACAGTGCCCA AATCGTTACG CCTTTCGTGC 240  
GGGTCGGAAC TTACCCGACA AGGAATTTTCG CTACCTTAGG ACCGTTATAG TTACGGCCGC 300  
CGTTTACTGG GGCTTCGATT CGTAGCTTCG CAGAnAAACG CACTTCCTGT TAAACCTTTC 360  
CAGCACCGGn CAGGCGTTCA CCCTnATTAC ATCAACTTTA 400

(2) INFORMATION FOR SEQ ID NO: 4121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4121:

AATAAATCTT GCTTTATTCT TTTTACCAGT AATATCTAAA TGAGTTGGAT ATTTAACTTT	60
CGCATTAAATT TCAATATTAA ATTGCGTTAC CGCGACAAGC GCAAACACAA CATAcataAT	120
AAGATTGGCT AAAAAGATAT AGTTAAAGCT AAATTCTGCG ACAAAGCCGC CCATTGCAGC	180
ACCGACAGCC ACACCAATAT TTTGCGCTAA GTATATCGCA TTAAACGTTT GTCTTCCGCC	240
ATTTGGCCAC ACTGCTCCAG CCATAGCGTA TATCGCAGGA ATAATCATTG CGCCACCAA	300
CCCTAACATT ACCAGGCCAT ACCAGCATAC CCAGGGCCAC CCGnGGAAGG AAATTAAGTA	360
CGGTGGTAC TACCAAnGAC CAGTGGAAGG TnCCAATTAA	400

(2) INFORMATION FOR SEQ ID NO: 4122:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 362 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4122:

GATAACTAAT AAAGTTTAGT TAAGTATTTT AATAACAAGT AGTATGTCAT TCTAGTAGCT	60
AGAACAGATA TACTACTTGT TTGTTTTTGT GGAAAATTGA GTATATTCAA AAGGATAAGn	120
ACGAGAATTT CGTTATTAAA CTACGAATTC TCGATTTTTT TATATTTTAA GATAGGTTTA	180
TTTCTGAAAA CTTAATAGAA AGGGGTTTGA CAAAGCTAAA GTGAAGTTTG ACGgTATAAA	240
CGCAAATTAA ATATACTTTT ATAGAAAATT AACTCAGGCT GGGACATAAA TCAATATTCT	300
ATGCTCTACG GAGGTATATT GGCAGTAGTT GACTGAACGA AAnGCGCTTG TnACCAGCTT	360
TT	362

(2) INFORMATION FOR SEQ ID NO: 4123:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 352 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4123:

CGCGAGGTGG TTTACAAGGA TTGTTGACAT TTCAAGACTT ACCAGTAACA AGTTATACAA 120  
 TCTGGGGTGG TGTCTCAGAT ATTGATTTAA TGTATGAAGA ACGTGTGCAT TTAAGAGGCA 180  
 5 TGCTACGAAG AATGATTGGT CATCCGAAAA AAGATCGAGC GGGCATATGA GGCACGCCAA 240  
 GCGATTCCAA ACATTAATGA AACAGTCCG CCAATATTAA TTGTACATnG GAGGGGAAAG 300  
 10 ACCCAGCAAG TTGGGTATTh CATCATGCGT ATTATTTTAA GCGGACCAAC TA 352

## (2) INFORMATION FOR SEQ ID NO: 4124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4124:

AACCAGGTGA TCTACCCTTG GTCAGGTTGA AGTTCAGGTA ACACTGAATG GAGGACCGAA 60  
 CCGACTTACG TTGAAAAGTG GAGCGGATGA ACTGAGGGTA GCGGAGGAAA TTCCAATCGA 120  
 25 ACCTGGAGAT AGCTGGTTCT CTCCGAAATA GCTTTAGGGC TAGCCTCAAG TGGATGATTA 180  
 TTGGGAGGTA GAGCACTGTT TGGACGAGGG GCCCTCTTC GGGTTTACCA ATTCAGACA 240  
 AACTTCCGAA TGCCAATTAA TTTGAACTTh GGAGTTCAGA ACATGGGTGA TAAGGTCCnT 300  
 30 GTTTCGnAAn GGGAAACAGC CCAGACCACC AGTTAAGGTC CCCAAATGTA TGTTTAAAGT 360  
 GAAAAGGGTT TTGGCGTTGC CCCGACAACT AGGATGTTGG 400

## (2) INFORMATION FOR SEQ ID NO: 4125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4125:

GGCTTATTAA TCAAAAAATT TATAAAGAAT ATGTAGAAAA CTTTATTTA CATCGAGGCT 60  
 ACACGCTACA ACAGAAAATT AAAATTTTAA TTAGCTTATA CATTGTAATA GGTTTTTCAA 120  
 50 TTTATATGGT GGATGTTCTT GCACTCCGTG TAGGATTAAT CATAATGGTT ATCATACAAA 180  
 CCGCTGTACT CTTTACATTT GTAAAAACAT TACCCAAATC AAATCATAAA ATAGAGGAGT 240  
 GATTGCCCAT GTTTATGGCA GAAAATAGAT TACAATTACA AAAAGGCAGT GCGGAAGAAA 300

TTGTCACTAA AACATTAAAT ACCGGGATAC AGCCGAGTAA

400

(2) INFORMATION FOR SEQ ID NO: 4126:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4126:

15	AATCTATATT TIACTTACTT ATCTAGTTTT CAATGTACAA TTTCTTTTTA GTCAAGCGCT	60
	CGCATAAGCA ATATCACTTT AACCAAAAAA TATTTGAATG TTAAATAAAC ATTCAAACCT	120
	GAATACAATA TGTCACATTA TTCCGCATCT TCTGAAGAAG ATGTTCCGAA TATATCCTTA	180
20	GAAAGGAGGT GATCCAGCCG CACCTTCCGA TACGGCTACC TTGTTACGAC TTCACCCCAA	240
	TCATTTGTCC CACCTTCGAC GGCTAGCTCC TAAAGGGTT ACTCCACCGG CTTGGGGTGT	300
	TACAACTCT CGTGGGTGTG GACGGGGCGG TGTGGTACAA nGACCCGGGG AACGThATTC	360
25	AnCGGTAGCA TGGCTGGATC TAACGATTTA CTAnGCGGAT	400

(2) INFORMATION FOR SEQ ID NO: 4127:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4127:

40	CGAAATTTGT AGTAAAAGAT GTGCAACCAG CGAAACCAAC TGTGACTGAA ACAGCGGCAG	60
	GAGCGATTAC AATTGCACCT GGAGCAAACC AAACAGTGAA TACACATGCC GGTAACGTAA	120
	CGACATACGC TGATAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTACAC	180
45	GTCGCAATAA TACGAGTCCA TGGGTGAAAG AAGCATCTGC AGCAACTGTA GCAGGTATTG	240
	CTGGAATAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GGATACAATT	300
	CCAAGTTGGT TGCAACGCCA AGGAAGCGGA GAGACCAGTG AAGTGATTGA GCCACCGTAA	360
50	TGGTTGGnTT CCCAGTTTG TCGGCAnCCA CAACCGGAAC	400

(2) INFORMATION FOR SEQ ID NO: 4128:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4128:

GATTAGTGAA AAGTTGGTTG TACTATTACC GTTAAAATTT GGAGATTATC TGTCGTCTTC	60
AAGTATGCGT TCATTAATTG ATATTGGCGC ACCGTATAAC CATGTCAAAG TACCATTGCG	120
AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GCCTACGCGT TACATGAAAA ACGGAGAACA	180
AGCAGAACAA TTATTACGTC AGCTTATAGA AAAAGATGAA GCACTAGCTA AGTATGTCAT	240
GGGTGTGAT GAAACAGCTT GGTGGTCATA TATGGGTCCA GATAATGATA TTTTCCAAGA	300
TCCATTAnGG CCATCTAACT GTTCCAGCTA AGGAAAGTAT CCCCGAAGTG GCTAAGCCCA	360
AAAATGATTA CGCCAACCAG CTAGTGGTCC ATnGGCCAGC	400

(2) INFORMATION FOR SEQ ID NO: 4129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4129:

AGAGGTCCGT TGCCTTACCG CTTGGCTATA GCCCAATATA TAGATGGnGG AGGGGGGCG	60
ATTCGAACTG CCGAACCCGA AGAGCGGATT TACAGTCCGC CGCGTTTACC ACTTCGCTAC	120
CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG GGTTCGAACC	180
GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGG AGCTAATTCT CCAAATAAT	240
GACTCCTGAC GGGACTCGAA CCCGTGTTAC CGCCGTGAAA GGGCGTGTTT TTGAACCGCT	300
TGGACCAAGG GAGCCATGGC TCCAACAGGT GAGGGACTCG AACCTnACGG ACCGATTCGG	360
TThAACAGCC GGAT	374

(2) INFORMATION FOR SEQ ID NO: 4130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4130:

ATTAAATTC AGTTGTTGCA ATTTCTTCAT CTGTAGGTAC ATCATCGTTA AGGCCAACAA 120  
 GTGCTTCAGA AACATTTTCGT GAATGATAAC CGATACGTTT AAGAACrCsa ATCATATCGA 180  
 5 TATATAGTAA TCCGCCTTTT GTTGTACATT CACCACGATT AAGGCGTTTA ATATGACCTT 240  
 TCGTAGTTT ATGTTCAATA TTAAATGATT CTCTACTACG TTCTACAATT TCATCTTTT 300  
 10 TCGTTTGTG ATAACATCT AACATGTCGA TGGCTTTATC AAATGACTCA GCAACATGGT 360  
 TGAATAAnt TATCCATACC GCGTTGTGCA TCTnCTGGTA ATGCGAATAT CTTTCATCATG 420  
 TTGGCGGTTT T 431

(2) INFORMATION FOR SEQ ID NO: 4131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4131:

TTTAGTTGAA GCGGGTGTG TCGCATTTGC TGTTTGTTGC GGTGCTTCTA CTTTAGTTGA 60  
 GGGCGGTGTT GTCGCGTTTG GTTTTGATTG CCGTGCTTCT ATTTTAGTTG AGGGCGGTGT 120  
 TGATGTGGTG CTCCACTTT AGGnAAntGA GTGTTGTCGC GTTTGCTGCT TCGGTTGTGC 180  
 30 TTGTGATTAC ACCTGTTGTT AAAAGGCCTA GTGCTAACT TGTTTTAGCA ATCGTTGTGA 240  
 TTTTCATAGT TGTATGCTCC ATTCGTAATT ATTAGATTG TTCGATACAT TCATTGAATC 300  
 ATACAGCTTT ATTATAGAGG CGTATTGCTC CATTACATT AAACCTGTnT AACCAGATTG 360  
 35 GAAGCAGCGT TGAATnAAAT GAAGAAAGCC AGAAGTTCGT 400

(2) INFORMATION FOR SEQ ID NO: 4132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4132:

CCATTCACCTG TATGTCCTTG GCCACCACCT TGACGTTGTT GTTGCTGTTG TTGATTTTGA 60  
 50 TTAGCTTGTT GTTGATTTTG ATTATTTTGT GCTTGATTGT TCGCTTGATT AGCGTTGTTT 120  
 TGATCATTAT CAGATTCATC TTTAGTCGCT TTGTCTTGAT CCTCTTTTGA TTTATCACTG 180

TCAGCATTAT TTTTATTTGT ATTGCGGATT TTATTTTCTT TTGTACCATT ATTATGATTG 300  
 TTTAATGCCA TGCCTCCAAA TATCGCTAAA TGCACCGATA AATnAGTACA GCTGCAATGA 360  
 5 ATGGAACAA TACTTTGGGC CAGnCACCGT TTTTACGGTn 400

## (2) INFORMATION FOR SEQ ID NO: 4133:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4133:

TTGAATACTT TTCTTCCACA CAAATGTATA TCTATTGGCA TTAGCTTCTA CTTTTGTACC 60  
 20 ATCAATAAAA ATTGAATTAT TATCAATAAG ATTTTGCTTT AAACATTGAC TATGGAACGT 120  
 AATAAATAAA GATTCAATTA ACGCATCAGT ATTAGGATTC ACTCTAAAAC GATTAATAGT 180  
 TTTATAAGAA GGTGTTTGAT TTTGAGCTAA CCACATCATT CGAATACTGT CATGAAGTAA 240  
 25 TTTCTCTATT CTTCGACCAG AAAATACAGA TTGAGTATAT GCATATAAGA TGATTTTTAA 300  
 CATCATTTTT GGGATGATAG GATGTTGCGC CACGATGATG TCTGAATTCA TCGAATTCGC 360  
 TAnCGGGTAC CGTTCACCA ATTCCATTAA CATATCGCGG AATATCATT TGAAGAA 417

## (2) INFORMATION FOR SEQ ID NO: 4134:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4134:

GGTTTAATAT GGACCTTTGC CGTnTTTATG TTCAATATTA AATGGATTCT CTACTACGTT 60  
 CTACAATTTT ATCTTTTTTT GTTTTGTTCAT AAACATCTAA CATGTCGATG GCTTTATCAA 120  
 45 ATGACTCAGC AACATGGTTG nAATAATTTA TCCATACCGC GTTGTGCATC TTCTGTAATG 180  
 CGnAATATCT TCATCATGTT GGTGTTTTTA ATTGAGCGAC ATACTCTTCT GTTAGCTCTG 240  
 CTACTTTTAA AATAGAGCGA TTGACATCAA ACATAACTGC TAAACGCTCA ACGTCTGCCT 300  
 50 TCGTAATGGC TTTTGTAGAA ATTCTAACTA AATAATTCG AATGCTATCA TTGT 354

## (2) INFORMATION FOR SEQ ID NO: 4135:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4135:

CTGGGATCGC CACCTTTAAG TCTAACAACC TTGTTATATC GACGCGCTGC TTCCACGATA 60  
 CAGTCATTTA TTTTCTTG CTGAATATGT TTTGCATACG GCTTTTACC AACATCGATA 120  
 ATTTCACTAG TCAAATTCGC ATATTGTAAA ATTAACGGAT TCACTAATCG ATCATATAGA 180  
 ATGACATCCG CTTACAGTAT TAAACGCTCA GCCTTTTTCG TCAAATAATT CGGATTACCT 240  
 GGACCCGCAC CTATCAAGTA AACCTTGCCA TATTCCTCTA CAGACATATA TATACGGTCC 300  
 CGTCTGTAAC TTCTACCTCA TAAACATCTA CACAACCTTC ATCAGGTCTG GACAATACCT 360  
 GATTAAACA ATTTTGTATC GTGGGGGGGC AAATACATAT 400

## (2) INFORMATION FOR SEQ ID NO: 4136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4136:

ACCACTGAAT CGTTCATCAT TTTCAAATTT TGAATCTGCT GTCCATTTTCG CACTGTATGG 60  
 TGGGTTTCGCA ATAACCGCAT CAAATGTATT GCCTAAAAAG GCTGGATTTT CCAATGTGTC 120  
 ATCATTACGG ATCTCGAAGT TCTCATAACG CACATCATGT AATAACATAT TCATGCGTGC 180  
 TAAGTTGTAT GTAGTATTGn TACGTTCTTG TCCGAAATAA CGATACACTT GCGTTTCTTT 240  
 ACCAACACGT AACACAATG GAACCGGAnC CACATGTTGG GTCGTACACG TGGACGTAAT 300  
 TTATChTTAC CGTGCTGTGA CAATCTTCGC CAGTATCTTA GATACTTG 348

## (2) INFORMATION FOR SEQ ID NO: 4137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4137:

EP 0 786 519 A2

TGGACAATAC AAAGGGCAGC GAAACCGCGA GTCAAAGCAA ATCCCATAAA GTTGTCTCTCA 120  
 GTTCGGATTG TAGTCTGCAA CTCGACTACA TGNAAAGCTGG nAATCGCTAG TAATCGTAGA 180  
 5 TCAGCATGCT ACGGTGAAAT ACGTTCCCGG GTCTTGATACA CACCGCCCGT CACACCACGA 240  
 GAGTTTGTAAC CACCCGAAGC CGGTGGAGTA ACCTTTTAAG GAGCTAGCCG TCGAAAGTGG 300  
 10 GGACAAATGA TTGGGGTGAA TCGTAACAAG GTAAGCCGTG ATCGGnAAGG TCGGGCTGGG 360  
 AT 362

(2) INFORMATION FOR SEQ ID NO: 4138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4138:

ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTTCGAAAT CTCTGGATCA 60  
 25 AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA 120  
 GTGCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCAC CATTTTTATA 180  
 30 AGTCAAACGC TCACATACGG CTTCGTTTTT ATTATTTTAA ATGCTCATT ACATAAGTAA 240  
 ACTCTGCTTT AAAATAATTT AACTGCATTG TCTGCTAAAC GTTTTCTTT ATAAAAAGAT 300  
 TTAAACGCGT TATTAATCTT GTGAGTGTTT TTTCGAACAC CAGCGATTAT TTCnTGAGGA 360  
 35 ATTCAAGCCT ANTAAAAACC CTTA 384

(2) INFORMATION FOR SEQ ID NO: 4139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4139:

CTCATTATGG GACGTGCACA AGATGGTTTT CTTGATCAAG ACAAATATGA CATTATTTTC 60  
 50 AAAACAGCTG AAAATTTAGA CGTACCGATT TATCTACATC CCGCGCCAGT TAACAGTGAC 120  
 ATTTATCAAT CATACTATAA AGGAAATTAT CCTGAAGTAA CTGCGGCAAC ATTTGCTTGT 180  
 TTTGGTTATG GTTGGCACAT TGATGTCGGC ATTCATACAA TACATCTnGT nTnATCTGGT 240

TCCTTAGAAC GAATGGATGA AGCTTATCCG TGAACATTTG AACCACCCCG GAAGCAATAC 360  
 TTAAAAATAA ATTTAnTATC ACACCGGGTG GCATGGTACC 400

(2) INFORMATION FOR SEQ ID NO: 4140:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4140:

CAACCACATT CGCTCGGCTC ACCTTAGAAT TCTCATCTTG AACTACCTGT GTCGGTTTGC 60  
 GGTACGGrCA CCTATTTTCT ATCTAGAGGC TTTTCTCGGc AGTGTGAAAT CAACGaCTCG 120  
 AAGACTCAAT GTCTTCTCCC CATCACAGCT CAGCCTTAAC GAGTACCGGA TTTGCCTAAT 180  
 ACTCAGCCTT ACTGCTTAGA CGTGCAATCC AATCGCACGC TTCGCCTATC CTACTGCGTC 240  
 CCCCCATCGA TTAAAACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT 300  
 AAGCCTGTGC GGCTCAGCTT AAGGACCCGA CTAACCCCGAG AACCGGAAGA GCCTTCCTCT 360  
 GGAAAACCTT AGTCAATCCG TTGGACCGGG ATCTCAACCG 400

(2) INFORMATION FOR SEQ ID NO: 4141:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4141:

CATATCGATA ACATGACATA ACTCATGCTG GGTTCCTCCA TTCGGAAATC TCTGGATCAA 60  
 AGCTTACTTA CAGCTCCCCA AAGCATATCG TCGTTAGTAA CGTCCTTCAT CGGCTTCTAG 120  
 TGCCAAGGCA TCCACCGTGC GCCCTTAATA ACTTAATCTA TGTTCACC ACCATTTTATAA 180  
 GTCAAACGCT CACATACGGC TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA 240  
 CTCTGCTTTA AAATAATTTA ACTCATGTGC TGCTAAACGT TTTCTTTTAT AAAAAGATT 300  
 AAACGCGTTA TTAATCTTGT GAGTGTCTT TCGAACATAG GCGGAGTATT TCTTAAGGAA 360  
 TnCAAGCnTA TTTAAAACTC TTAATCACnT GGTTTTGCT 400

(2) INFORMATION FOR SEQ ID NO: 4142:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4142:

10 GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTTC ACTTCGCCAA GCCATTTTTC 60  
 TTTGTGTTTA CTTTTTATTT TGACGTTTTA GACATAAAAA AAGAGACCTC ACGGTCTCAA 120  
 CTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC 180  
 15 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCTCTCC TTCGGCTCTC GCTTACTCAT 240  
 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGGTTCGT CAGATTCAAA CGTTTCACTC 300  
 GCCAAGCCAT TTTCTTGCGG TTACTTTTAA TTTGACGTTT AAGGCATAAA AAAAAGAGAC 360  
 20 TTGCGGGCTC AAATGCGGnT CATCGCATCC ATTTTnGnCh 400

## (2) INFORMATION FOR SEQ ID NO: 4143:

25

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 369 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4143:

TTTAAAATTG ACATTATTAC TGACCAAACA AGTGACATG ATCCGCTAAA TGGATATGTG 60  
 35 CCACAAGGAA GCGAAAGTAT TGCCTGAAAA AGATCCGAAA AAATATGTTG AACTGTCACA 120  
 AGCTTCAATG GCAAAGCATG TTGAATTAAT GCTTGGAATT CCAAAAACGT GGCGCTGTAG 180  
 CATTGATTA TGGTAACAAT ATTCTGCAAG TAGCCTTCAA TAACGGAnGn ATAAATGCTT 240  
 40 TTGGACTTCC CAGGTTTTGT ACCAGCTTAC ATTAGACCAT TnATTCTGTG TAGGTTAAAG 300  
 GGCCATTCCG CTTTGCTGCG TTGGAGTGGT GGATCCAAAA GATATCGAGC GTGCCGGATG 360  
 45 GAGGAAATG 369

## (2) INFORMATION FOR SEQ ID NO: 4144:

50

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

GGAAAGATAA ATAGCTTCAT CAATGTCATG CGTCACTAAA ATAATAGTTG ATTGCGTTTT 60  
 ATGTTTTAGT TGCAC TAGTT GATCCTGAAG TTTATAACGT GTAAATGCAT CTAATGCACC 120  
 5 TAATGGCTCA TCCATCAATA TAACGTTAGG CTTATGCACA TCGCTCGAC ATAGTGCCAC 180  
 ACGTTGTTTC ATACCCCCGG ACAGTTGCTC GGGAAAATGC TTTCCCCTGT CTTCTAAATC 240  
 AACTAATTTA AGCTGTGCTT TAATCTCTTC ATCACTAATT TTCTGTTGTA ATCCAATCCT 300  
 10 AATGTTGTCA TTAATCGTTT TCCAGGCAGC AAATTATGGT GTTGAAATAG CATAAACAA 360  
 CGGGAGnGGC 370

## (2) INFORMATION FOR SEQ ID NO: 4145:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4145:

CGAGGTAGCA AAGAACAAAT TCGGAAATAT GTACCTAAAT TACAGTCACA TGAAGTTCGT 60  
 ACATGCTTTG CTTTAACTGA ACCAGAACAC GGTTCCGACG TTGCGGGAGG TCTTGAAACA 120  
 GTCGCTGAAC GCCAAGGCCA TACTTGGGTT ATCAATGGTG AAAAGAAATG GATTGGTGGT 180  
 30 GCACATGTAT CTGATGTCAT TCCAGTATTC GCAGTAAATA AAGAACTGG GCAAACCCCA 240  
 TTGCTTTGTA GTCAGACCAG AACAGATGG GCGTCGATAT TGAAGTCATT GGATAATAAA 300  
 ATCGCACTTC GGCATTGTTC CTAACGCCCT AATTTnAATT AAnTAATGTT CAAAGTAGGA 360  
 35 TTGAAGCGGG 370

## (2) INFORMATION FOR SEQ ID NO: 4146:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4146:

TGGGGTGTTC TTACCAATAA AGCGTTGCAA GGTGGCGGTA GTTTAATCGA TTATGGTTGC 60  
 50 CACTTGTTAG CTACTAGGTA AAGATATGGT GCCGCATGAA GTCTAGGAAA AACATATAAT 120  
 CAATTGAGCA AACAAACGAA TCAAATTAAT GATTGGGGAA CATTGATCA TACTAAATTT 180

GAATGTTTCGT GGTCTGCAAA TATCAAAGAA GATAAGGTTT ACGTThTTTT ATCAGGAGGA 300  
 GGATGGCGGT ATCCAATTTA TTTCCATTG GAAATATATG GnCCCCCGTT TTGGGAACnC 360  
 5 ATTTTTTGGG AAGCCAAGCT 380

## (2) INFORMATION FOR SEQ ID NO: 4147:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4147:

TACTTATCTA GTTTTCAATG TACAATTTCT TTTAGTCAA GCGCTCGCAT AAGCAATATC 60  
 20 ACTTTAACCA AAAAATATTT GAATGTTAAA TAAACATTCA AAAGTGAATA CAATATGTCA 120  
 CATTATTCCG CATCTTCTGA AGAAGATGTT CCGAATATAT CCTAGAAAG GAGGTGATCC 180  
 AGCCGCACCT TCCGATACGG CTACCTTGTT ACGACTTCAC CCAATCATT TGTCCACCT 240  
 25 TCGACGGCTA GCTCCTAAAA GGTACTCCA CCGANTTCGG GTGTTACAAA CTCTCGTGGT 300  
 GTGACGGGCG GTGTGTACAA GACCCGGGAC GTATTCACCT GGCAGCTTg CTGGGTTTAC 360  
 nT 362

## (2) INFORMATION FOR SEQ ID NO: 4148:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4148:

CACCATACAT GCGAAATGGA CAGCAGATTC AAAATTGAA AATGATGAAC GATTCAGTGG 60  
 TTACGGCAAG CTTGCGCCAA AATCCAAAGC AGACTTTGCC TTTATTCAAC ACATGGTACA 120  
 45 TTACCTAGAC GATGAAGGTA CCATGGCAGT CGTACTCCCA CATGGTGTAT TATTCGTGG 180  
 TGCCGCAGAA GGTGTGATTC GTCGCTATTT AATAGAAGAA AAGAACTACT TAGAAGCCGT 240  
 GATTGGGTTA CAGCCAATAT TTTCTATGGG nCAAGTATTC CAACATGTAT TTAGTATTAA 300  
 50 AAATGTCGCC ACAAGACGCC ACGTACTATT ATCGATGCAT CCAATGATTT GAAAAGGAAA 360  
 AATCAAACCA TTAAGCGTGC CAAGCGACGA TATnGnCTA 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4149:

10	CAGCTATTGA TATCGATTAC CATACTGCTG TGGATAGCGA CAGGTTACAG TTGGAGGATA	60
	CACTGAGTCC TCTGAGGAAT CAAATCCAAT TGACTTTGAA GAATCTACAC ATGAAAATTC	120
15	AAAACATCAC GCTGATGTTG TTGAATATGA AGAAGATACA AACCCAGGTG GTGGTCAGGT	180
	TACTACTGAG TCTAACTTAG TTGAATTTGA CGAAGAGTCT ACAAAGGTA TTGTAAGTGG	240
	CGCnTGAGCG ATCATACAAC AGTTGAAGAT ACGAAGAATA TACTACTGAAG TAATCTGATT	300
20	GAATAGTGGA TGAATACCTG AAGAGCATGn TCAGCACAAG ACCAGTCGAG GAATnACTAA	360
	AACCATCATC ATATTCnCAT CTGGTTAGGA CTGAAATGGC	400

(2) INFORMATION FOR SEQ ID NO: 4150:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4150:

35	AAGGACGACA TTAGACGAAT CATCTGGAAA GATAATCAAA GAAGGTAATA ATCCTGTAGT	60
	CGAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG GAGCACGTGA AATCCGTCG	120
	GAATCTGGGA GGACCATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCACT	180
40	ACCGTGCAGG AGAAGGTGAA AAGCACCCCG GAAGGAGTTG AAATAGAACC TGAACCGTG	240
	TGCTTACAAG TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTTGTA GAATGAACCG	300
	GCGAGTTACG ATTTGATGCA AGTTAAGCAT AAATGTGGAG CCGTAGCAGA ACnnGTTnTG	360
45	AATAGGCGTT A	371

(2) INFORMATION FOR SEQ ID NO: 4151:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 366 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4151:

TCAGCTTTT TGATATGTAT TTTATAATGT ACAGCTCGTT GACnnTAATT TTCCTTATAT 60  
 5 TAAGTGCCAT CAATACAAA CCTAGCTCTC GTTTAACTTT ATTTATTCCT CGAACTGACA 120  
 TTCGAGTGAA CCCAAAATAG CCTTCATAAA TCCAAAAGCA GGCTCTACAT CAATTTTTCT 180  
 TTGACTATAG ATGTTTTTCG TTTCTGGTTC AGAAAGCTTT TGATTAATTT GGACTTTAAA 240  
 10 GTATTCCCAA TTATAATTCT TCATGGATTT TCTTATTGGG ATTTCGAATT TGGTTTCATG 300  
 CATTGATGTC TCAAAGAACA TGATGGAACA GTCCAnCACA TTCCAGATAG TTTGGAAGTC 360  
 15 TCGTTT 366

## (2) INFORMATION FOR SEQ ID NO: 4152:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4152:

TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC 60  
 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCTCTCC TTCGGCTCTC GCTTACTCAT 120  
 30 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 180  
 TCGCCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAA 240  
 35 GAGACCTTGC GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGCA ACGTTCTACT 300  
 CTAGCGGGAC GTAAGTGGCT ACCATCGACG CTAAGAACCT TTCCTGGACT TGGTGGACAA 360  
 TCGCnTGCCT CCTTCCTCCT CCTCGGGCTC TCGGCTTACG 400

## (2) INFORMATION FOR SEQ ID NO: 4153:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4153:

TGATATTCCT GTACCACCTA TAATCGTTTT AATCGATGGG GGGACGCATA GGnATAGGCG 60  
 ACGTGCGATT GGATTGCACG TCTAAGCAGT AAGGCTGAGT ATTAGGCAAA TCCGGTACTC 120

CCGAGAAAAG CCTCTAGATA GAAAATAGGT GCCCGTACCG CAAACCGACA CAGGTAGTTC 240  
 AAGATGAGAT TCTAAGGTGG AGCGAGCGAA CTCTCGTTTA AGGACTCGGG CAAATGGACC 300  
 5 CCGTTACTTC GGGGAGAnGG GTGCTCTTTA nGGGTTTACG CCCAGAAGAG CCGCATTGAA 360  
 TAAGGCCCAA GCGnTGTTTT ATCCAAAACA CGGTCTCTGC 400

## (2) INFORMATION FOR SEQ ID NO: 4154:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4154:

20 TTTTAGCAAT CATTTTAACA GTCAGTCATA TTAAAGGCTG GCTAACGATT GTTATCTnGT 60  
 nCAGATTTGT AAGTTAAGAT TTCTTGTAAT GTGTATGCAG CACCATATGC TTCAAGTGCC 120  
 CATACCTCCA TCTACCAAAA ACGTTGTCCA CCGAATTGCG CTTTACCGCC AAGTGGTTGT 180  
 25 TGTGTAACAA GTGAATATGG TCCTGTTGAA CGCGCATGTA ATTTATCATC AACCATGTGC 240  
 GCAAGTTTCA ACATGTACAT TACACCTACT GAAATACGGT TATCGAATGG TTCACCTGTA 300  
 CGTCCATCAT AAAGTACAGT TTTACCATCA CGAGCCATAC CAGCTTCTTC AATTGTTGGA 360  
 30 CCATACATCG TCATCGTTTG CACCGTCAAA TACTGGTGGA 400

## (2) INFORMATION FOR SEQ ID NO: 4155:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4155:

45 GATCCGAAGT TACCAACAGG AGAGAAAGAG GAAGTTCCAG GTAAACCAGG AATTAAGAAT 60  
 CCAGAAACAG GAGATGTAGT TAGACCACCG GTCGATAGCG TAACAAAATA TGGACCTGTA 120  
 AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCG AGAAAGAACG TAAATTTAAT 180  
 50 CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG TGAGAAGACA 240  
 ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA AGGTGAATCG 300  
 AAAGAAGAAA TCACAnAAGT CCAGTTAATG AATTAACAGA TTCGGTGGCG AGAAATACCG 360

## (2) INFORMATION FOR SEQ ID NO: 4156:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4156:

CAAAGTGACA GGTGGTGCAT GGTGTGCGTC AGCTCGTGTC GTGAGATGTT GGGTTAAGTC 60  
 CCGCAACGAG CGCAACCCCTT AAGCTTAGTT GCCATCATTAGTTGGGCAC TCTAAGTTGA 120  
 CTGCCGGTGA CAAACCGGG GnaAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA 180  
 TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG CGAGTGAAG 240  
 CAAATCCCAT AAAGTTGTTC TCAGTTCGGA TTGTAGTCTG CAACTCGACT ACATGAAGCT 300  
 GGGAAATCGCT AGTAATCGTT AGATCCAGCA TGGCTAACGG TGGATACGT TTCCCGGGGT 360  
 CCTTGTTACA CACCGCCCGT 380

## (2) INFORMATION FOR SEQ ID NO: 4157:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4157:

TGGAGAAGGA CCCAAAAATG TTGCCGTTTC AAGGTTATGT TTTACAACAT TTCGAACCTTA 60  
 TGGATGATGG ATTCTGCCAA GTTAAATAA CTGAAGATGT ATTGGAGCAA TTCGGTATTC 120  
 AGCCAAATGA AGCATCTCAG TTTGTTAATA CAATTGCTGA CATCAAAGGC TTGAAAATAT 180  
 GGGTATTGTC AGTCGATGGA AGGTAATGAA ATCAGATGTC GATTACGTTT TAAAGGGCAA 240  
 TTGGATTATT AATGATATTG CGCAGATTTT GGTGGCGGTG GTCATCCGAA TGCCTCAGGA 300  
 GTTTCAGTGG ACCAGCTGGG GTGGANTTGA GCCACTTGCT ACCAGCTTTA CGGCACCAA 360  
 ACTTnACTTA TAGGAAGGGG CCCATTCCAT CCAGGTGGGC 400

## (2) INFORMATION FOR SEQ ID NO: 4158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4158:

5 AAATCTCTGG GATCAAATCT TACTTACAGC TCCCCAAAGn CATATCGTCG TTAGTAACGT 60  
 CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGCC CTTAATAACT TAATCTATGT 120  
 TTCCACCATT TTTATAAGTC AAACGTTAAC ATGAAGTTAC GTTCTTTTAT AAAAAGATTT 180  
 10 AAACGCGTTA TTAATCTTGT GAGTGTTCCT TCGAACACTA GCGATTATTT CTTATGAATT 240  
 CAAGCTTATT TAAAACTCTT TATTCACCTG GTTTTGCTTG GTAAATCTA TATTTACTT 300  
 ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGn n 351

## (2) INFORMATION FOR SEQ ID NO: 4159:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 420 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4159:

25 AGTTAAAGGA ACTTTTAAAG TGGTTGGCCG CCGTnATTGC CTTCTnACC TTTTGTCTT 60  
 TCTCTGTgTA CTTTTTCTGT CCCTGGTGCT AAATCnGGAT TAAATTTACG TTCTTTCTTG 120  
 30 AATGGAATyT CTTCTTTTTC TACAATCGAG TCTCCTTTTA CAGGTCCATA TTTTGTTACG 180  
 CTATCGACCG GTGGTCTAAC TACGTCTCCT GTTCTCGGAT TCTTAATTCC TGGTTTACCT 240  
 GGAACCTCyT CTTTCTCTCC TGTTGGTAAC TTCGGATCAA ATTCGTCTCG ATGACCTGGT 300  
 35 GTTATCGTTT CTGGTCCGTA TTCTGTTAAT TCATTAATCG GATCTTTTGT GATTTCTTCT 360  
 TTTGGTTCAC CnTTnACGAA TAATnACTCC AGTAAAGGAT TTTTAAAGTG TTGGTGTCTG 420

## (2) INFORMATION FOR SEQ ID NO: 4160:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 359 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4160:

50 ACGATAATGG TGACGGGTTA CAAAGCCAAC ACAGCTAGGG TAGTATCCCA CCAGCGTCCT 60  
 CCACGTAATC TAGCGCTCAC GTTTCAAAGG CTCCTACCTA TCCTGTACAA GCTGTGCCGA 120

TGCATCTTCA CAGGTACTAT GATTTCACCG AGTCTCTCGT TGAGACAGTG CCCAAnTCGT 240  
TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAnT TTCGCTACCT TAGGACCGTT 300  
5 ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAAn TAACCACTC 359

## (2) INFORMATION FOR SEQ ID NO: 4161:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4161:

ATTGACTAAG GTTTCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA 60  
20 GGCCCGnAAC GGTAGGGCGA TGGATAACAG GTTGATATTC CTGTACCACC TATAATCGTT 120  
TTAATCGATG GGGGGACGCA TAGGGATAGG CGAACGTGTC GATTGGATTG CACGTCTAAG 180  
CAGTAAGGCT GAGTATTAGG CAAATCCGGT ACTCGTTAAG GCTGGAGCTG TGATGGGGAG 240  
25 AAGACATTGT GTCTTCGAGT CGTTGATTTT AACTGCCGA GAAAAGCCTC TAGATAGAAA 300  
ATAGGTGCCC GTGACCGCAA ACCGACACAG GTAGTnCAAG ATGAGAAnTC T 351

## (2) INFORMATION FOR SEQ ID NO: 4162:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4162:

AnCGTCCTGC TTTGCACGCC AGAGGTCAGC GGTTTCGATCC CGCTAGTCTC CACCATTAT 60  
TTTTTACACG ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT TCCAAAAAAC 120  
GTAActATAA GTTACAAACA TTATTIAGTA TTTATGAGCT AATCAAACAT CATAATTTTT 180  
45 ATGGAGAGTT TGATCCTGGC TCAGGATGAA CGCTGGCGGC GTGCCTAATA CATGCAAGTC 240  
GAGCGAACGG ACGAGAAGCT TGCTTCTCTG ATGTTAGCGG CGGACGGGTG AGTAACACGT 300  
GGATAACCTA CCTATAAGAC TGGGGATAAC TTCGGGGAAC CGGAGCCAAT ACCGGATAAT 360  
50 AnTTTGAACC GCATnGGTCC AnAAGTGAAA GACCGGCTTG 400

## (2) INFORMATION FOR SEQ ID NO: 4163:

(A) LENGTH: 342 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4163:

10 ATTTTATATA TGAAATAATC TGGGACAACA TTCATAAATC TTATTGTCGT CCATTTTTTTT 60  
 AAAATAATAC CAATCTCATT TTAAATTCT AACTTGGTT TCGTATAATA CGCTCTTAAA 120  
 TCTTTAAATT TAGGATTTAT TTCTGTTGGT ACTTGTTTTG TGGTTGGCGA TTGTGGTGTG 180  
 15 TCTGATTTAG TAGATTGCAT TGGTTGTGGC GTGTTTGTG ATGGAGGTGT TGTCACTTTA 240  
 GTTGnAAGGC GGTGTTGTCTG CATTGCTGT TTGTTGCGGT GCTTCTACTT TnATTGCAGG 300  
 CGGTGTTGTC GCGTTTGGTT TTGnATGCGG TGCTTCTATT TT 342  
 20

(2) INFORMATION FOR SEQ ID NO: 4164:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4164:

TCACGACACG AGCTGACGAC AACCATGCAC CACCTGTCAC TTTGTCCCCC GAGGAAGGGC 60  
 TCTATCTCTA GAGTTGTCAA AGGATGTCAA GATTTGGTAA GGTTCTTCGC GTTGCTTCGA 120  
 35 ATTAAACCAC ATGCTCCACC GCTTGTGCGG TTCCCCGTCA ATTCTTTGA GTTTCAACCT 180  
 TGCGGTCGTA CTCCCCAGGC GGAGTGCTTA ATGCGTTAnT GCCAGCACTA AAGGGGCGGA 240  
 AACCCCCTAA AACTTAGCA CTCCATCGTT TACGGCGTGG AACTACCAGG GTATCTAATC 300  
 40 CTGTTTGATC CCCACGCTTT CGCACATCAG GTCATTAACA GACCAGAAAT CGCTTGGCCA 360  
 nGGGGGTnCC nCCAAACTT TGGGGATTTA ACGGTAAAAA 400

45 (2) INFORMATION FOR SEQ ID NO: 4165:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4165:

GCATTAATTT CATGTGTACC TTCGTACGTG TAAATCGCTT CTGCATCAGA GAAGAAACGT 120  
 GCAATATCAT AATCGTCAGC TAGTATGCCA TTACCACCTG TAATACCGCG GCCCATAGCT 180  
 5 ACTGTCTCAC GCAAACGTAA GGCATTTCATC ATCTTCGCCG TTGAAGTTGC AACCTCGTCA 240  
 TATTCAACCAT GTGCTTGCAT ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGAGCTAAA 300  
 10 TTAnCTTGCA TCATTGCTAG CTTTCCTGTA TTAACGGATA TTAATAATnG GTTGCCGAAT 360  
 GCTTACGCTC AGGGACnTAA CnAAGTGGCA CGTAAGCGGC 400

## (2) INFORMATION FOR SEQ ID NO: 4166:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4166:

AAAGTTCTTT GGAAATAGTA ACGTTGAAGT TGTACTCACT GGTGATACAT TTGATCACTG 60  
 25 TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTATAG ATCCATTCAA 120  
 TAATGTTTCAT ACAATTTCTG GACAAGGTAC GCTTGCTAAA GAAATGCTAG AACAAGCAAA 180  
 30 GTCTGACAAT GTTAACTTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTT 240  
 AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG GAAAATTATA GGTGTTGGAA 300  
 CCTTCAGGTG GCAAGTAGTA TGGTATGGAA TcGGTGGTG GGTAAATAAT CcGGTnGTC 360  
 35 CACATTGGCC CTAATAACCG ATAAAATTG GGGGGCCGGG 400

## (2) INFORMATION FOR SEQ ID NO: 4167:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4167:

CTTATAATCC ACACCCTGAG CAAACGCTnC TTATGACAGA GTATTAAAAT AAGCCGATAA 60  
 50 AGATACACAC CTTTACCGAC TATTTAAAAT ACACCTCACC AATTCAATTTT AATTTAATGG 120  
 ATTGAAGTAA CTAAATTAAT ATTATGTTGT TCAATTAAAA GCTTCATACA AACCTAATCT 180  
 ATTTGCACTC CACCGGTAAC ACCGAACACT TGTCCGGTTG TATAACTTGA TTCTTCTGGA 240

GTTTTTTGTA CCAAATGnTT GGGGATTTTA CTTnGTGGGT TGTCCACCAG AAATTTGT

358

(2) INFORMATION FOR SEQ ID NO: 4168:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4168:

15	TTTCTTGACC ATATGGACGT AAAGAGATGT TAGCATCACA ACGTAAAGAT CCCTCTTCCA	60
	TCCTAACGTC TGATACACCA GTGTATTGAA TAATTGAACG CAATTTTCT AAATATGCAT	120
	ATGCTTCTTT AGGTGAACGA ATATCTGGTT CAGATACGAT TTCAATTAGC GGTGTACCTT	180
20	GACGGTTCAA GTCAACTAAT GAATACTCAC CTTTATGTGT TGACTTACCA GCATCTTCTT	240
	CCATGTGGAA GACGAGTAAT ACCGATTCGT TTTGTTTCAC CGTCGACTTC GATATCGATA	300
	TATCCATTTT CACCAATTGG TTGATCAAAT TGAGAAntTG AGAGCTTnTG GnTTAGCTGG	360
25	ATAGAAATAG TTCTTACGGT CAACTTAGAT CCGTTGCGAT	400

(2) INFORMATION FOR SEQ ID NO: 4169:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4169:

	ACCATGTTTG AATGAATCCA TTGGAATCAT TATTGAAGTA AATTAAGGAA TCTATAATGT	60
40	TCGTAAATA AACTGATCC CGTTGTGCTT CACACCCGAT AGATAGGGAT TTACAGATAA	120
	ATTCAGGTCT CTCCACGTC ATATTTGGAC CCATCGAAAA TTCGGGTTCT CAAATCATCG	180
	AACATAACAA AAGAAGCTAA GCAACATGTA GGCCGTTGTC ACTTAACTTC TTGTTTTTCC	240
45	GATGACAGCT TCTATTTAGA GAATGTCATG ATTATTTTAT ATTCATTCA ATGTTATCAA	300
	TATTAGTGCC ATCTATGACA TCTGCCATGC GATTTTCTTG TAATTTTTTG TGCAATCAAC	360
50	GTGTACnTCC ACGGTTTTCA TTTAAAnACA ATTTACCGGA	400

(2) INFORMATION FOR SEQ ID NO: 4170:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 395 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4170:

TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCCTAA GGTAGCGAAA	60
10 TTCCTTGTCG GGTAAGTTCC GACCCGCACG AAAGGCGTAA CGATTGGGC ACTGTCTCAA	120
CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG ACAGGACGGA	180
AAGACCCCGT GGAGCTTTAC TGTAGCCTGA TATTGAAATT CGGCACAGCT TGTTACAGGA	240
15 TAGGTAAGGA GCCTTTGGAA ACGTGAGCGC TAnTTTACGT GGrAGGCGCT GGGTGGGGAT	300
ACTTACCCTA AGCTGTGTTG GCTTTCTAAC CCGCACCAnt TATCGTGGTG GGGAGACCAT	360
GGTCAAGCGG GGCATTTTGA ATGGGGGGCG GTTCG	395

20

(2) INFORMATION FOR SEQ ID NO: 4171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 371 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4171:

TACATTATAG CTTTAATCGT TTGAAGTATA GTTTGAAACC AGTAGTCACA GCTGTTCAAG	60
GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG TACTTTACTC ACCTATTGTT GTCGCTGCAA	120
35 GTGAAACATA TATCGGTCTT GTTGAAGCAG GTGTTGGCTT ATTACCGAGT GGCGGTGGCC	180
TTGCAGAAAT GGCTGATCGC ATATTACGCA CATCGCATAA GTTTGATGAC AAACAAGCTT	240
CCATGACAAA AGTACTGACG AATATCGCAT TCGGAAnGCT CTACAAATGC CTTTGAGGCA	300
40 CGTCGTATGG GTATTTACCG TGGATACAGA TACGATnATT TCCAATACAG CACAACGnGT	360
CGAAGTGGCG C	371

45

(2) INFORMATION FOR SEQ ID NO: 4172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4172:

55

GCTGAGCTAA GCCCCATAA TAATTACAGT ATATCGGGAA GACAGGATTC GAACCTGCGA 120  
 CCCCTTGGTC CCAAACCAAG TGCTCTACCA AGCTGAGCTA CTTCCCGTAT AATTAACGCG 180  
 5 CCCGATAGGA GTCGAACCCA TAACCTCTTG ATCCGTAGTC AAACGCTCTA TCCAATTGAG 240  
 CTACGGGCGC ATATGTTTTT ATTGAAAATn GTGCCGAGGA CCGnGAATGAA CCGGTACGTG 300  
 ATCATTACCG CAGATTTTAA GTCCTGTGCG TCTGCCAGTT CCGCAnCCCG GACTATAAAA 360  
 10 T 361

## (2) INFORMATION FOR SEQ ID NO: 4173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4173:

GTACAGATGC ATTGTTAAAC AATCAGTTGC AACAGCTGTT GAAACTGGTA GAGTATCTAA 60  
 25 TGGTGATTTA ATCATTATTA CTGCTGGTGT ACCAACTGGT GAAACTGGAA CTACTAATAT 120  
 GATGAAAATC CACCTAGTTG GTGACGAAAT TGCTAATGGT CAAGGTATTG GACGTGGATC 180  
 AGTTGTTGGT ACTACGTTAG TTGCTGAAAC TGTTAAAGAT TTAGAAGGTA AAGATTTATC 240  
 30 TGACAAAGTT ATCGTTACTA ACTCCATCGA TGAAACGTTT GTACCTTATG TAGAAAAAGC 300  
 TTTAGGCTTA ATTACAGAAG AAATGGTATT nCACACCCAG TGCCATGGTT GGTTAGGAAA 360  
 AGnAATCCCA CCGTTGTAnG 380

## (2) INFORMATION FOR SEQ ID NO: 4174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4174:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAG 60  
 CTGAGCTGTG ATGGGGAGAA GACATTGAGT CTTCAAGTC GTTGATTTCa CACTGCCGAG 120  
 50 AAAAGCCTCT AGATAGAAAA TAGGTGCCCG TACCGCAAAC CGACACAGGT AGTCAAGATG 180  
 AGAATTCTAA GGTGGAGCGA GCGAACTCTC GTTTAAGGAA CTCGGGCAAA ATGGACCCCG 240

GCCCAAGCGC TGTATTATCCA AAACACAGTC TCTGCTnAAC CGTAGGGGAT TGTATAGGGG 360  
 CTTACGCCTG CCCGGTGCCT GGAAGGTTTA AAAGGGTGGT 400

(2) INFORMATION FOR SEQ ID NO: 4175:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4175:

AGCCATGGCT CAGCGAGGTA GGA CTGGAAC CTACGACCGA TCGGTTAACA GCCGATAGCT 60  
 CTACCACTGA GCTACTGTGG ATTAATATTA TGCTTGCAA CGTTCTACTC TAGCGGAACG 120  
 TAATTCGnAC TACCATCGAC GCTAAGGAGC TTAAGTTCTG TGTTCGGCAT GGAACAGGT 180  
 GTGACCTCCT TGCTATAGTC ACCAGACATA TGAnTGTAAT TTATACATTC AAAACTAGAT 240  
 AGTAAGTAAA AGTGATTTTG CTTGCAAAA CATTATTTT GGATTAAGTC TTCGATCGAT 300  
 TAGTATTCGT CAGCTCCACA TGTGCACCAT GCTnCCACC TCGAACCT 348

(2) INFORMATION FOR SEQ ID NO: 4176:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 344 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4176:

CATTTTTTTA AAATAATACC AATCTCATTT TTAAATTCTA AACTTGGTTT CGTATAATAC 60  
 GCTCTTAAAT CTTTAAATTT AGGATTTATT TCTGTGGTA CTTGTTTGT GGTGGCGAT 120  
 TGTGGTGTGT CTGATTTAGT AGATTGCATT GGTGTGGCG TGTGTGTTGA TGGAGGTGTT 180  
 GTCACTTTAG TTGAAGGCGG TGTGTGCGA TTTGCTGTTT GTTGGGTGC TTCTACTTTA 240  
 GTTGAGGGCG GTTGTGTCG GTTGGTTTT GATTGCGGTG CTTCTATTTT AGTTGAGGGC 300  
 GGTGTTGAnT GTGGTGCTTC CACTTTAGGG nAAGATnAGT GGTG 344

(2) INFORMATION FOR SEQ ID NO: 4177:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 362 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4177:

5 CAGAACCTTG NAATGAATCG CGATGGAATA TCTCTATCTG NAAACAGATT TCTTTTTGTC 60  
 CGCCAATGGC CTTGGAATTG TTAAATAAA TCTATTTGCG CTTCTTTATC AATGTCATAA 120  
 CCTAATGCIT TTAACCTCTC TGAGAAGCGT GTTTACCAGA TAATTTTCCT AATGGAAGTT 180  
 10 CAGTCGTGCT TACACCAACA AGTTGAGGTG TCATAATTC ATATGTTTCA CGATGTTTTA 240  
 ATACGCCATC TTGGTGAATA CCTGATTCAT GACTAAATGC ATTTGGCCAA CAATTGCTTT 300  
 ATTTCTAGGC ACTCGAATAC CTGCATATCT TGAATATAAA TCCGAGGTTT TAGTTCCTCG 360  
 15 AG 362

## (2) INFORMATION FOR SEQ ID NO: 4178:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4178:

25 GGAGCTAATA CCGGATAATA TTTTGAACCG CATGGTAAAG NTGGAAAGAC GGTCTTGCTG 60  
 30 TCACTTATAG ATGGATCCGC GCTGCATTAG CTAGTTGGTA AGGTAACGGC TTACCAAGGC 120  
 AACGATGCAT AGCCGACCTG AGAGGGTGAT CGGCCACACT GGAAGTGA GA CACGGTCCAG 180  
 ACTCCTACGG GAGGCAGCAG TAGGGAATCT TCCGCAATGG GCGAAACTTn ACGGAGCAAC 240  
 35 GCCGCGTGAG TGATGAAGGT CTTGGGATCG TAAAACTCTG TTATTAGGGG AGGACATATG 300  
 TGTAAGTAAC TGTGCACATT TTTGACGGTA CCTnATCAGG AAGCCACGGT TTACTAGGGG 360  
 CCCAGAAGCC CCGGTTAATA CGTGGGTGGG nAAGGGTTTT 400

## (2) INFORMATION FOR SEQ ID NO: 4179:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4179:

50 GTTGTTCAG CAGCGACACA GTGTATTCCA TTCTTAGAAA ATGATGACTC AAACCGTGCA 60

GTTGGTACAG GTATGGAACA CGTTGCAGCA CGTGATTCTG GTGCGGCTAT TACAGCTAAG 180  
 CACAGAGGTC GTGTTGAACA TGTTGAATCT AATGAAATTC TTGTTCTGTCG TCTAGTTGGA 240  
 5 AGAGAACGGC GGTGGAACAT GAAAGGTGGA TTAAGATCGC TATCCATTAG CTAAATTTAA 300  
 ACGTTCAAAC TCAGGTACAT GTTACAACCA ACGTCCAATC GTTGCCAGTT GGGAGATGTT 360  
 10 GTTGGnnnTA C 371

## (2) INFORMATION FOR SEQ ID NO: 4180:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4180:

AAAGGGAATC GAATTTTCTT TCTCTTCCTC CGGGTACTAA GATGTTTCAG TTCTCCGGGT 60  
 25 GTGCCTTCTG ATATGCTATG TATTCACATA TCGATAACAT GACATAACTC ATGCTGGGTT 120  
 TCCCCATTCTG GAAATCTCTG GATCAAAGCT TACTTACAAC TCCCCAAGC ATATCGTCGT 180  
 TAGTAACGTC CTTATCGGC TTCTAATGCC AANGCATCCA CCGTGCGCCC TTAATAACTT 240  
 30 AATCTATGTT TCCACCATT TTTATAAGTCA AACGCTCACA TACGGCTTCG TTTTCATTAT 300  
 nTnAAATGCT CATTTACATA AGTAAACTCT GCTTTAAAT-AATT 344

## (2) INFORMATION FOR SEQ ID NO: 4181:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4181:

CCGTGATCGG AAGGTGCGGC TGGATCACCT CCTTTCTAAG GATATATTCG GAACATCTTC 60  
 45 TTCAGAAGAT CGGGAATAAC GTGACATATT GTATTCAGTT TTGAATGTTT GTTCATTCAA 120  
 ATTAATGGGC CTATAGCTCA GCTGGTTAGA GCGCACGCCT GATAAGCGTG AGGTCGGTGG 180  
 50 TTCGAGTCCA CTTAGGCCCA CCATTAATTT AATACCTATT TGGGGGCTTA GCTCAGCnGG 240  
 GAGAGCGCCT GCTTTGCACG CnGAGGTCAG CGGTTTCGATC CCGCTAGTCT CCACCATTAT 300  
 55 TTGTACATTG AAAACTAGAT AAGTGAnGTA AAAATATAGA TTT 343

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4182:

CAGAGCCAAC TCGTATGTGA TTTGTCTGCG CCAATGTATG CATCATCAAA AGTTCTGGAC 60  
 TACTACACGC AAACGCTGGT ACATTATGAT GTTCCGTAAA CCAAATTCGC TTAAAGCCAA 120  
 GTCGATCTGC TAATTTTGCA AGTGCTACTG AATCTTGCAA TGCCTTTTGT GCATCCTTAC 180  
 CTTTCATCTAT TAAGGCATAG TCTAATACGC TTAATTTAAC CAATCCGTCA TCTCCAAACT 240  
 TATCCTGTCA TGTCAAACCG ACATAACATT TTAGCGTCTT AATACCATTG CCTCTTCATA 300  
 TACCCACGTA TATGATAACG TTTTCAATAA CTTTATATCT TTCGCCTTAT TTTCTTTTCA 360  
 TATCATATTT CAGACTACAA ATGCATCATA GTTAATTAAA 400

(2) INFORMATION FOR SEQ ID NO: 4183:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4183:

AAAGTATGAA AGATGGTAGT GACGCGGTTG GTGATTGGGC TGTATTGAAT GCACTCATTG 60  
 ACACAGCTGC AGGTGGTTCA TGGATTTTCA TCCATCACGG TGGCGGTGTT GGCATGGGAT 120  
 ATTCACTTCA TCGGGGTATG GTTGTGTAG CAGATGGATC AGAGCGTGCT GAAGGAAGAT 180  
 TGGAACGTGT ATTGACGACT GACCCAGGTA TGGTGTGGCC CGACATGTTG nATGCTGGCT 240  
 ATGACATCGC TATTCAAACA GCTAAAGAAA AAGGTATTCA nATTCCAATG ATTGGTGAAA 300  
 GCAGGTGATA AGTAATGAAT GATTTAATAT TAATCAnATA GCAGnTATT TTTACCGGT 360  
 CCAACAGATA AACCTTTGAA GGGTTAGGTA TTAGATGCAT 400

(2) INFORMATION FOR SEQ ID NO: 4184:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 342 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4184:

TTCCCTGTGC ATCGGCATCA CTATTATTAG CATGACTCAA TTATTGGCAT CACAATATGT 60  
 5 CATTGCAGTT ATCATTGGTT TCGTCATATG TCGGATAGGT AATGGTTTAG TCGCAACACC 120  
 TGGACTTACG ATTGCAATTT TCAGTATGCC TAATGAnAAA GTTGGTTTAG CTACAGGATT 180  
 ATATAAAATG AGTGGTACAT TAGGTGGCTC CTTTGGTATA GCACTAAGTA CTACAGTTTT 240  
 10 CAGTATGTTA CAACTAACT ATGCACCAAG TGTAGCTGCA ACCGTAACAT TTATAGTCAG 300  
 CATTGTATTG ATGnTCCTTG GGTnCATTTG CTGCATACAT GA 342

## (2) INFORMATION FOR SEQ ID NO: 4185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4185:

AAGCATACTC TGAAGCGTG AACAAAAATA GAACAGATCA CATTAGACAT TTACTTGAAT 60  
 25 TTAAAGCATG TACACCGATT GACATCGACC AAGTTGAACC GGTAAGTGAC ATTGTCAAAC 120  
 GCTTTAATAC AGGGGCGATG AGTTATGGAT CGATTTCAGC GGAACACATG AAACGTTAGC 180  
 30 ACAAGCCATG AACCAATTAG GTGGAAAGAG TAATAGTGGT GAAGGTGGCG AnATGCAAAA 240  
 CGTTATGAAG TACAAGTTGA TGGAAGCAAC AAAGTAAGTG CGATTnAACA AGTTGCTTCT 300  
 35 GGGCGTTTTG GTGTACTAGT GATTATTTAC CACCTGCCAA GGAATTCCAA TTAnACTTGC 360

## (2) INFORMATION FOR SEQ ID NO: 4186:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4186:

CCCAAGCGGA ATTCTAAAAT GATCGTCGCT CCATTCTTCA TTTTAATAAA TCCAAACGCA 60  
 50 GAATCTTCAA CTGTAAATTC ATCTGGATTC CATGAACCCC AAGCGTTTGC CGCATGATGC 120  
 TGTATTATTA ATTTATGGAA TGTTGAACCC ATCACTGATT CTGGTTCATA ATTATCCATC 180  
 ATCCATAACG TTAAATCTAA AGCGTGTGTA CCGATATCGA TTAATGGTCC TCCACCTTGG 240

nCTTTCCGAA GTTAAATGTC TCCTAAGTCG CCACGTTGGC GCTGCCTGGA TGGAAAATTG 360  
GACGATCTGC TCGGGAAACG AATTTGGATA AACnGATGGG 400

(2) INFORMATION FOR SEQ ID NO: 4187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4187:

GAATCATCTG GCAACnCCC CCAAAGAAGG TAATAATCCT GTAGTCGAAA ATGTTGTCTC 60  
TCTTGAGTGG ATCCTGAGTA CGACGGAGCA CGTGAAATTC CGTCGGAATC TGGGAGGACC 120  
ATCTCCTAAG GCTAAATACT CTCTAGTGAC CGATAGTGAA CCAGTACCGT GAGGGAAAGG 180  
TGAAAAGCAC CCCGGAAGGG ATGTGAAATA GAACCTGAAA CCGTGTGCTT ACAAGTAGTC 240  
AGAGCCCGTT AATGGGTGAT GGCCTGCCTT TTGTAGAATG AACCGGCGAG TTACGATTTG 300  
ATGCAAnGTT AAGCAGTACA TGTGGAGCCG TAGCGAAAGC GAnGTCTGA 349

(2) INFORMATION FOR SEQ ID NO: 4188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4188:

TGGATCCTGA GTACGACGGA GCACGTGAAA TTCCGTCGGA ATCTGGGAGG ACCATCTCCT 60  
AAGGCTAAAT ACTCTCTAGT GACCGATAGT GAACCACTAC CGTGAGGGAA AGGTGAAAAG 120  
CACCCCGGAA GGGGAGTGAn ATAGAACCTG AAACCGTGTG CTTACAAGTA GTCAGAGCCC 180  
GTTAATGGGT GATGGCGTGC CTTTTGTAGA ATGAACCGGC GAGTTACGAT TTGATGCAAG 240  
GTTAAGCAGT AAATGTGGAn CCGTAGCGAA ACGAGTCTGA ATAGGGCGTT TAGTATTTGG 300  
TCGTAGACCC GAAACCAGGT GATCTACCCT nGGTCA 336

(2) INFORMATION FOR SEQ ID NO: 4189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4189:

5 CAAAGGATGT TAAGAAATAC AATTTATTAC CCAGCATTTA ATAATGGTGC TATAGAAGGA 60  
 ATTAATAATA AGATAAAATT AATCAAGTGA ATTTCCTTTG GTTACAGAAA TTTCAACAAC 120  
 TTAAAGCAC GTATAATGAT GATTTTCAGC TTGTACAAAG GAGAAAAAAA GAAGACAACC 180  
 10 AAGCCCAATA ATGGACTGGC CGCCTAATAA TAAAAGCTCT AAAAGTTGTA TTTTAAAAAT 240  
 AGTTCTTTAA ATTATATACC CACCACATTT GGTGGAGGAC CTAAAAAAA GCACITCCCC 300  
 AAAAATGGGA AAGTGCAAGT AGTGAGCCnT AGGAGGGTTC GGACCCTCTn nCCCCCTCT 358

## (2) INFORMATION FOR SEQ ID NO: 4190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4190:

25 TCACCAAGTT GAGCAAAGAA GATGTTCTGC GTACCTTGAA CTAAGTGCCC TTTGACTTCT 60  
 AAnGTACCAC CAAGTGCCGT CTGCCAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT 120  
 30 GGACCTAACA ATCTTAAGAT GAAGCCATAA ACAAAGTAC CGATGGCACC TGTTTTCGTT 180  
 ACAATCCAC CAACATGATA AATGCCGGCT TGTATGCTTG GCCAAATGAA AAACATCAAT 240  
 ACACCTAAAA AGATTGCGGC AAATGCTGTG ACAATAGGGA CAnATGTAGA GCCACCAAAG 300  
 35 AAACCTAAAT ACGGTGGTAA TACCATTGTG GnTATTTGTT GTGAAGTATT GCGGTCATAA 360  
 TA 362

## (2) INFORMATION FOR SEQ ID NO: 4191:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4191:

50 TGATCACCCA TGTTCTGGAC TCCAATTGA AATTGAATTG GGCAATCGGA GTTTGTCTGG 60  
 nATTCGGTAA CCCGnGCAGG GTCCCCTCGT GCCAAACAGT GCTCTACCTC CAATAATCAT 120

nATTTCTCCG CTAACCTCAG TTCATCCGCT CACTTTTCAA CGTAAGTCGG TTCGGTCCTC 240  
 CATTCA GTGT TACCTGAACT TCAACCTGAC CAAGGTAGAT CACCTGGTTT CGGGTCTACG 300  
 5 ACCAAATACT AAACGCCCTA TTCAGACTCG CTTTCGCTAA GGCTCCACAT TTA CTGCTTA 360  
 AC 362

(2) INFORMATION FOR SEQ ID NO: 4192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4192:

20 CGTGTATTAT GCCTTCTACA TTGGCCATTA TGAAACTTA TTATCAGGGT GCTGAACGTC 60  
 AGCGTGCCTT AAGTTATTGG TCTATCGGTT CTGCGGGTGG CAGTGGTATC TGTTCACTCT 120  
 TCGGTGGTGC AGTTGCGACA ACTATGGGTT GGAGATGGAT TTTATCTTC TCAATTATCG 180  
 25 TTGCCGTA CTCAATGTTA CTCATCAAAG GGACGCCTGA AACGAAATCA GAAATTACCA 240  
 ATACACATAA ATTTGACGTT GCAGGGCTAA TTGTTCTAGT AGTATGTTGC TAAGTTAAAC 300  
 GTTGTCACTA CTAAAGGTGC AGCACTTGGT TACACATCAT TATGGGTCTT GGGTTGAATG 360  
 30 CCAATCGGAA ATTGTAGCAT CnTTAATTTC CTAAAAGGTG 400

(2) INFORMATION FOR SEQ ID NO: 4193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4193:

45 AATCCCATGG ACCCTCAAAT TCTTTATCTA AATAGTACCC TAATGAAGTT TTTCTGTGCA 60  
 TGTGATTAAT TTCATGTAAA CCGATGACAC CAACTAGCGT TCCTTCATAC CAAATGCCAC 120  
 ACTGAAATCC ATTACCATCA GCAAATTGCA AAAGTCCTCT TTTAATAAAT GCACGCGTAT 180  
 50 CTGATGGTTG CTCAGTTGCA TCTACCCAAG GTAACCATT CTAAGTGAA TTTCTTGAAC 240  
 GATTGACTAA ATTGAAAAGC GCTTCTGTGT CATGAGCTTC TAAAATTTTA ATGTTATTGT 300  
 TCAATCACTT TCATTCCAAA CATACnATCA CATCCTCATT CATnTCATA TAATCCGGnA 360

## (2) INFORMATION FOR SEQ ID NO: 4194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4194:

ACAAAGGACG ACATTAGACG AATCATCTGG AAAGAGAATC AAAGGTAATA ATCCTGTAGT 60  
 CGAAAATGTT GTCTCGAGTG GATCCTGAGT ACGACGGAGC ACGTGAAATT CCGTCGGAAT 120  
 CTnGGAGGAC CATCTCCTAA GGCTAAATAC TCTCTAGTGA CCGATAGTGA ACCAGTACCG 180  
 TGAGGAAAGG TGAAAAGCAC CCCGGAAGGG AGGTGTAAAT AGAACCTGAA ACCGTGTGCT 240  
 TACAAGTAGT cAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGAAT GGAACCGGCG 300  
 AGTTtACGAT TTGgAtTGCA AGGTTAAGCA GTAAATGTGG GAGCCGTA 348

## (2) INFORMATION FOR SEQ ID NO: 4195:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4195:

AAGGCAGATG CTCTCCCAGC TGAGCTAATT CTCCGATTTA AAAGTGCCTG GCAACGTTCT 60  
 ACTCTAGCGG AAnTAAGTnG GACTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCCG 120  
 CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA 180  
 TTCAAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAAG 240  
 TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC TCGAACCTAT 300  
 TAACCTCATC ATCTTTGAGG GATCTTATAA nCGAGTTGGG 340

## (2) INFORMATION FOR SEQ ID NO: 4196:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAAATTAA TGAAAGATAC AGTAGGTGCT 60  
 GATGTAGAAG TAAAAGCATC AGGTGGCGTA CGTAATTTAG AAGATTTCAA TAAAATGGTT 120  
 5 GAAGCAGGTG CGACACGTAT TGGTGGGAGC GCnGTGTTCA AATTATGCAA GGTTTAGAAG 180  
 CAGATTCAGA TTTACTAATAT ATATnAATnT TGGGAGTGAT AGCTATGACA AGACCATTTA 240  
 10 ATCGTGTA TTTAATCGTA ATGGATTTCAG TAGGTATTGG TGAAGCGCCA GACGCAGCTG 300  
 ATTTTTAAAG ATGGAGGTTT ACATACTTTT A 331

## (2) INFORMATION FOR SEQ ID NO: 4197:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4197:

GTAGACGTCC CGATAGCCGT TACGCATGGT TACGATGTGT ATTGGTGTCTG GCATGGGTGC 60  
 25 AGCTGCTATA TTTGAATATG TCGTTAGAA TGGTTGATTT TGGATGAAGC GGATTCGTTT 120  
 TGTATTGAA TGAAGTAGGC TGAAGTTGAA GCCAGTTGAA GTTGAAGCGG GTTGAAGCAA 180  
 30 TTTCGTTTTA TTGAATGAAG CTGTGTGAAA TATAGTGATT GAACAAAAAA AGTGGTTTAA 240  
 TGGGATGGTG GTTATTCCG TTTTAGAATT TAACATTAC ACGTCTAATT TTAAATCATT 300  
 GTTTTAAATT TTATGAATCG AAGCCCTTTG GATTTAATAN TATTGCTAAT GCnAGTAACT 360  
 35 nATCTGATTG T 371

## (2) INFORMATION FOR SEQ ID NO: 4198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4198:

GCGACCCCAA CCTTGGCAAG GTTGTTnATTC TACCGCTGAA CTACTTCTGC ATATGCGGGT 60  
 50 GAAGGGAGTC GAACCCCCAC GCCGTAAGCT nAGnATCCTA AGTCTAGTGC GTCTGCCAAT 120  
 TCCGCCACAC CCGCAAATGG TGAGCCATAG AGGATTTCGAA CCTCTGACCC TCTGATTAAA 180  
 AGTCAGATGC TCTACCAACT GAGCTAATGG CTCTTCCATG GTGCCGGCCA GAGGACTTGA 240

TAAGAATAAA TGGTGGAGAA TGACGGGTTT G<sub>n</sub>ACCGTCGA CCCTGTGCTT GTTAAGGCAG 360  
 ATGGTTTTCC CACTGGGGTA AATTTTCCGA TTTAAAAATG 400

(2) INFORMATION FOR SEQ ID NO: 4199:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4199:

ATCAGTTGCT GTTGC GCCTT GTGGAATGA ATTTACTAGT CGTACACCAA TAACCTCTGG 60  
 AATTGGGAAA TAAGAAGGTT GTCCAAGCAT TCCAGCTTCA GCTTCAATAC CACCAACACC 120  
 CCATCCTAGT ACGCCAATAC CATTTATCAT TGTGTATGT GAATCAGTAC CAACTAATGT 180  
 ATCTGGAAAT GCAGTTTTTT CACCATCTAC ATCAGGAACA TGTACAACAC TTGCTAAATA 240  
 TTCTAAGTTA ACTTGGTGAA CTATTCCAGT TGCAGGAGGG AACTGCATTG TAATTATCAA 300  
 ATGCTTTTCGG TTGGCCCAAT TTAaaaaaCT GGATAACGTT CATnGTTACG TTCCAATTCC 360  
 TAATTTCCnA ATTACGGTTC CAnGAGCTTC TGGGATTTTG 400

(2) INFORMATION FOR SEQ ID NO: 4200:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 335 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4200:

CAACCTTTAT TGGTAAAAAC ACCCCAGCCA GGCACCTTAC GCCTACGCAT CGCTTGTACA 60  
 CGTGCTACTA nAGGTTTACC AACCACACCT GATTCAATTG CTTTTTTAGC AGTAATTGCC 120  
 ACATCTGTGT GACGATAATG ATATGCGACA GTTAATAATT TGTGATTTTT ATTAGCCGCT 180  
 TCAATCATGC GATCACACTC TTCCGTCGTC ATCGCCATTG GCTTTTCACA CAATACATGG 240  
 CACACCATGG TTCAATGChT CTATAGAAAG ATCAGCAGGA ATTTATTAGG TGTACAAATG 300  
 ACCCATCAAC AAGTTTAAAC AGCTCGCTAG GTGnC 335

(2) INFORMATION FOR SEQ ID NO: 4201:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 370 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4201:

ATGATGTGGC GGTGGTGAAA TCAGACCGAT ACCTGGCGTT GACCCTCTTG TCTTCGCAAT	60
CCACGGATAT ACCTTAGTAC CAGGTAATTG ACCACCTTCA CCAGGCTTTG CACCTTGCGC	120
AACTTTAATT TGAATTTCTT TGGCATGTTG TAAATAATCA CTAGTTACAC CAAAACGCCC	180
AGAAGCAACT TGTTTAATCG CACTTACTTT GTTGCTTCCA TCAACTTGTA CTTCATAACG	240
TTTTGCATCT TCGGCAACTT CACCCTATT ACTCTTTCCA nCTAATTGGG TCATGGGCTG	300
TGCTAACGTT TCATGTGCTT CCGnTGnAAT CGATCCATAA CTCATCGGCC CCGTATTAA	360
GCGGTTGGAC	370

(2) INFORMATION FOR SEQ ID NO: 4202:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 380 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4202:

CAGCTAGCGA CTTACCTTGA CGTTTTGnGT ATTCATTCCA GCTTTGTnGG AATGAGtCGG	60
gATATAAGCA TCTTTAGATA ATGCACCATC AACTAATGGA TATTTATGTC CAGTTGGaGC	120
CAGAAATCAT AAACGTCTTC AGTGTAAGCA ACAGCATCTT CaTTTAATGC CAAAATGCTT	180
GGaTTAgTGC AATAACCATC GCAACTGnGC CAaACCTTGT GTTGGCTCGC CGCCTGAATT	240
CAATCCATAA CGTGCTGTAT CTGTAGCAAT AACTAATACT TTTTCATTG GTCTAGTTGC	300
TAAATAATCT TTAGCTAATT GAATTGCTGG TGTTGCAGCA TAACAAGCTT CTTTCATTTC	360
AAAGCAGCGT GCAAAAGGTT	380

(2) INFORMATION FOR SEQ ID NO: 4203:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4203:

GACATGTCAC CAAGAGCATT AGAAGAAGTT ATTTACTTTG CTTCTTATGT TGTGTAGAT 120  
 CCAGGTCCAA CTGGTTTAGA AAAGAAACT TTATTATCTG AAGCTGAATT CAGAGATTAT 180  
 5 TATGATAAAT ACCCAGGTCA ATTCGTTGCA AAAATGGGTG CAGAAGGTAT TAAAGATTTA 240  
 CTTGGAAGAG ATTGATCTTG ACGAGGAACT TAAATTGTTA CGCGATGAGT TGGGAATCAG 300  
 10 CTACTGGGTC CAAAGACTTA CTCCGTGGCA ATTAACGGTT TAGAAGTTGT TnGAATCATC 360  
 CCGTAATCCA GGGTACCACC CTCCnnGGnT GGATTTAGGA 400

## (2) INFORMATION FOR SEQ ID NO: 4204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4204:

AAATTCTTCC GCCCTGTAAT TCCTTAACCG CTTCAACGGC ATCGTnAATn TCTTACATTT 60  
 25 AGATAAAGAT GCATTGCAAG ATATCGTCAA CTTATTATTA GACGATGTAC AAGTTACATT 120  
 AGACAAAAAA GGTATTACGA TGGACGTTTC TCAAGATGCG AAAGATTGGT TAATTGANGA 180  
 30 AGGCTATGAT GAAGAATTAG GTGCACGTCC ATTAAGACGT ATTGTTGAAC AGCAAGTACG 240  
 TGACAAAATT ACAGATTACT ATTTAGATCA TACAGACGTT AAACATGTGG ATATAGATGT 300  
 TGAGGATAAC GAATTAGTCG TAAAAGGTA 329

## (2) INFORMATION FOR SEQ ID NO: 4205:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4205:

GGTAAACAAA AAACCTCCCT TTGGAAGCGA ATTATGGAGC GGAAGATAGG ATTTACACCT 60  
 ATACCTCGTT CCGGGAAGGG CTGTTTCTAA AAGTTGAACT ACTCCCGCAA ATATTAAATT 120  
 50 ATGGAGCGGA AGATAGGATT TACACCTATA CCTCATTCCA GGAAGGAATG TATTCTAAGA 180  
 GTTGAAATAC TCCCGCATTA TTATTAAATT ATGGAGCGGA AGTAGGATTT GCACCTATAC 240  
 CTCGTTCCGG GAAGGAGCTG TTTCTAAAAG TTGAACTACT ACCGCATAAA CCTGGTGGCG 300

## (2) INFORMATION FOR SEQ ID NO: 4206:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4206:

TACTTTGTGA ATCCAGAAAA CTTTGAGGAT GTCACATAATA GTGTGAATAT TACATTCCCA	60
AATCCAAATC AATATAAAGT AGAGTTTAAT ACGCCTGATG ATCAAATTAC AACACCGTAT	120
ATAGTAGTTG TTAATGGTCA TATTGATCCG AATAGCAAAG GTGATTTAGC TTTACGTTCA	180
ACTTTATATG GGTATAACTC GAATATAATT TGGCGCTCTA TGTCATGGGA CAACGAnnAG	240
CATTTAATAA CGGATCAGGT TCTGGTGACG GTATCGATAA ACCAGTTGTT CCTGAACACC	300
TGATGAGCCT GGTGAAATTG AACCAATCCA GGGATCAGAT CTGACCCAGG TCAGATCTGG	360
CAGCGATCTA ATCAGnAGCG GTCAGATCGG GnAGGATCAC	400

## (2) INFORMATION FOR SEQ ID NO: 4207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4207:

AAAAAGTTGA GAAAAATGTT TGAATCAGCA AACGTTGTGC AATCGAAATT TCCACACCAT	60
CAAAACCTGC TTTAATCGCG CGTAATGTAG CATCGCnGwk ACTGCTGAAT GATGCTATTG	120
ATTTTCTCAT GAGACATGGC GATAACATCG TGTTtCAATC GGTGAATGCA ATGwCATAGG	180
GCTTGGTCCA TACACCTTTC CAAAATTTAA AATGGCTTGA TTTGAAAAAC GACCAGCATG	240
CGCTACTGGG ATAATAGCGA GGCTACCATG TTGTTTCATC GTAGATCCCA TGTTAGTTAA	300
TCCAGGGATA CAACCATCAT GATCAATATT AAAnCATATC CAACCATTGA CCATAAGGTC	360
AATGTAACAC GCCGGTGACT TCATCCAGCT GAATAGACGC GT	402

## (2) INFORMATION FOR SEQ ID NO: 4208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4208:

5 GAAGAGTTGC AGCAGCAGAT ACAATTTATC CATTCACTCA AGCTGAAAAT GTTTGGTTAC 60  
 CAAACAAAAA TGACATCATC GAAAAAGCAA AAGAACTTT AGAATTTTAA TACATTTTAA 120  
 AAGTTAACGA ATTAGCCGTG ATTTIAGTCT CATTGATTAA AATGAAATnG TTAATTTACG 180  
 10 AAATCTTAGG AGGGCAAAAA CGTGGGCATT TGAATTTAGA TTACCCGATA TCGGGGGAAG 240  
 GTATCCACGA AGGTGAAATT GTAAAATGGT TTGTTAAAGC TGGAGGATAC TATnGGAAGA 300  
 AGACGATGTT TTAGCTGGAG GTACAAAACC GATAAATCAG TAGTAGAAAT CCCCATCCAC 360  
 15 CAGCATCTGG TACnGGTAAG 380

## (2) INFORMATION FOR SEQ ID NO: 4209:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4209:

25 AATAAACCTC AGGCTATTCA ATGGCATACA AATTTAACGA ATGAGCGATT CACTACTATC 60  
 30 GCACATCGTG GCGCAAGTGG CTATGCACCC GAGCATACGT TTCAAGCATA TGATAAGAGT 120  
 CATAATGAGT TAAAAGCATC TTATATCGAA ATTGATTTAC AACGTACCAA AGATGGCCAT 180  
 TTAGTTGCTA TGCATGATGA AACTGTTAAC CGTACAACAA ATGGACACGG TAAAGTTGAG 240  
 35 GATTATACCC nTGATGAATT AnAACAGTTA GATGCAGGAA GTTGGTTAAT AAAAAATATC 300  
 CnAAATACGC CAGAGCAGTA TTAAAATGCT AAAGTACCAC TTAGGTGGAA TTTAGGACGT 360  
 ATTGGCCCCG TGCCAACnTT TATATTGAAC CAAGCACCTG 400

## (2) INFORMATION FOR SEQ ID NO: 4210:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4210:

50 GCCCCACAACC ACAAGGCTG TAGGCTACAA ATATGGAGAC GCGGGGATTT GAACCCGCGT 60

55

AAAAGTGATA AACAAACCAAC ATGATGCTAG TTTGATTAAAG TTTCTTCTAA ACAGACTTCA 180  
 AACGGCATnG TTAGCATATC CTATTAAGGT TGAATCGCGT TAACAGCACA TAGGAAATGC 240  
 5 TGTTAGGCCA TGCAGAGTGC GATTAGGCAG CTA CTGCGAA ATTATTGTnT GATTTGCCAG 300  
 TTATTATnAA CTGTGTGGTG TTGATGACGA 330

## (2) INFORMATION FOR SEQ ID NO: 4211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4211:

AAATCATCTT ATGACTGCTT TTTATTATAC TTTACATTTC TCGTTTCGTC AGATTCAAAC 60  
 GTTTTCACTT CGCCAAGCCA TCTTTCTTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT 120  
 AAAAAAAGAG ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTG CCTGGCAACG 180  
 25 TTCTACTCTA GCGGAACGTA AGTTCGACTA CCATCGACGC TAAGGAGCTT AACTTCnGTG 240  
 TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC CAGACATATG AATGTAAATT 300  
 ATACATTCAA AACTAGATAG nAAGTAAAAG TGATTTTGC 339

## (2) INFORMATION FOR SEQ ID NO: 4212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4212:

GCGATGGTTG AAACATTGAC TGATATTAAA GAGTTTATGA ACCAAGTTGA GTCGCATAGC 60  
 TAGTATGAAA CGTGGTGTGC GCATGGGAAC TATCAAGCTT TGAAGATGTG GTACTACATG 120  
 45 CGTTGAATTA GGGATCGGTA CTTTATATGA AGACGTGCTG CTTCCATTAA ATGAGTGATG 180  
 CGATTTTGGC ATGAAGGTCA CCTnAAATGT ACATTGTTGT AATAAAATTG CCTATAAAAT 240  
 TTTTAGCACA TAAAATAAGA GGGGCCAnCC ATTTTAGACT ATAACAACGG TTGGCTCTTT 300  
 50 GAATTGTAAA AAGAAAACCA TACGCTATGn TATT 334

## (2) INFORMATION FOR SEQ ID NO: 4213:

(A) LENGTH: 332 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4213:

10 CTATGATTTC ACCGAGTCTC TCGTTGAGAC AGTGCCCAAA TCGTTACGCC TTTCGTGCGG 60  
 GTCGTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT ATAGTTACGC CGCCGTTTAC 120  
 TGGGGCTTCG ATTCGTAGCT TCGCAGAGTA NACCCACTCC TCTTAACCTT CCAGCACCGG 180  
 15 GCAGGCGTCA CCCTATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT TTGATAAACA 240  
 GTCGCTTGGG CCTATTCACT GCGGCTCTTC TGGGGCGTTA ACCCTAAAGA GCACCCCTTC 300  
 TnCCGAAGTT TACGGGGTCA nTTTGCCGAG TT 332

20

## (2) INFORMATION FOR SEQ ID NO: 4214:

## (i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 363 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4214:

CGCCTGGCAA CGTTCTACTC TAGCGGAACG TAAGTTGGCT ACCATCGTCG CTAAGACCT 60  
 TTCTTGACTT GTGACAATCG CTTCCTTCTT TCCTCTCCTT CGGCTCTCGC TTACTCATTT 120  
 35 AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC 180  
 GCCAAGCCAT TTTTCTTTGT GTTTACTTTT TAnTTTGACG TTTTAGACAT AAAAAAAGA 240  
 GACCTTGCGG TCTCAATGCG GTCATCGCA TCCATTTTTT GCCTGGGCAA CGTTCTACTC 300  
 40 TAGCGGAACG TAAGTTGGGT ACCATCGACG CTAAGAACCT TCTTGGAnTG TGGACAACGn 360  
 TGG 363

45

## (2) INFORMATION FOR SEQ ID NO: 4215:

## (i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 338 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4215:

TTATTTGTAT TGTATAGAGA GAAATAAAAA GAAACCTTGT TTTACAAGGT TTCTAATACG 120  
 TTATGTTATG TAAATAACAG TTAATTATAC CGGTGGTCCG GGTGGAACCG ACACTCCACA 180  
 5 AGTGAACCGG GGATTTTGAG TCCCGCGCGT CTGCCAATTC CGCCACACCG GCTTAATGGT 240  
 AAACAAAAAA CTTCCCTTTG GAAGCAATTA TGGAGCGGAA GATAGGATTT ACACCTATAC 300  
 10 CTCGTTCGGG GAAGGACGTG TTCTAAAAGT TGAATACC 338

## (2) INFORMATION FOR SEQ ID NO: 4216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4216:

ACGGTGATCC CATAATGCTT GAACATCAAT TTCATCCATT AATGTTACAT GAGGTGCAGT 60  
 ATGCTTAGAG TTAACCATTG CTTTCGCAAT TGCTCTACGC ATAGCAGGGA TTTTTCAGT 120  
 25 TGTTTCTGGG AAGTCGCCTT CTAATGTTAC TGCTGCAGGT GCTGCAGGAG TTTAGCAAC 180  
 TTCTTCACTT GTAGCTGAAG CAGCTGATTC ATTTGAAGCT GTTGGTGCAC CACCATTAA 240  
 30 GATGCATCT ACATCTTCTT TTGTAATACG ACCATTTTAA CCAGATCCAG AAATGCTTT 300  
 AATGnTAACA CCTnTTTCAC GTGCGTATTA CGACTGAAGG CATGCCTTAA CAGTCnGGTT 360  
 CACCACTCTC AGTTGAGAGC ACAGGGCTGC nCGCTGGCGC 400

## (2) INFORMATION FOR SEQ ID NO: 4217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4217:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGTACTAAGA TGTTCAGTT CTCCGGGTGT 60  
 GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC 120  
 50 CCCATTCGGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA 180  
 GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA 240  
 TCTATGTTTC CATCCTACAG GAAACGCGTT ATTAATCTTG TGAGTGnCT TTCGAACATA 300

## (2) INFORMATION FOR SEQ ID NO: 4218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4218:

```

GGCGCCCTCG TGCCAAACAG TGCTCTACCT CCAATAATCA TCACCTGAGG CTAGCCCTAA      60
AGCTATTTTCG GAGAGAACCA GCTATCTCCA GGTTCGATTG GAATTTCTCC GCTACCCTCA      120
GTTTCATCCGC TCACTTTTC ACGTAATCGG TTCGGTCCTC CAnTCAGTGT TACCTGAACT      180
TCAACCTGGA CCAAGGGTAG ATCACCTGGn TTCGGGTCTA CGACCAAATA CTAAACGCCC      240
TATTCAGACT CGCTTTCGCT GACGGCTCCA CATTTACTGC TTAACCTTGC ATCAAATCGT      300
AACTCGCCGG TTGCATTCTA CAAAGGCAC GCCATGCACC CATTA                          345

```

## (2) INFORMATION FOR SEQ ID NO: 4219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4219:

```

TCTTATGACT GCTTTTTATT ATACTTTACA TTTCTCGTTT CGTCAGATTG AACGTTTTTC      60
ACTTCGCCAA GCCATCTTTC TTGTGTTTGG CTTTTATTTT GACGTTTTAG ACATAAAAAA      120
AGAGACCTTG CGGTCTCAAT GCGGCTCATC GCATCCACTT TTGCCTGGC AACGTTCTAC      180
TCTAGCGGAA CGTAAAGTTC GnACTACCAT CGACGCTAAG GAGCTTAACT TCTGTGTTTCG      240
GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGGAAT GTAAATTATA      300
CATTCAAAC TAGATAGTAA GTAAAGTGGn TTTGCTTCGC AAACnTTAT TTTGGTTAGT      360
CTTCGTC                          367

```

## (2) INFORMATION FOR SEQ ID NO: 4220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4220:

AAGAGCCTTT CTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCACTT 60  
 ACTCATTTAG CTCTACTAAA CTCGTTGCGT TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 120  
 TTCACTTCGC CAAGCCATTT TTCTTTGTGT TTGCTTTTAA TTTTGACGTT TTAGACATAA 180  
 TAAAAAGAGA CCTTGCGGTC TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT 240  
 TCACTCTAGC GGAANTAACT CGAACTACCA TCGACGCTAA GGAGCTTAAC TTTCTGTGTT 300  
 CGGCATGGGA ACAGGTGTGA CCCCCnTGGC TATAGTCACC AG 342

## (2) INFORMATION FOR SEQ ID NO: 4221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4221:

ACCGGATGAC AGCCCCAGGA TGCGATGAGC CGACATCGAG GTGCCAAACC TCCCCGTCGA 60  
 TGTGAACTCT TGGGGGAGAT AAGCtGTTAT CCCCggggTA GCTTTTATCC gTTGAGCGAT 120  
 GGCCCTTCCA TGCGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG CTCGACTTGT 180  
 AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACTCTCTAT GAATGATTTC CAACCATTCT 240  
 GAGGGAACCT TTTGAGCGCC TCCGTTACCT TTTAnGAGGC GACCGCCCCA GTCAAACGTC 300  
 CCGCCTGACA CTGTCTCnCA CCACGATAAG TGGCGnG 337

## (2) INFORMATION FOR SEQ ID NO: 4222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4222:

GCGCCTTGAC TAAAAAGAAA TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT 60  
 TTACCAAGCA AAACCGAGTG AATAAAGAGT TTTAAATAAG CTTGAATTCA TAAGAAATAA 120  
 TCGCTAGTGT TCGAAAGACA TCCACCAAGn TTAATAACGC GTTTAAATCT TTTTATAAAA 180  
 GAAAACGTTT AGCAGACAAT GAGTTAAATT ATTTTAAAGC AGAGTTTACT TATGTAAATG 240

ACATAGATTA AGTTATTAAG GGCGCACGGT GGGTGCCnTG GCACTTAGAA GCCGCTGAAG 360  
G 361

(2) INFORMATION FOR SEQ ID NO: 4223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4223:

CGGTAGAATA CAACCTTGCC AAGGTTGGCG TCGCGGGTTC GAATCCCGTC TTCTGCTCCA 60  
TTATTTTGCC GGGGTGGCGG AACTGGCAGA CGCACAGGAC TTAAATCCTT GCGGTGAGAG 120  
ATCACCGTAC CGGTTGCATT CCGGTCCTCG GCACCATTTT AGCGCCCGTA GCTCAATTGG 180  
ATAGAGCGTT TGACTIONGGA TCAAGAGGTT ATGGGTTCTGA CTCCTATCGG GCGCGCCATT 240  
TTTAAATTAA TTGAATAACG GGAAGTTAGC TCAGCTTGGT AGAGCACTTG GTTTGGGGAC 300  
CAAGGGTCGC AGTTCGAATC CTGTCTTCCC GATTACTCnT AAnTCCATTT AnGGGGGCTA 360  
GCTCAGTGGG GAGAGCGCTG CTTGCACGCA GGAGGTCACG 400

(2) INFORMATION FOR SEQ ID NO: 4224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4224:

CATAATATAC TCTTAAGTGT AAAGGGGAAT TTCCTGGGTA ATAATTCGCG TGTGCACCTT 60  
GAGTGACTTC TACCATTTTA TAGTCAAATT GCTTTAGTTC GTTTGGTTTA ACGCCGACAC 120  
TCGCAAATGT ATAATCAAAG AACTTCACAA TATTGTTGCC TAAGAAGCCT TTGAATTCAA 180  
TAGTGTCATT TCCAGCAATT TGTTCCGGCA CAATACTTGC TGCACGGGTG AGCGCCCCCA 240  
GnCAAAAGGA CCACTAGCCG GTAGAATCGA CATGTCGATA ATGTGATGGT TGCCAATAAT 300  
CGCCTATTGC ATAATGTTTG GACCATTTGGT TCCAAATTTA TCGTTACCGG TATGAAACCT 360  
TTCGATCCAG TTGATAATT GAACTTCGnA AATTTGATTG 400

(2) INFORMATION FOR SEQ ID NO: 4225:

(A) LENGTH: 328 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4225:

GGGTTCAATT TCTGCATACC AATCGATGCC AGCTCTATTT CTGACAATAT CCATATATTT 60  
 TGAAATTTTC TCTAATTCCT TGCCACTAAC CTTTTACCA TTCAACCAAA ATTGATCCTG 120  
 TGTTAACTGG TCGTTAAAAG TGACTTTCGT TTCAGTGTA AATTTTCTA ATGTAACAGA 180  
 TATGCTATTA TTCATTGGAA TGATTAGTGC TTCATCTTTT TTACCCCAAT ATTTTATnAG 240  
 TGCAATATTC GTATGTGCAC GTGCTTTGCC ACTnnTAATC AACGCATTAA CCTCCTAAAT 300  
 TCTCAATCCA AGTATGTGCT GCACCAGC 328

20

## (2) INFORMATION FOR SEQ ID NO: 4226:

## (i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4226:

30

TGACGGGTTT GAACCGCCGA CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA 60  
 TTCTCCGATT TAAAACTGCC TGGCAACGTT CTA CTCTAGC GGAAnGTAAG TTCGnACTAC 120  
 CATCGACGCT AAGGAGCTTA ACTnCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 180  
 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAA ACTAGATAGT AAGTAAAAGT 240  
 GATTTTGCTT CGCAAAACAT TTATTTTGAT TAAGTCTTCG ATCGATTAGT ATTCGTCAGC 300  
 TCCACATGTC ACCATGCTTC CACCT 325

40

## (2) INFORMATION FOR SEQ ID NO: 4227:

## (i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4227:

GCGCAACTCA CACAACAAGG TGGCAATCAC TCTGAACAAA GTGCGGCAAn TThTTCAACA 60

55

AACCTTACGC AAGAAGCACG TGACGGTTTA TTAGATCCAG TCATTGGTCG TGGATAAAGA 180  
 AATTCAAGnA ACTGCTGAAG TTTTAAGTAG ACGAACTAAA AACAATCCTA TATTAGTTGG 240  
 5 AGAAGCTGGT GTTGGTAAAA CTGCGATTGT TGGAAGGTTT AGCACAGGCA ATCGTTGGAA 300  
 GGAAATGTAC CAGCAGCAAT CAAAGACAAA G 331

## (2) INFORMATION FOR SEQ ID NO: 4228:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4228:

AGAGGTCCGT TGCCTTACCG CTTGGCTATA GCCATTAATA ATAAGGGCGG CTGAAGGGGA 60  
 TCGAACCCTC GAATGTCGGA ACCACAATCC GATGTGTAA CnCTTCACCA CAGCCGCCAT 120  
 GGCAGGGGCA GTAGGAATCG AACCACACACC AAAGTTTTGG AGACCTCTAT TCTACCGTTG 180  
 25 AACTATGCCC CTATTAAAA TAATAAATGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA 240  
 AGAGCGGATT TACAGTCCGC CGCGTTTAnC CACTTCGCTA CCCCTCCATA AATGGTGCCG 300  
 GCCAGAGGAC TTGnAACCCC CAACCTAATG GTT 333

## (2) INFORMATION FOR SEQ ID NO: 4229:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4229:

CTCTTACTTT GTAAACCAAA TCTTAAATTA AAATATTGAA AATGCAATGn ATCCTTAATA 60  
 TTTTATTAAA CCTATAATTA CTTATTAAAA ATAACACACA ATATTCATAA AGTTTTAAAA 120  
 45 ATATTCTGTT TTATCACCTA CTATTAGTGG AAAAGTACAA TTGCAATTGT ATATAGTTTG 180  
 CATAACGCTT CAAAAGTAAT TTCTTTTTTG TTTAGTTCAA AAAAATTTAG AGGTGATGTT 240  
 ATATGAATAA CGGTTTTTTC AATAGCGACT TTGATTCAAT TTTTCGAGGA TGATGAAAGA 300  
 50 TATGCAAGGT TCAAATCAAG TCGGAAACAA AAGTACTATA TThATGGTAA GGAGTTTCAC 360  
 CTGAGGACTG GCGCAACTnC ACACACCAGG TGGCCATCAC 400

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4230:

CATTAACGGG CTCTGACTAC TTGTAAGCAC ACGGTTTCAG GTTCTATTTT ACTCCCCCTC 60  
 CGGGGTGCTT TTCACCTTTC CCTCACGGTA CTGGTTCACT ATCGGTCCT AGAGAGTATT 120  
 TAGCCTTAGG AGATGGTCCT CCCAGATTCC GACGGAATTT CACGTGCTCC GTCGTA CTCA 180  
 GGATCCACTC AAGAGAGACA ACATTTTCGA CTACAGGATT ATTACCTTCT TTGATTCATC 240  
 TTTcCAGATG ATTCGTCTAA TGTCGTCCTT TGTAACCTCG TATAGAGTGT CCTAsAACCC 300  
 CAACAAGCAA GCTTGTTGGT TTGGGnTCTT GCCGTTTCG 339

## (2) INFORMATION FOR SEQ ID NO: 4231:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4231:

GAAGTCATAT GCATACACTT GGTTATCATT ATTCATACGT TCAATCGCAT CTGTAACTG 60  
 AATTTGTTA CCTGCGCCTT CTTTTGCGT TTTTAAATAA TCGAAAATTT CAGGCGTTAA 120  
 TACATAACGT CCCATAATAG CTAGnTTGA TGGTGCCGTA CCTTGTGCTG GCTTTTCAAC 180  
 AAACTTTTTC ACTTCAGACT GACGTCCGn TTTAGTTAAT GGGTCAATAA TTCCATAACG 240  
 ATGAGTATCT GCTTCCGGAA CTTCTTGGAC ACCTATAACT GAGTGCCCTG TnTCTTCATA 300  
 AACGTCAATC AACTGTTTCA CTGCTGGCAC TTCAGAGTCA ACAATATCG 349

## (2) INFORMATION FOR SEQ ID NO: 4232:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4232:

CCAGGATGCG ATGACCGACA TCGAkGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG 120  
 GAGATAAGCC TGTTATCCCC GGGGTAGCTT TTATCCGTTG aGCGATGGCC CTTCCATGCG 180  
 5 GAACCACCGG ATCACTAAGT CCGTCTTTTCG ACCCTGCTCG ACTTGTAAGT CTCGCAkTCA 240  
 AGCTCCCTTA TGcCTTTACA CTCTATGAAT GATTTCCAAC CATTCTGAGG GAACTTTGaG 300  
 10 CGCCTCCGTT ACCTTTTAGG AGGCGACCGC CCAGTCAAAC TGCCCGCCTG ACACTGTCTC 360  
 CCACCACGAT AAGGTCG 377

## (2) INFORMATION FOR SEQ ID NO: 4233:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4233:

GGCTAGCCTC AAGTGATGAT TATTGGAGGT AGAGCACTGT TTGGACGAAG GGCCCCCTCTC 60  
 25 GGGTTACCGA AGTTCAGACA AACTCCGAAT GCCAATTAAG TTAACTTGG GAGTCAGAAC 120  
 ATGGGTGATA AGGTCCGTGT TCGAAAGGGA AACAGCCCAG ACCACCAGCT AAGGTCCCAA 180  
 30 AATATATGTT AAGTGAAAAA GGATGTGGCG TGGCCAGAC AACTAGGATG TTGGCTTAGG 240  
 AAGCAGCCGT CATTTAAGA GTGCGTAATA GCGCACTAGT CGAGTGACAC TGGGGGGAAA 300  
 GGGTACCGGG GCTGAACATA TTACCGAAGC TGGTGGGTTG TCCTTTGGAC AnTTh 355

## (2) INFORMATION FOR SEQ ID NO: 4234:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4234:

ATCCGCCTCC CGCAATATTT TATAGGTCTC GTAGTGTAGC GnTTAACACG CCTGCCTGTC 60  
 45 ACGCAGAGAT CGCGGGTTCG ATTCCCGTCG AGACCGCCAT CATTACATTT TTATTATGGT 120  
 TCAGTAGCTC AGTTGGTAGA GCAATGGATT GAAGCTCCAT GTGTCGGCAG TTCGACTCTG 180  
 50 TCCTGAACCA TTTCTTAGCC GGCCTAGCTC AATTGGTAGA GCAACTGACT TGTAAATCAGT 240  
 AGGTGGGGG TTCAAGTCCT CTGGCCGGCA CCATTTATGG AGGGGTAACG AnTGGGCTAA 300

TTAATAATTT TAATAAGGGG CATAnTTCAA CGGTAnAATA

400

## (2) INFORMATION FOR SEQ ID NO: 4235:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 341 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4235:

ATGCCATGTT CACCTTGTTT AAAATCAAGG TTTGTAATGT TTCCTTGTTT CACGATAATA 60  
 GCGTAATAT CACTCTTTC ATGATTGCGG ATGTAGTCTA AATCAAAGTT GATTAATAAA 120  
 TCACCTTCTT TAACTnTTG ACCTTCCTCA ACATGTAAAG TAAAGCCTTC TCCGTTTAAT 180  
 TTAACAGTGT CTAAACCGAT GTGGATTAAT AGTTCTAAAC CACTATCTGA TACAAGACCA 240  
 ATTGCATGnT TTGTGGGAA AATCATTTGT ACTTTACCGT TGAATGGTGC ACGAACTTCA 300  
 CCTGTGAGG TTTGATAGCG ATACCGTCAC CCATGCATTT T 341

## (2) INFORMATION FOR SEQ ID NO: 4236:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4236:

GTTGATGCAG CCCGTTGAGC TCTAAACCAA CTGAGCTAAA GGTCCTAAAT ATAATTTTAC 60  
 AACTAATAAA TAGTGGCGGT GGAGGGGATC GAACCCCGA CCTCACGGGT ATGAACCGTA 120  
 CGCTCTAGCC AGCTGAGCTA CACCGCCTTA TATAGTTTGT AAATAATATG GTGGAGACTA 180  
 GCGGGATCGA ACCGCTGGAC CTCCTGCGTG CAAAGCAGGC GCTCTCCAG CTGAGCTAAG 240  
 CCCCCATAAT AATTACAGTA TATCGGGAAG ACAGGATTCG AACCTGCGAC CCCTTGGTCC 300  
 CAAACCAAGT GCTCTACCAA GCTGAGCTAC TTCCCGTATA ATTAACGnGC CCGTAGGAGT 360  
 TGAACCCATG AACCTnTTGA TCnTAGTnC AAACGGTCTA 400

## (2) INFORMATION FOR SEQ ID NO: 4237:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 376 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4237:

5 nAntTTCTTGA CCTGACATCA CCTGAAATTG AATGGACATG GTCCACCAGG TCATATACTC 60  
 TAATCCATGG GTCGCCGATA CCTTCAACGn ACAACATCTA CACCACTATT TCTAATACAG 120  
 AATCTTTCTC CTGCACTACC GTTAATAAAT GCCTTACCAC TTGTCGCACC ATAGAATGAG 180  
 10 ACGTTACCAG CAATAATTTT ATTTTGTCTG TCTTCAAAAG GTGCTTTGAC AATGACCGTA 240  
 CCACCAGATA ATCCTTTACC AACATAGTCA TTCGCATCTC CAGTATGATG AATCATTAAAG 300  
 CCTTTCGGTG CATATGCTGC AAGACTTTGA CCAGCATGAC CATTCGTATA AACATTAATT 360  
 15 GTATTTTCAG GAAGTC 376

## (2) INFORMATION FOR SEQ ID NO: 4238:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 335 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4238:

25 CGATTTAAAG CTAAGCCCAT TTTCGCTCTT TCTCCATAGC CTAACCAAGC AATACGTGAT 60  
 GGTAGTCCTT GATATGAAAT TTTTCTTCA GCTAAATCAA GCCATCTTAA TAACTTTTCA 120  
 30 TTTTCTGGGA AAAGTTTGCG CATTTCITCA TCCGCAAGCT CGATATCTTT TGGATCACCA 180  
 CTCAACGCAG CAAAGCGGAA TGGCCCTTTA CCTTCACAGA ATAATGGTCT AATGTAAGCT 240  
 35 GGTACAAAAG CTGGGAAGTC AnAAAGCATT TTCACTCCG TATTGAAGGC TACTTGACGA 300  
 TATGnTACCA TAATCAATGC TACAGCGCCA CGTTG 335

## (2) INFORMATION FOR SEQ ID NO: 4239:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4239:

50 CCACAnTTAC AAGCAACTAC TGAAGGCGCT GTATTATTAA AAGGTGGCGA CGGTTTTGAT 60  
 TTCGGACACG TAGAAAGATT TATTCAAAAC CCGCCACATG GGGCAACGGT TGCATGGCAT 120

TTACCTAATG GTCAAGGTAC GCGTAATGTT GAAGTTCCAG TCAAAGTTTA TCCAGTTGCT 240  
 AATGCAAAGG CGCCATCACG TGATGTGAAA GGTCAAAATT TGCTGTTGGA CGGATGCGAT 300  
 5 GAACTACATT ACATTTGTCC AATACAACAC AGATnGTATC ACTGCAGC 348

## (2) INFORMATION FOR SEQ ID NO: 4240:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4240:

TTGATGTTAA AGATTTAGCA AGGGGCGAGA GAACTGGAGA AGAGGTTGCC AAACGAATGG 60  
 AACGTGCTTC TGTATTGGCC CAAGTAGATA TTCATCGTGC AGCAACACAT AATAAAGGTG 120  
 20 TTATGAATGG CATACATGCT GTTGTTTTAG CAACAGGAAA TGATACGCGT GGTGCAGAAG 180  
 CAAGTGCACA TGCATTACGC GAGTTCGTGA CGGACAGTAT CGTGGTATTG CTACATGGCG 240  
 25 TTACGATCAA GATCGTTCAA CGATTTGATT GGTACATTGG AAGTGCCTAT GACATTGGCA 300  
 ATCGTTGGCG GTGGGTACAA AAGTATTACC AATTGCTAAG CCTTCATTAG GAGnTACTAA 360  
 ATGGTAGAGT CCGCCCCAAG AATTAnGnCC CTGTA 395

## (2) INFORMATION FOR SEQ ID NO: 4241:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4241:

ACTAATGATT TATTATGTAG TGGTTCCTTG TCATTAGCCA CAGCTATTGT GTACTTAAAA 60  
 ATAGGAATGC ATGAGTGCAA CTCTAnAnGn AGCATACTAA TTTCTAAAGA AAAAGTATTT 120  
 45 CTTTATGTTG GGGCCCCGCC AACTTGCATT GTTTGTAGAA TTTCTTTTCG AAATTCTTTA 180  
 TGTGGGGGCC CCGCCAACTT GCATTGTTTG TAGAATTTCT TTTGAAATT CTTTATGTTG 240  
 GGGCCCCGCC AACTAATTCC AATATATCAT TGTAGAGCTT AGGTCATTGA TTTTGGCTC 300  
 50 GGACTTTTAT GGCGATATGA ACCATGTAAA T 331

## (2) INFORMATION FOR SEQ ID NO: 4242:

- (A) LENGTH: 389 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4242:

10 TGCAATTGCAT TATTGTACTG CGTAATTGTA CCTGGCTTTT TACCTTCAGT GCTTACTGGA 60  
 TCATCTAAAT GATTTTTAGC TGTGATTAAC TCACGTTTAT CCGCTTTTGT GAAAATGGAC 120  
 TCTTGTA CTTT CAGTACT ACCATCATTG TAAGTTACTG TCACAGGAAT CGTCGTTGTG 180  
 15 CTACCACCAG CTAAATTAGT AGGCATTGCT GTGCCATTTT TAATCGTTGC AGTACGTTTA 240  
 TTAGCAACTT GAACTGCATT GTTAATTTCA GCTGCTGTTA CATTTGAACC ATAATCTTTC 300  
 20 ACAATTn CAG TTGTGTTGAC AGATGAGnGG CCGTG CAGTA AGGACTGGAT ACACTACGAG 360  
 TGACCGGACT GCTTCGGGnA ATGTGATGA 389

## (2) INFORMATION FOR SEQ ID NO: 4243:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4243:

ATACGCATGT TAACGATCGA ATGCTTAATG TCCCGGGAAA TAAATCTATC ATAAGTTACT 60  
 35 TTAATGAAGT TGTCTCACGA CAAGGTAATC ATGTTGCGCT ATCATGAATG ATTTGACAAT 120  
 GACGTATGAA CATTACGCAA CTATGTGGAT GCCATTGCGC ACATGCTCCT ATCAAATGGT 180  
 40 GTGGGCAATG GTCAACGGGT TGCCTTGTTT ACAGAACGTn TTTTGAAAT GATTGCGGCG 240  
 ATGTTGGCGA CAGTTAAAGT AGGTGCATCT TATATACCTA TCGATATTGA TTTTCCGAAT 300  
 AAACGACAAG GTGCAATTTT GG 322

45

## (2) INFORMATION FOR SEQ ID NO: 4244:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4244:

55

CAGTTCTCCG GGTGTGCCTT CTGTATATGC TATGTATTCA CATATCGATA ACATGACATA 120  
 ACTCATGCTG GGTTTCCCCA TTCGGAAATC TCTGGATCAA AGCTTACTTA CAGCTCCCCA 180  
 AAGCATATCG TCGTTAGTAA CGTCCTTCAT TGGCTTCTAG TGCCAAGGCA TCCACCGTGC 240  
 GCCCTTAATA ACTTAATCTA TGTTCACACC ATTTTATATA GTCAAACGTT AACATGAAGT 300  
 TACGTTCTTT TATAAAAAGA TTAAACGCG TTATTAATC 339

## (2) INFORMATION FOR SEQ ID NO: 4245:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4245:

CCATTAAACGG GCTCTGACTA CTTGTAAGCA CACGGTTTCA GGTTCATTTT CACTCCCCTT 60  
 CCGGGGTGCT TTTCACCTTT CCCTCACGGT ACTGGTTCAC TATCGGTCAC TAGAGAGTAT 120  
 TTAGCCTTAC GAGATGGTCC TCCCAGATTC CGACGGAATT TCACGTGCTC CGTCGTACTC 180  
 AGGATCCACT CAAGACAGAC AACATTTTCG ACTACAGGGA TTATTACCTT CTTTGGAATC 240  
 ATCTTTCCAG ATGATTCGTC TAATGTCGTC CTTTGTAAC TCCGTATAGAG TGTCTACAA 300  
 CCCCACAAG CAAGCTTGTT GGTnTTGGGC nACTTCCCGG TTTCGGTTCG GCCGnAA 358

## (2) INFORMATION FOR SEQ ID NO: 4246:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4246:

AAAGAGACCT TGCGGTTAGA TGCGGCTCAT CGCATCCATT TTTGCCTGG CAACGTTCTA 60  
 CTCTAGCGGA ACGTAAGTnG AnCTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCCG 120  
 CATGGGAACA GGTGTGACCT CTTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA 180  
 TTCAAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAAG 240  
 TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC TCGGAACCTA 300  
 TTAACCTCAT GCATCTTTGA GGGGnGCTTG ATAACCGA 338

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4247:

CCCCGGGTAG CTTTTATCCG TTGAGCGATG GCCCTTCCAT GCGGAACCAC CGGATCACTA	60
AGTCCGTCTT TCGACCCTGC TCGACTTGTA GGTCTCGCAG TCAAGCTCCC TTATGCCTTT	120
ACACTCTATG AATGATTTC AACCATTCTG AGGGAACCTT GAGCGCCTCC GTTACCTTTT	180
AGGAGGCGAC CGCCCACTCA AACTGCCCGC CTGACACTGT CTCCCACCAC GATAAnGGCG	240
GGGGTTAGAA AGCCAACACA GCTAGGGTAG TATCCCACCA GCGCTCCACG TAACTAnCGC	300
TCACGTTTCA AAGnTCTACC TATCCTGTAC A	331

(2) INFORMATION FOR SEQ ID NO: 4248:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4248:

ATAATCATAC AGATGGCAAT ACAACAGCAA CTGAGACAGT GTCAAACGCT AATAATAATG	60
ATGTAGTGTC GAATAATACC GCATTAAATG TACCAACTAA AACAAATGAA AATGGTTCAG	120
GAGGACATCT AACTTTAAAG GAAATTCAAG AAGATGTTTG TCATTCTTCA AATAAACCAG	180
AGCTAGTTGC AATTGCTGAA CCAGCATGCT AATAGACCGA AAAAGAGAAG TAGACGTGCG	240
GCACCGGCAG ATnCCTAAAT GCAACTTCCA GCCAGATCCA GCGGCTGCAG CGGTAnGGAA	300
ACGGTGGTGC CACCAGTTTG CCAATTTACA GCGCCCATAT TACGCCAACA ACTGGTnCCC	360
TAATGCCCAA T	371

(2) INFORMATION FOR SEQ ID NO: 4249:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 357 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AATTGCATGG CATAACATCG GCGATTAAAA GATGGACGTT TTGATGATGT ACAACAAGAC 60  
 ATTGAAGCAG TGGTGAAAGC TGCGAAGGTC ACACAGTAAA AGTGATTATT GAGACGGTAT 120  
 5 TGTGACCA TGACGAAATT GTAAAAGCGA GTGAATTAAC AAAAGCGGCT GGTGCGGACT 180  
 TCGTTAAAAC TTCAACAGGT TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAATTAAT 240  
 10 GAAAGATACA GTAGGTGCTG ATATAGAAGT AAAAGCTCAG GTGGCGTACG TATTnTAGAA 300  
 GTTTCAATGA AnGGTTGAAG CAGGTGCGAC ACGTAnTGGT GCGAGCGCAG CGTTCAA 357

## (2) INFORMATION FOR SEQ ID NO: 4250:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 352 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4250:

25 GAGCCCAAAC CAACAAGCTT GCTTGTGGG nGTTGTAGGA CACTCTATAC GGAGTTACAA 60  
 AGGACGACAT TAGACGAATC ATCTGGAAG ATGAATCAAA GAAGGTAATA ATCCTGTAGT 120  
 CGAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG GAACACGTGA AATTCCGTCG 180  
 30 GAATCTGGGA GGACCATCTC CTAAGGCTGA ATACTCTCTA GTGACCGATA GTGAAGnAGT 240  
 ACCGTGAGGG AAAGGTGAAA AGCACCCCGG GAAGGGGAAG TGAAATAGAA GCTGGAAACC 300  
 GGTGTGCTTA CAAGGTAGTC AnAGCCCGTT AATGGGTGAT GGCCTGCCTT TT 352

## (2) INFORMATION FOR SEQ ID NO: 4251:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 331 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4251:

45 CATTTACTGC TTAACCTTGC ATCanATCGT AACTCGCCGG TTCATTCTAC AAAAGGCACG 60  
 CCATCACCCA TTAACGGGCT CTGACTACTT GTAAGCACAC GGTTCAGGT TCTATTTTAC 120  
 50 TCCCCTCCG GGGTGCTTTT CACCTTTCCC TCACGGTACT GGTTCACTAT CGGTCACTAG 180  
 AGAGTATTTA GCCTTAGGAG ATGGTCCTCC CAGATTCCGA CGGAATTTCA CGTGCTCCGT 240  
 55 CGTACTCAGG ATCCAACAA GAGAGACAAC ATnTTCGACT ACAGGATTAT TACCTTCTTT 300

## (2) INFORMATION FOR SEQ ID NO: 4252:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4252:

TATTTGATAT TTTGTGCATT GCAGTCAAAC CATGGCGGAA ATTGAACCAA TACCATTGCT 60  
 AATTTTCTCT GTGTATGTAA GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTnGC 120  
 CTTGTATCTG CAAATGTTTT GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTTGACC 180  
 ACAAATTCAA ATGTATCAGG CGTTTCTTTT ATCCATTTCa ATATATTTCT TTCCGGTTGT 240  
 ATCGCATAGT ATGTCGCATC TAATTCGCAA CCGGAAAATG TCCAGCATAT GTTTTAAGGT 300  
 TATCGGTTTG GCGTTCTAAA TCTGCATATA ATGAATAGTG ATCACCCCAA CCTGTAAAT 360  
 CCGATGGTTA TCCAnATGAT GATCACCATG TCATCAnACC 400

## (2) INFORMATION FOR SEQ ID NO: 4253:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4253:

AAAGGTATCA AAGATGTAA AGTTACTTTA TTAAATGAAA AAGGCGAAGT AATTGGnACA 60  
 ACTAAACAG ATGAAAATGG TAAATACTGC TTTGATAATT TAGATAGCGG TAAATACAAA 120  
 GTTATTTTnG AnaAGCCTGC TGGCTTAAAC ACAAACAGTT ACAAATACAA CTGAAGATGA 180  
 TAAAGATGCA GATGGTGGCG AGTTGACGTA ACAATTACGG ATCATGATGA TTTCACACTT 240  
 GATAACGGAT ACTTCGAGGG GATGACATCA GACAGCGATT CAGACTCCAG ATAGTGACTC 300  
 AGnCAGCGAC TCAGACTTCA GACAGCG 327

## (2) INFORMATION FOR SEQ ID NO: 4254:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4254:

5 AGATGACATT AAATAGCATC TCCTCGTGTT GATTATTTTG GTTGGCTGAC CAATATTTAT 60  
 TCTAGCACGT AGAGATGCAT TTTTGTGAC AATGGTAGAA CCTTTTCTGA ACCATACGCA 120  
 TAGGATTGTh CThTTTTACA ATTAAAGAGC CAACCGTTGT TATAGTCTAA CAATGGTTGC 180  
 10 CCTCTTATTT TATGTGGCTA AAAATTTATA GGCAATTTTA TTACAACAAT GTACATTTAA 240  
 GGTGACCTTC ATGCCAAAT CGCATCACTC ATTTAATGGA AGCAGCACGT CTTCATATAA 300  
 AGTACCGATC CCTAATTCCA ACGCATGTnG 330

## (2) INFORMATION FOR SEQ ID NO: 4255:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4255:

25 ATTAGTGATT GTAAAAAGT AAACTATTC TTGGGAGTCG GACATAAATC AATGTCTAGA 60  
 CTCTATAGTG TTGATTTGG CAGTAGTTGA CGGGGCCCCA ACATAAAGAA ATACTTTTTC 120  
 30 TTTAGAAATT AGTATTTCTT ATACATGAGT TTTACTCAGG ATATCCTATT TTAAATACA 180  
 CATTAGCTGT GTTAAATGAT AAAGAACCAC TACATCATAA ATCTTTAATG GTTCTTTATC 240  
 AATTCCTTCC CCCCTCTCAT GTTTTGTATC TTAAATCAA TATAATTCAA AAAAGGGTCG 300  
 35 AAGATATGAn ATCACATCTT CGACCCTThn TTGTACTAAT TTAA 344

## (2) INFORMATION FOR SEQ ID NO: 4256:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4256:

50 CCAGTAATAT CTAAATGAGT TGGATATTTA ACTTTCGCAT TAATTTCAAT ATTAAATTGC 60  
 GTTACCGCGA CAAGnCATnA CACAACATAC ATAATAAGAT TGGCTAAAAA GATATAGTTA 120  
 AAGCTAAATT CTGCGACAAA GCCGCCCAT TGCAGCACCGA CAGCCACACC AATATTTTGC 180  
 55 GCTAAGTATA TCGCATTAAA CGTTTGTCTT CCGCCATTG GCCACACTGC TCCAGCCATA 240

TACCAAGGCC ACCCGTGGan AGA

323

## (2) INFORMATION FOR SEQ ID NO: 4257:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 369 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4257:

15	GCTGACTTTC CACCAGCCTC TGTGTTGGGG CCCGACTAT TTTTGAAAAG AGCGTGTTAC	60
	ACGGTCATTG TTTTACAGTC AACTACTGCT AAAATAAAAT TAACGAGCTT AGGGCTTTGT	120
	TTTCTGTCCTC AAGCTCGTTA AATCATATAT GATAATTAAT TATGCCCAAC CACGATATCT	180
20	AGCTGCTTCT GCTGTACGTT TAATACCTAT GGATATATGC TGCAnTCTGC ATATCTATTT	240
	TTCGGTTTTG AGACAATTG TAAATCGTAT CAAATGCCGC TTCTAATTTT TnCACGTGGC	300
25	TTTTGCATTG AACTTCTTCT nGCAGGACCA ATAATAACCT TGGATTATTT TGTGACCCAT	360
	GCGGAGTGA	369

## (2) INFORMATION FOR SEQ ID NO: 4258:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 335 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4258:

40	CCTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT	60
	TTTTTAAATA CTAAAATACA TGTTGGAATA CTGTGCCAT AGAAAATATT GGCTGGTAAC	120
	CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT AGCGACGAAT CACACCTTCT	180
45	GCGGCACCAC GAATAATACA CCATGnGGAG TACGACGCCA nGTACCTTCA TCGTCTAGTA	240
	ATGTACCAGT GTTGAATAAA GCAAAGTCTG CTTTGATTTT GCGGCAACTT GCCGTAACCA	300
50	CTGAATCGTT CATCATTTCA AATTGAACT GCTGT	335

## (2) INFORMATION FOR SEQ ID NO: 4259:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 324 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4259:

5 ATTTGCTAC CTTACGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTTCGTA 60  
 GCTTCGCAGC nACAACCACT CCTCTTAACC TTCCAGCACC GGGCAGGCGT CACCCTATAC 120  
 ATCACCTTAC GGTTTAGCAG AGACCTGTGT TTTTGATAAA CAGTCGCTTG GGCCTATTCA 180  
 10 CTGCGGnTCT TCTGGGCGTT AACCTAAAG AGCACCCCTT CTCCCGAAGT TACGGGGTCA 240  
 TTTTGCCGAG TTCCTTAACG AGAGTTCGCT CGCTCACCTT AGAnTTCTCA TCTTGACTAC 300  
 CTGTGTCGGT TTGCGGTACG GGCA 324

## (2) INFORMATION FOR SEQ ID NO: 4260:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4260:

25 AAGCGTTGT TAGACAATGC ATTAAGAAAA ATTAAAGCGG AGTTTACTTT TGTAATGAG 60  
 CATTTGATTT TTTGAAAATA AAGCAGTATC GGGCGCTTGA CTAAAAAGAA ATTGTACATT 120  
 30 GAAACTAGA TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAGAG 180  
 TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ACGACGAAGA 240  
 TTAATAACGC GTTTAAATCT TTTTATAAAA GAAACGTTT AGCAGACAAT GAGTTAAAnTT 300  
 35 ATTTTAAAGC AGAGTTTACT TATGTnAATG GAGCATTGAA AATnATGAAA ACGAGCCCGT 360  
 ATGTGGAGCG TTTGGACTTA TAAAAATGGT GGGAAACATA 400

## (2) INFORMATION FOR SEQ ID NO: 4261:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs  
 (B) TYPE: nucleic acid  
 45 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4261:

50 AATTAATGTG CGAGTTGGGG TGGGACGACG ATAAAGAAAT ACTTTTTCTA TAGAAATTAG 60  
 TATTTCTTAT GCATGAGTTT TACTCAGTAA TTCCTATTTT TAAGnACACA TTAGCTGTGG 120

CTCCCCTGAG AAGTTTAAAA TTTTATATGT TGGCTTGTTA TGTTAAGGGA ATTAACATGG 240  
 TTGTCTTGTT TATATTATGT GATTCAAACA TTAGTAGTCT TGGTAAATCT AATTCGTAAA 300  
 5 ATGCTAAATC TAACCATCTA TTAAATTTAA AACC 334

## (2) INFORMATION FOR SEQ ID NO: 4262:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4262:

TTTCGGTCAT ATTCAAACGT TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT 60  
 20 ATTTTGACGT TTTAGGCATA AAAAAAAGAG ACCTTGCGCG TCTCAATGCG GCTCATCGCA 120  
 TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGnAGTA ATTGGGCTAC CATCGTCGCT 180  
 25 AAAGACCTTT CTGACTTGT GACAATCGCT TGCnTCTTTC CTCTCCTTCG GCTCTCGCTT 240  
 ACTCATnAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 300  
 TTCACTTCGC CAAGCCATTT TTCTTTGTGT 330

## (2) INFORMATION FOR SEQ ID NO: 4263:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4263:

GAGGTATACC CCGGGACGGC TGAAGGGGAT CGAACCCTAC GnAATGTCGG AACCACAATC 60  
 CGATGTGTTA CCACTTCACC ACAGCCGCCA TGGCAGGGGC AGTAGGAATC GAACCCACAC 120  
 45 CAAAGGTTTT GGAGACCTCT ATTCTACCGT TGAACATATGC CCCTATTAAA AATAATAAAT 180  
 GGAGGGGGGC AGATTGGAAC TGCCGAACCC GAAGAGTCGG ATTTACAGTC CGCCGCGTTT 240  
 AGCCACTTCG CTACCCCTCC ATAAATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC 300  
 50 TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG 339

## (2) INFORMATION FOR SEQ ID NO: 4264:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4264:

	GTATTTCAAA GTAAAATTAC ATGTTAATAC GTGnTTAATG GCGGAGACTC CTGAGGGAGC	60
10	AGTGCCAGTC GAAGCCGAGG CTGAGACGGC ACCCTAGGAA AGCGAGCATT CAATACGAGA	120
	TnTnATGAAA TAGAGAACAG CAGTAAGATA TTTTCTAATT GAAAATTATC TTAGTGCTGT	180
	TTTTTAGGGA TTTATGTCCC AGCCTCTTAC TCTAATTATA TTCACTATCA ATTAGACAAA	240
15	ATGGCCATTT TCAAATATCA CGCGTTGTTT CTGACCTTGA ATATATTTAT TATAATTCTC	300
	TTTTTGAAA ATCAGTTAAC ATTAATTTAG ATGTACCGTA TTTTAAACAC T	351

(2) INFORMATION FOR SEQ ID NO: 4265:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 346 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4265:

30	ATTTTCACTT TAAAACCTGC TTCTTTGGCT TTTTGCATAT AATGTGCGA TTGTTCTATT	60
	GTAAATACAC CTGTTTCACA GAAAATATCC GCAAAGTCTG CATATTGTTT TACTTCCGGA	120
	AGTAACGCAA TCATTTCTTC TAAAAATGCC TCATTTGAAC TTGCCTCTTT AGGTACAGCA	180
35	TGAGGCCCTA GGAAAGTATG TTTTATGTCT AAATCATATT TCTCAGCTAA ACGnTTAGAC	240
	ACTTTCAATT GCTTCAGTTC ATTTTCTCTA TCTAATCCAT AAACCACTCT TGACTTTCAA	300
40	CTGCAGTCAC GCCGTGTTTn AATCCATAGT AAGACAAAnC ATGACT	346

(2) INFORMATION FOR SEQ ID NO: 4266:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 347 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4266:

	TCAAACGCTC TATCCAATTG AGCTACGGGC GCATATGTTT TTATTGAAAA TGGTGCCGAG	60
55	GACCGGAATC GAACCGGTAC GTGATCACTC ACCGCAGGAT TTTAAGTCCT GTGCGTCTGC	120

CCAACCTTGG CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA 240  
 5 GTCGAACCCC CACGCCGTAA GGnTGAGATC CTAAGTCTAG TCGTCTGCC AATTCCGCCA 300  
 CACCCGCCAA TGnTGAGnCA TAGAGGnTTC GAACCTCTGA CCCTCTG 347

(2) INFORMATION FOR SEQ ID NO: 4267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4267:

GACTTGTCTTCT CTTGGACCTA TATCATGTTTCT TTTATTTTCT AATGCAGGAT CTTTAATTGC 60  
 20 ATCTTTAAGT GATTCATCCG CTGCAGGATA GTTTTTCGCA GTGTTTGCTG GTTGCGTGAG 120  
 GTnTGTGTTT GATTTGTATC CTTAGGTGGC TGAGTTGTAG TTGCATTATT ATTTTGATT 180  
 25 TCCGAGATTT TATCTGAAGT APTTGATTT TCTGCTGCTT GTGCTTGATG TTGAGAAGTA 240  
 ATTAAAAATA GTGTACTGAC AATGACCGAT GCAACGCCTA GAGTTGATTT TCTAATAGAA 300  
 TAGGAAAGAC CnTnAATTTT GGGTGGATGT TTGTTCA 337

(2) INFORMATION FOR SEQ ID NO: 4268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4268:

ATACATGTTG GAATACITGT CCCATAGAnA ATATTGGCTG GTAACCCAAT CACGGCTTCT 60  
 AAGTAGTTCT TTTCTTCTAT TAAATAGCGA CGAATCACAC CTTCTGCGGC ACCACGGAAT 120  
 45 AATACACCAT GTGGGAGTAC GACTGCCATG GTACCTTCAT CGTCTAGGTA ATGTACCATG 180  
 TGTGAATAA AGGGCAAAGT CTGCTTTGGG ATTTTGGCGC AACTTGGCCG TTAACCACTG 240  
 GAATCGTTCA TCATTTTCA nATTTTGGAA TCTGGCTGGT TCCATTTTCG GCACTGGTAT 300  
 50 GGTGGGGGTT TCGGCAATAA ACGGCATTCA AATGGTATTT GGCCTAAACA AGGCCGGGAT 360  
 TTTTCCAATG GGGGTCATCA TTAAnGGGAT CnTCGAAGTT 400

(2) INFORMATION FOR SEQ ID NO: 4269:

(A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4269:

10 GGCTCATCGC ATCCTGGGGC TGTAGTCGGT CCCAAGGGTT GGGCTGTTTCG CCCATTAAAG 60  
 CGGTACGGAG CTGGGTTTCAG AACGTCGTGA GACAGTTCGG TCCCTATCCG TCGTGGGCGT 120  
 AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG 180  
 15 TACCAGTTGT CGTGCCAACG GCATAGCTGG GTAGCTATGT GTGGACGnGA TAAGTGCTGA 240  
 nAGCATCTAA GCATGAnGCC CCCTCAAGAT GAGATTCCCA ACTTCGGTTA TAAGATCCCT 300  
 CAAAGATGAT GAGGATATAG GTCGAGGTTG GAGCATGGTA CATGT 345

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(2) INFORMATION FOR SEQ ID NO: 4270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4270:

30 AAGAATTAAT TATACATTTT ATTAACATTT AAGTCAATAA CTTTTTTTAT CTTGTCCATT 60  
 TTATTTTTTA ACCAAAATTT GATTAAAAAA CTGCCTGGCA ACGTTCTACT CTAGCGGAAn 120  
 35 TAAGTCGaCT ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG 180  
 TGACCTCCtT GCTATAGTCA CCAGACATAT GaATGTAATT TATACATTCA AAAGTAGATA 240  
 40 GTAAGTAAAA GTGGATTTTG CTTGCAAAAc ATTTATTTTG ATTAAGTCTT CGATCGATTA 300  
 GTATTGCTCA GCTCCaCATG GTCACCAGCT TCCACCTCGA ACCTATTGGn CGCATCATCT 360  
 CGCAGGGGAnC 370

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(2) INFORMATION FOR SEQ ID NO: 4271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4271:

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ATTAACAAAA GGCATTGATT TAGAAGGGCG GACATTTTAA CACAATTATG ATTGGCGTAA 120  
 AGATAAAGAT GGCACATTAT TAAATACCAT CATTTCTGGT CCGGCACTTG TGGCACAATG 180  
 5 GaTTAATTTA CAATATTATG CGTCGACAGT TGCGCCGCAT TTTTaCGGtA ATGGGAATAA 240  
 AGCGACACAA ACCGTCACGT CAGTGTGGT GTCATGCAAG GTAATGCGAG TGCATCTGAT 300  
 10 GTAGGGCTTA TCATGGCCAA TCTGTTA 327

## (2) INFORMATION FOR SEQ ID NO: 4272:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4272:

CATTCTTTAA ACTCTGTAAG TACTTCTTCA ATCTCAGGGG CATCTACTAA CATATCATCA 60  
 GTAATATGCG TCAAATTGAT AATCGTTTCC GATAATCGTT CATGCGGATT ACTAAACCTT 120  
 25 TCAAACCTTAT CGATGATTTT ACCGTTATGA ACTTTACAG CTGCAANTCG ATGATTTTAT 180  
 CATACTGATT TGATAAACCA GTTGTCTCAA CGTCGAACAC AACATAAGTA GCATCTTTTA 240  
 ATACGACATC TTGTGGGTTG TATGCAATCG GGAACACCAT CATCAACTAA CATACCTTCC 300  
 30 ATACCGGnAT ATCATTTTAA nGCCA 325

## (2) INFORMATION FOR SEQ ID NO: 4273:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4273:

TCCGGCCTTG ACCTGAAGAA CACTTGTCTT GTCGTTAAGA TGACTCTAGA CTCTTATGTT 60  
 45 TATTATCAAC CGTTAATAAA CTTACCATCA AGAGTGCACC TACCCATACT GACAGTGCAG 120  
 TATAGAATGG TGTCATACCT GAACCATAAT CCTTAACTGG GAAAACATCA ACAGTCTTCT 180  
 50 TATTAATAGG ATTTGCAATA ATACCCGCTT GCTTTTTTCAA ATCATTCTTA AGTGTGTCGA 240  
 TnAATTTGTC GACTGCATCA TCTnTGTCTA ATTTCTTGAA AATTTTGATT CGCTTTTTTC 300  
 CAAATCCTTn TCCAACATCA GGCAATTTTA TTTTGAGAAA AATCAGCCAA ATCCGGA 357

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 bas pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4274:

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ACGTTAGCAC AAGCCATGAA CCAATTAGGT GGAAAGAGTA ATAGTGGTGA AGGTGGCGAA      60
GATGCAAAAC GTTATGAAGT ACAAGTTGAT GGAAGCAACA AAGTAAGTGC GATTAAACAA      120
GTTGCTTCTG GCGGTTTTGG TGTAAGTAGT GATTATTTAC AACATGCCAA AGAAATTCAA      180
ATTAAAGTTG CGCAAGGTGC AAAGCCTGGT GAAGGTGGTC AATTACCTGG TACTAAGGTA      240
TATCCGTGGA TTGCGAnGAC AAGAGGGTCA ACGCCAGGTA TCGGTCTGAT TTCACCACCG      300
CCACATCATG ATATTTnATT CCATAnGAGG ATTTAGCCGC CACCTGATAC CTGGATTTTG      360
GAAAAATGGC GAATTAAGGT TGCnGATTTT CCCCggGTAA      400

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(2) INFORMATION FOR SEQ ID NO: 4275:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 341 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4275:

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AACGTCGTTA ATTGAATAAC GCTTATGTTA TAAGAGCACT CATACCAAAC CATAATCATC      60
TATAGATATA ACAATTCACG ATATAAGGGC TGTGTTTGGC ATAGCCTTTA GATATACACT      120
TAATTCCTAT TAAATAGTA GGGATTAAAA GGGGGCTTGT CATGGATTAA AATTCAACAA      180
TTACAACATC ACTTTGGATC ACATAAGTA ATTCATAACT TTAATTTGGA CATTAGCAAG      240
GGAGAAATAG TCACTTTCAT AGGGGAAAAG TGGTTGCGGA AAGTCTACTT TACTCAATAT      300
TATCGGTGGA TTTnTTCCAT CCATCGnCTG GTCGTGTCCA n      341

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(2) INFORMATION FOR SEQ ID NO: 4276:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 368 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TAGTGATATA CGACATCACA GCATAATATT GCTTTAGAAA GTCGTGCCGA ACTGGAACCT 60  
 ACAAGTCTAG TTCGAACACA CACTGATGTG AGTGGTTTTT TTTATTTTAA ACATGAACAA 120  
 5 TCAGATAAGT TACTAGCATT AGCAAATATT ATTAAATCAA AGGGCTTCGA TTCATAAAAT 180  
 TTAAAACAAT GATTAAAATT AGACGTGTAA ATTGTAAAT TCTAAAACGG AAATAACCAC 240  
 10 CATTCCATTA AACCACTTTT TTGTTTCATCA CTATATTTCA CACnGCTTCA TTAATAAACG 300  
 GAATGCTTCA nCCGCTTCAA CTTCAACTGG CTTCAACTTC nGCCTACTTC ATCATACCAA 360  
 ACGGTCCG 368

(2) INFORMATION FOR SEQ ID NO: 4277:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 318 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4277:

25 ATGGAAGTAC GTGACGTTCA CTACTCTCAC TATGGCCGTA TGTGTCCAAT TGAAACACCT 60  
 GAGGGACCAA ACATTGGATT GATTAACTCA TTATCAAGTT ATGCACGTGT AAATGAATTC 120  
 30 GGCTTTATTG AAACACCATA TCGTAAAGTT GATTTAGATA CACATGCTAT CACTGATCAA 180  
 ATTGACTATT TAACAGCTGA CGAAGAAGAT AGCTATGTTG TAGCACAAGC AAACTCTAAA 240  
 TTAGATGANA ATGGTCGTTT CATGGGATGA TGAAGTTGTA TGTGTTTCC GTGGTAACAA 300  
 35 TACAGThATG GCTAAAGn 318

(2) INFORMATION FOR SEQ ID NO: 4278:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4278:

CACTTGTA CTCTGATGTT GAGCCAGACT CTGATGTA CTACCGATGTA GATAAACTTG 60  
 50 CAATGGTCGA CATGCGGTTT GAAGTTGATG TACTTAGCGA ATCACTTAAT GATGCTGATG 120  
 TGCTTTGTGA ATCGGATTCG CTCGTGCTTG TACTTGTGTA GTTTGAGGCA CTTTGGCTTG 180  
 CTGAGTTTGA GTCTACTCCG CTTTGATTCA TTGAGGCACT TAGTGACAAT GATGTACTCG 240

TACTTATGCT CATTGGATGT TGAATCGGAT TTA~~CTTT~~CAC TTGAATGATG TTGAGTCGGA 360  
 TTCAC~~TTT~~CA CTGTAGAAC CACTTAATGA TGTGGGATGT 400

(2) INFORMATION FOR SEQ ID NO: 4279:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4279:

TTGTACTTC GATTTAAAAG ATATTAGACA TAAATCTAA AAnCAGCAGT AAGATGATTT 60  
 ATGATTAAAA ACTATCTTAC TGCTGTTTAC TTTTATAAT ACTTCTGAAT GTCTTCACTT 120  
 ATACTTCTAG TCACAGATTT AAATAATCAA AAGTGCACAT TATTAAAATA TCAATTTTAC 180  
 ACTCAATGCG GCTCATCGCA TTCATTTCTT GTCTAGCAAC GTTCTACTCT AGCGGAAGTA 240  
 AGTTAGCTAC CATCCTCGCT AAGAACCCTT CTTGACTTGT GACAAATCGCT TGCTTCTTTC 300  
 CTCTCCTTCG GCTCTCGCTT ACTC 324

(2) INFORMATION FOR SEQ ID NO: 4280:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4280:

CTCACTAGTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT 60  
 GTGGATTGTC CTTTGGCATG TGnTTAGGAG AGCGTTCTAA GGGCGTTGAA GCATGATCGT 120  
 AAGGACATGT GGAGCGCTTA GAAGTGAGAA TGCCGGTGTG AGTAGCGAAA GACGGGTGAG 180  
 AATCCCGTCC ACCGATTGAC TAAGGTTTCC TGnGGAAGGC TCGTCCGCTC TGGGTTAGTC 240  
 GnGTCCTAAG CTGAGGCCGA CAGTAGGGCG ATGGGATAAC AGGTTGATAT TCCTGTACCA 300  
 CCTATAATCG TTTAATCGAT GGGGGG 326

(2) INFORMATION FOR SEQ ID NO: 4281:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4281:

5 TCGAACATGA GCGATTATTT CTTATGAATT CAAGCTTATT TAAAACTCTT TATTCACCTG 60  
 GTTTTGCTTG GTAAAATCTA TATTTTACTT ACTTATCTAG TTTTCAATGT ACAAATAATG 120  
 GTGGGCCTAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGCGTGCG CTCTAACCAG 180  
 10 CTGAGCTATA GGCCCATTTT TTTGAATGTT AAATAAACAT TCAAACTGG AATACAATAT 240  
 GTCACGTTAT TCCGCATCTT CTGAAGAAGA TGTTCGAAT ATATCCTTAG AAAGGnAGGT 300  
 15 GATCCAGCCG CACCTTCCGA TACGGGCTGA CCTTGTGAC GACTTGCACC CCAAGCATT 360  
 GTGCCCAnCn 370

## (2) INFORMATION FOR SEQ ID NO: 4282:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4282:

30 GAGAGATGAC ACGGnACTGA ATTGGTTTGA CACCACGTGA TGAATGTGAT CGTCGGCCTT 60  
 CTTACAGATT GnaATACTTT TACATCAAGA ACGATACCGC CAGCGCCGTG AGGTACACGT 120  
 AATGAAGTAT CTCTAACTTC ACGTGCCTTT TCACCAAAGA TTGCATGTAA CAATCTTTCT 180  
 35 TCGGCAGTTA ACTCAGTTAC ACCTTTAGGC GTTACTTTAC CAACTAAAAT ATCTCCATCT 240  
 TTTACTTCTG CACCAATATA AACGATACCA CGATCGTCTA AGTTCTTAAG TGCACCTTCA 300  
 GAAACATTAG GnatATCTCT TGTGATTTCC TCAGGGCCTA ACTTAGTATC ACGTGCCTCT 360  
 40 GAATCCATAC TCCTTCAATA TGAATAGAAG TATACACGGn 400

## (2) INFORMATION FOR SEQ ID NO: 4283:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4283:

55 AATTCTACAG GCAATGCGAG TTGGGGTGTG GGCCCCAACA AAGAGAAATT GGATTCCCAA 60

TCTGTCCCAC TCCCGATTAT CTCGTGCGAA TATTTTTTTC AAAGCGATTT AAATCATTAT 180  
 CATGTCCAAT CATGATTAAA ATATCACCTA TTTCTAAATT AATATTTGGA TTTGGTGAAA 240  
 5 TGATGGACTC TTTGCCTCGT TTAATTGCCA TAATGTTAAT nCCATATTGT GCTCTTATAT 300  
 CTnAATCCAT GATAGACTGn CCCG 324

(2) INFORMATION FOR SEQ ID NO: 4284:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4284:

20 AAATCGTAAC GAGTGAACCTT TCTTATTTAG GTGGCGAAGT AACTTACTAG CACCTGACGA 60  
 AACGGTTTTA GATCGTATTC AATTGAAAAG GCCGGTATTG AATGAATCAC ACTTAGCAGC 120  
 GATTGATCAG GAACATTTTA AATTAACCTA TTTATCAACG GTATATGAAG GGGATTTGGC 180  
 25 AAGATGCGTT ATAAGCATTG GGCCGTAGAA GCAGTGAAAT GCTGTnAAAC AAGGGCGCTC 240  
 AAATTCTAGT GTTAGATGAT AGTGGATTAG TTGGATAGCA ATGGCTTTGC AATGCCGATG 300  
 TTTACTCGCA ATGAAGTGCA TGTGCCATGC AATTGACTTC TTTAAAGCCA GATTTACGTG 360  
 30 ATGTCTAACA AGTTTTnTnC GCTAAAATCh GGGTGGAGAC 400

(2) INFORMATION FOR SEQ ID NO: 4285:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 560 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4285:

45 CATTTTCTT TGTGTTTACT TTTATTTTG ACGTTTTAGA CATAAAAAA GAGACTCAGC 60  
 GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC 120  
 TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCATCTTT CCTCAnCATC GGnTnTAGCT 180  
 TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT 240  
 50 TTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGGCATA 300  
 AAAAAAAGAG ACCTTGnCGG TCTCAATGCG GGCTCATCGC ATCCATTTTT TGCCTGGCAA 360

TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA 480  
 ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACCTCG CCAAGCCATT 540  
 5 TTCTTTGTG TTTACTTTTT 560

## (2) INFORMATION FOR SEQ ID NO: 4286:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4286:

GTAACACTCG GtATAACCTA CCTATAAGAC TGGGATAACT TCGGGAAACC GTAGCTAATA 60  
 20 CCGGATAATA TTTTGAACCG CATGGTTAAA AGTGGAAAGA CGGTCTTGCT GTCACCTATA 120  
 GATGGATCCG CGCTGCATTA GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA 180  
 TAGCCGACCT GAGAnGGTGA TCGGCCACAC TGGAAGTGA ACACGGTCCA GACTCCTACG 240  
 25 GGAGGCAGCA GTAGGGAATC TTCCGAATG GGCGAACTG GACGGAGCAA CGCCGCGTGA 300  
 TGnATGGAAG GTCTTCGGAT CGTAAAACTC TGTTATT 337

## (2) INFORMATION FOR SEQ ID NO: 4287:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4287:

CAATCGTGCT CAnTGCGCAT CGTnACTCAT CTGTATGTGT TCCAGCATAT ACAATTTTGC 60  
 CATCTTTAAT GACAACTGTA CCATTTTTCA CAACATTAA TTCATCTAAT TCCTTACCCT 120  
 TCAAAGGTTT ATCTGTTGAT CTCGGTAAAA TTAATTCGCG CTATATGATT AATTATTAAA 180  
 45 TCATCATTAC TTATCACCTG CTTTATCAAT CATGGAATAT GAATACCTTT TTCTTTAGCT 240  
 GTTTGAATAG CGATGTCATA GCCAGCATCA ACATGTCGGG CAACACCCAT ACCTGGGTCA 300  
 50 GTCGTCAATA CAGGTTCCAA TCTTCTTTCA GCACGCTCTG AATCCATCTG G 351

## (2) INFORMATION FOR SEQ ID NO: 4288:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4288:

CTATTC	ACTG	CGGCTCTTCT	GGGCGTTAAC	CCTAAAGAGC	ACCCCTTCTC	CCGAAGTTAC	60
GGGGT	CATTT	TGCCGAGTTC	CTTAACGAGA	GTTGCTCGC	TCACCTTAGA	ATTCTCATCT	120
TGACTA	CTG	TGTCGGTTTG	CGGTACGGGC	ACCTATTTTC	TATCTAGAGG	CTTTTCTCGG	180
CAGTGT	GAAA	TCAACGACTC	GAAGACACAA	TGTCTTCTCC	CCATCACAGC	TCAGCCTTAA	240
CGAGTA	CCGG	ATTTCCTAA	TACTCAGCCT	TACTGCTTAG	GACGTGCAAT	CCAATCGCAC	300
GGTTTn	GCCT	ATCCTA					316

20

(2) INFORMATION FOR SEQ ID NO: 4289:

25

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 322 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4289:

TTnTTT	ATGT	CTAAACGTC	AAAATAAAAG	CAAACACAAA	GAAAGATGGC	TTGGCGAAGT	60
GAAAAC	GnTT	GAATCTGACG	AAACGAGAAA	TGTAAAGTAT	AATAAAAAGC	AGTCATAAGA	120
TGATTT	CAAT	TAGAAATCAA	TTTATGACTG	TTTTTCTTAC	TATGTGTTAA	ATTAACAATG	180
AATATA	ACAT	CTTATTTTCA	TTAATATAAA	TATTGGAAGG	ATCGAnATGA	TTTACACGTT	240
GTTTGAG	TG	TATTAAATCA	TCATGATCTT	TAAGTTGAAT	ACCAATAATG	ACAGTACCTG	300
TATTTTG	GAGA	GATTTTTTAA	GT				322

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(2) INFORMATION FOR SEQ ID NO: 4290:

45

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 338 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4290:

TCATTT	AGCT	CTACTAAACT	CGTTGCGCTC	TTTTCTCGTT	TCGTCAGATT	CAAACGTTTT	60
CACTTC	GCCA	AGCCATTTTT	CTTTGTGTTT	ACTTTTTATT	TTGACGTTTT	AGGCATAAAA	120

55

CTCTAGCGGA AATAATTGGC TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC 240  
 GCTTGCTTCT TTCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCnACT AAATCGTTG 300  
 5 CGCTCTTnTC TCGTTTCGTC AGATTTCAAA CGTTTTCA 338

## (2) INFORMATION FOR SEQ ID NO: 4291:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4291:

AATTGGTTTA CACCAGGTGA TAATGTATCG TCGCCTTCTT CACGATTGAA TACTTTTACA 60  
 20 TCAAGAACGA TACCGCCAGC GCCGTGAGGT ACACGTAATG AAGTATCTCT AACTTCACGT 120  
 GCTTTTTCAC CAAAGATTGC ATGTAACAAT CTTTCTTCGG CAGTTAACTC AGTTACACCT 180  
 TTAAGGCGTT ACTTTACCAA CTAAAATATC TCCATCTTTT ACTTCTGCAC CAATATAAAC 240  
 25 GATACCACGA TCGTCTAAAG TTCTTGAAGT GCACTTTnCA GAAACATTGA GGAATGATC 300  
 TCTTGTGATT TCTCCAGGT CCTAACTTGA GTGATCACGT GGCTTCTGGA TTGCAGACGC 360  
 TTGCAAGATG GAATGAGAAG TGAhACACGT GCATCCTTGC 400

## (2) INFORMATION FOR SEQ ID NO: 4292:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4292:

AAACGTTTTC ACTTCGCCAA GCCATTTTTC TTGTGTTTA CTTTTATTT TGACGTTTTA 60  
 GGCATAAAAA AAAGAGACCT TCGGTCTCA AATGCGGCTC ATCGCATCCA TTTTTGCCT 120  
 45 GGCAACGTTT TACTCTAGCG GAACGTAATT GGGCTACCAT CGTCGCTAAA GACCTTTCTT 180  
 GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC 240  
 50 TACTAAACTC GTTGCCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA 300  
 GCCATTTTTC TTGTGTnA CTTTnT 326

## (2) INFORMATION FOR SEQ ID NO: 4293:

(A) LENGTH: 356 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4293:

GGGGACAATT CCCTGGGGGT TCAAGTCCTC TCGGGCCGGC ATCAAAATTC TTAATTTAAA 60  
 TAAGCGGGTG TAGTTTAATG GCAAAACCTC AGCCTTCCAA GCTGATGTTG TGGGTTCGAT 120  
 TCCCATCACC CGCTCCATAG ATAATTTTAA TGAACATTGA AACTGAATG ACAATATGTC 180  
 AACGTTAATT CAAAAACGT AACTATAAGT TACAAACATT ATTTAGTATT TATGAGCnAA 240  
 TCAACATCA TAATTTTTAT GGAGAGTTTG ATCCTGGCTC AGGATGAACG CTGGCGGCGT 300  
 GCCTAATACA TGCCAGTCGA GCGAACGGAC GAGAAGCCTG CCTCnGAT GTTAGC 356

(2) INFORMATION FOR SEQ ID NO: 4294:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 314 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4294:

TTATCACCCA TGTCTGACT CCCAAGTTAA ATTAATTGGC ATTCGGAGTT TGTCTGAATT 60  
 CGGTAACCCG AGAGGnCCCC TCGTCCAAAC AGTGCTCTAC CTCCAATAAT CATCACTTGA 120  
 GGCAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATTTCC AGGTCGATT GGAATTTCTC 180  
 CGCTACCCCTC AGTTCATCCG CTCACTTTTT AACGTAATCG GTTCGGTCCT CCATTTCAGTG 240  
 TTACCTGAAC TTCAACCTGA CCAAGGTAGA TCACCTGGTT TCGGGTCTAC GACAAATACT 300  
 AAACGCCCTA TTCA 314

(2) INFORMATION FOR SEQ ID NO: 4295:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4295:

AAGTGAAAGA ACTCGGCGTG ACACCTATTG CACGATTCGT TGGTTTTAAG GCAGTAGGCG 60

GCAATCTATC TGTGAAGAC ATTGATTGTA TCGAATTGAA CGAAGCATT T GCTTCTCAAA 180  
 CGATTGCATC TATTAAAGAA GTAGGTCTAG ATATATCAG TACGAATGTG AATGGTGGCG 240  
 CTATTGCTTT AGGTCATCCA TTAGGTGCTA CAGGCGCCAA TGTTAACCCG CGCGTTTACC 300  
 TAATGAAATG GGGTAAACCG nCCCGATAGn CCGTAnCGCA AGGGT 345

## (2) INFORMATION FOR SEQ ID NO: 4296:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4296:

TAAATTGATT TCTAATTGAA ATCATCTTAT GACTGCTTTT TATTATACTT TACATTTCTC 60  
 GTTTCGTCAG ATTCAAACGT TTTCACCTCG CCAAGCCATC TTTCTTTGTG TTTGCTTTTA 120  
 TTTTGACGTT TTAGACATAA AAAAAGAGAC CTTGCGGTCT CAATGCGGCT CATCGCATCC 180  
 ACTTTTTGCC TGGCAACGTT CTACTCTAGC GGAAnTAATT CnACTACCA TCGACGCTAA 240  
 GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGGCT ATAGTCACCA 300  
 GACATATGAA TGThAATTGA TACATTGCAA AACTAGGATA GTGAAGTAA AGTGATTTTG 360  
 C 361

## (2) INFORMATION FOR SEQ ID NO: 4297:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4297:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAAC TTTTCACTT CGCCAAGCCA 60  
 TTTTTCTTTG TGTTTACTTT TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG 120  
 TCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT 180  
 AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT 240  
 ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 300  
 TTCACTTCGC CAAGCCATTT TnCTTTGTGT nTACTnT 337

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4298:

GTATTCCTCC ATTATTATAG GTAAATCGCT ATTAATTATA AAATTAAATG GCGGTCTCGA 60  
 CGGGAATCCT GCGTGACAGn CAGGCGTGTT ACCGCTACAC TACGAGACCA TTAGTAA AAC 120  
 GGAGGAAGAG GGATTGGAAC CCCCGCGAGC CGTTAAGCCC CTGTCGGTTT TCAAGACCGA 180  
 TCCCTTCAGC CGGACTTGGG TATTCCTnCA AAATTATATG GACCTnGCAG GACTCGAACC 240  
 TGCGACCGAA CGTTATGAGC CTTAGCTCTA ACCAACTGAG CTAAAGGTCC TAAATATAAT 300  
 TTTTACAAC TATAAAATAG TGG 323

(2) INFORMATION FOR SEQ ID NO: 4299:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4299:

CTACATGCGT TGAATTAGGG ATCGGTACTT TATATGAAGA CGTGCTGCTT CCATTAAATG 60  
 AGTGATGCGA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT AAAATTGCCT 120  
 ATAAATTTTT AGCACATAAA ATAAGAGGnG CCAACCATTG TTAGACTATA ACAACGGTTG 180  
 GCTCTTTAAT TGTA AAAAGA AAACCATACG CTATGnTGT ACAAnGAAAA AGGTTCTACC 240  
 ATTGTCACAA AAAATGCATC TCTACGTGCT AGAATAAATA TTGGTCAGCC AACCAAATA 300  
 ATCAACACGA GGAGATGCTA TTT 323

(2) INFORMATION FOR SEQ ID NO: 4300:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 385 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4300:

TGAATCCAGA TAAAAATTGGA ATGATTAACG CGAATCACTT TTACTACCAA TGTTCCAAAG 120  
 CTGCTCTGCA AACGCATTGT ACTCTGAGCT TTTTGGATTA AATGAATTGG CTCCAAATAA 180  
 5 AAATACAATT GCCATTAAAA TACCACCAGA TATTACAAGT GGCAACATGT TAGAAACACC 240  
 GTTnCATTTGA AGTGTTTGAT AGAATGCTTT ACCTGGGGCT TGAATTTTTTC TTGGACTGTG 300  
 CATTTGAGTT ACCTTTTCTT TGGACCATCA CGGGGCAACA AAAGGTTTGA CGACTTGTGA 360  
 10 GCTGAATGGC TTTnGnTGAAT GAATT 385

## (2) INFORMATION FOR SEQ ID NO: 4301:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4301:

TCCTGTACCA CCTATAATCG TTTTAATCGA TGGGGGGACG CATAGGAATA GGCGACGTGA 60  
 25 CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA 120  
 GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTC ACACTGCCGA 180  
 GAAAAGCCTC TAGATAGAAA ATAGGTGCCC GTACCGCAAA CCGACACAGG TAGTCAAGAT 240  
 30 GAGAATTCTA AAGTGAACGA ACGAACTCTC GTTAAGGGAC TCGGCAAAAT GAnCCCGTAA 300  
 CTTCGGGGAA AAGGGTnCTC TTTAnGGTTA ACGCCCCAAA AAACCGCT 348

## (2) INFORMATION FOR SEQ ID NO: 4302:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4302:

AATGGAACGT GCTTCTGTAT TGGCCCAAGT AGATATTCAT CGTGCAGCAA CACATAATAA 60  
 AGGTGTTATG AATGGCATAAC ATGCTGTTGT TTAGCAACA GGGAAATGAT ACGCGTGGTG 120  
 CAGAAGCAAG TGCGCATGCA TnACGCGAGT CGTGACGGGA CAGTATCGTG GTATTGCTAC 180  
 50 ATGGCGTTAC GATCAAGATC GTTCAACGAT TGATTGGTAC AATTGCAAGT GCCTATGGAC 240  
 ATTGGGCAAT CGTTGGCGGT GGTACAAAAG TATTACCAAT TGCTAAAGCT TCCATTAGGn 300

TTTTGAGCGG CAAAACTTT GnCAG

385

## (2) INFORMATION FOR SEQ ID NO: 4303:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4303:

AGTGCGACGA TTGGTATTTT ACAAGAATTT TATCAACAAG ATTTAATTAG CTTAAACGCA 60  
 GCAATCCCTG TGTTACTAGG CGATAACATT GGTACCACGA TTACAGCTAT CTTAGCTAGT 120  
 TTAGCCGGCT CAATCGCTGC AAAACGTGCG GCGCTGTAC ACGTCATCTT TAACTTAATC 180  
 GGGGTAATTA TCTTCACAAT TTTCTTGCCA GTTGTGATTC ATTTGATTAG TTTGTTACAA 240  
 GATTTATGGG CACTTAAAC CAGCGATGAC GATTGCAGTA TCACATGGnA TCCTTCAACA 300  
 TAACCAATAC CTTGGATTCC ATTTACCAAT TTGTAGCCnG GTTTAGCATH GGATTGGTTA 360  
 CCAAGCCTTG TCCC 374

## (2) INFORMATION FOR SEQ ID NO: 4304:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4304:

AAAACAGGAT ACTTCGATAA GTTAATGATT TCTGTTGTGA ATCGCGCACC ACGTTTCTTA 60  
 ATTTTACCGA CTATTATATT AATTGGTATT TTAGGTAGTA CAGCCGGCGA TGCTGCGACA 120  
 ATTTCTTGCC GCGCTTGCA GCAATGCTTT TTATTAAAAT TGGCTATCAC CCTATCGCTG 180  
 GACTAACGAT GGCATATGCT TCCGCTGTTG GAGGATTTGC AGCAAATATA GTTGTGGTA 240  
 TGCAAGATGC TTTGGTCTAT TCATTACAG AACCGGCAAC ACGTATCGTT TCAGATTCTA 300  
 TTAAAACAAA CGTT 314

## (2) INFORMATION FOR SEQ ID NO: 4305:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4305:

5 CGTTGCAGAA TGTGTTGAAA TCATCAGAAA TATGCTTAGG CAAGCTAATA TCATTGTCAG 60  
 CCATTAATTT ACGGTTACCA ACCAATATAT GGTGATGATC AATCGTTGCT TCAATACCAT 120  
 GGCCAGGTAC TGCTTTAAAT GTTGTGTCT CAGTTAATAT TAATTGCTTT TCTTTTGCAT 180  
 10 AATTGACAAT GGCTTCTGCC AATGGGTGTT CAGAATCTTT TTCAGCAGTA GCAAGTAGTT 240  
 GTAGCGTTTG ATTGTCACCA TGATAATCTG TCACGACTGG GACGACCATT TGTAATGGnA 300  
 nCCGTCCTTA TCTAAAACGA TGGGTATCAA TTTGATGnGG GCGG 344

## (2) INFORMATION FOR SEQ ID NO: 4306:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 378 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4306:

25 AGTTTCCCTG AAAATTAATC AAGGACTTAA CATTGCGAGT CAAGGTATTG ATCAAGCTAA 60  
 TGGACAGTTA AATGATGCCA AAGCTTCGTC ACACAAGTTA GAAGTAGAGT CCGTGATTAT 120  
 30 CAAGATGCAA TTCGACGCGC GCAAGATTTA AATCGAAGAA ACCAGCAACA GATTCCTCAA 180  
 AATAGCGCGG CGAACAACGA AACATCAAAT AGTGCACCTG CAGCTGGTAA TGGTGTAGCA 240  
 35 TCAACGCCAC CAAGTGCACC AAGTGGCGAT ACTGCACCAA ATAATAATGT TACGCAAAT 300  
 ACCGCACCAG ATGAGTGAAT AATGCGCCTG TATCGACTAC ACCACAAATG ACAnnCCGGG 360  
 GAAAnAGATGG TCAAATTT 378

## (2) INFORMATION FOR SEQ ID NO: 4307:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 318 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4307:

50 GGAATTGGGT ATTCCTCCAA AATTATATGG ACCTTGCAGG ACTCGAACCT GCGACCGAAC 60  
 GGTATGAGC CGTTAGCTCT AACCAACTGA GCTAAAGGTC CTAnATATAA TTTTACAACT 120

CTAGCCAGCT GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG 240  
 GATCGAACCG CTGGACCTCC TGCCTGGCAA AGCAGnCGCT CTCCCAGCTG nGCTAAGCCC 300  
 5 CCATAATAAT TACAGTAT 318

## (2) INFORMATION FOR SEQ ID NO: 4308:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4308:

TGTACGTTTA ATACCTATGA TATATGCTGC AAGTCTCATA TCTATTTTTTC GGTTTTGAGA 60  
 20 CAATTCGTAA ATCGTATCAA ATGCCGCTTC TAATTTTTTCA CGTAGCTTTT CATTAACTTC 120  
 TTCTTCAGAC CAATAATAAC CTTGATTATT TTGTACCCAT TCGAAGTAAG AAACCGTTAC 180  
 ACCACCAGCA CTTGCTAATA CGTCTGGAAC TAATAATATA CCACGTTTACG TTTAAATACG 240  
 25 TGTTGCTTCT GGTGTGTAG GTCCATTAGC AGCTTCAACA ACGATACTAG CTTTAATATC 300  
 ATGTGCATTG TCCTCnGTAA TTGGGTTGAA TAGCGnGGGA CTAAATGCAC ATCnAATCAA 360  
 30 CAATCCTATT GGATGTCCCA AnaATTGTAC GACCAACACC 400

## (2) INFORMATION FOR SEQ ID NO: 4309:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4309:

CAAATAAACC AGAGCTAGTT GCAATTGCTG AACCACATCC TAATAGACCG AAAAAGAGAA 60  
 45 GTAGACGTGC GGCACCGGCA GATCCTAATG CAACTCCAGC AGATCCAGCG GCTGCAGCGG 120  
 GTAGGAAACG TGGGTGACC AGTTGCAATT ACAGCGCCAT ATACGCCAAC AACTGATCCT 180  
 AATGCCAATA ATGCAGGACA AAATGCACCT AACGAATnGT TGTTCAATTG ATGACAATGG 240  
 50 TATTAGACCA AGTACCAACC GTTCTGTGCC ACnTnAAACG TTGTTAATAA CTTGCCGGGC 300  
 TTCACACTAA TCAATGGTGG CAAAGT 326

## (2) INFORMATION FOR SEQ ID NO: 4310:

(A) LENGTH: 313 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4310:

10 TCAAAGCGCC AATAACATCT TCTACTGAAG TTTCTTTAGA TTTAGCATTC AGTGATAATG 60  
 TTATTGTTGC TTTTCTCTCC ATTGGAATAC TTTGATGAAT CGTTAATACA GATAGTTCTA 120  
 ACTTTGATAT AACATCTAGT ACACGTGCCA ACATACCAAC AATATCAGTT ACATATAAAA 180  
 15 TTAATGTAAA TTCTCGATGG TCAAGCATTT TATCGGCTAC TGGAAATATC GTTTCTCTAT 240  
 ATnTATAAnA AGCACTTCTA GATAGATCAA ACTGTTTAAC GGCATCATAA ATGGnCAATG 300  
 TCGGATCACT TTT 313

20

(2) INFORMATION FOR SEQ ID NO: 4311:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4311:

GGTTCGAATC CAGCTAGCCC AGCCATTAGA GCCATTAGCT CAGTTGGTAG AGCATCTGAC 60  
 TTTTAATCAG AGGGTCAGAG GTTCGAATCC TCTATGGCTC ACTACTTGCA CTTTCCATTT 120  
 35 TTGGGAAGTG CTTTTTTTGA GGTTCTCCAC CAAATGTGGT GGGTATATAA TTAAAGAAC 180  
 TATTTTTTAAA ATACAACTTT TAGAGCTTTT ATTATTAGGC GGCCAGTCCA TTATTGGGGC 240  
 TGGTTGTCTT CnTTTTTTCT CCTTTGTACA AGCTGAAAAT CATCATTATA CGTGCTTAAA 300  
 40 GTGGTGAATT CTGAACCAAA GAATCACTTG ATAATTTATC TATATAATCC TcNATAGACC 360  
 ATATAATGCT GGAATAATGG ATCTACAnCC TGAGTTCCAn 400

40

45 (2) INFORMATION FOR SEQ ID NO: 4312:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4312:

55

ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA 120  
 AGGCATCCAC CGTGCGCCCT TAATAACTTA ATCTATGTTT CCACCATTTT TATAAGTCAA 180  
 5 ACGCTCACAT ACGGCTTCGT TTTCATTATT TTAAATGCTC ATTTACATAA GTAAACTCTG 240  
 CTTTAAAATA ATTAACATCAT TGTCTGCAAA ACGTTTTCTT TTATAAAAAG ATTAAACGCG 300  
 TTATTAACT GTGGAGTG 318

10 (2) INFORMATION FOR SEQ ID NO: 4313:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 316 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4313:

ACGGTGATCA CTCACCGCAG ATTTTAAGTC CTGTGCGTCT GCCAGTTCCG CCACCCCGGC 60  
 ACTATAAAAA TGGAGCAGAA GACGGGATTC GAACCCGCGA CCCAACCTT GGCAAGGTTG 120  
 25 TATTCTACCG CTGAACTACT TCTGCATATG CGGGTGAAG GAGTCGAACC CCCACGCCGT 180  
 AAGGCATAGA TCCTAAGTCT AGTGCGTCTG CCAATTCCGC CACACCCGCA AATGGTGAGC 240  
 CATAGAGGAT TCGAACCTCT GACCCTCTGA TTAAAGTCA GATGCTCTAC CAACTGAGCA 300  
 30 AATGGTCTT CCATGG 316

(2) INFORMATION FOR SEQ ID NO: 4314:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 356 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4314:

AGGAAAAGTC GTTGTGATAC ATCAACCAGC TGAAGAAGTA CCACCAGGTG GTGCTAAAC 60  
 45 AATGATTGAA AATGGTGTAT TAGACGGTGT TGATCATGTA TTAGGTGTAC ACGTCATGAG 120  
 CACAATGAAA ACAGGTAAAA GTGTATTACC AGACCTGGTT ATGTTCAAAC AGGACGCGCA 180  
 50 TnCTTCAAAT TGAAAGTCAA GGTAAGTGG TCATGGTTCA TCACCACATA TGGCCAATGA 240  
 TGCCATTGTT GCAGGTAGCT ACTTCGTCAC AGCGTTACAA ACAGTGTATC TAGACGACTA 300  
 GGCCATTGTA ACCGGTGGTT TCACATCGGT CATTTnCCGT AAAAGnCCAT TCCATG 356

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4315:

10	TATCAGCATT TGTAAGTGT ATTGTTTATA ACTTCTGTGT GAAGCGCAAT ATTACAATTA	60
	AAATGCCGAA AGAAGTACCG CCGAATATTT CACAAGTATT TAAGGACTTA ATTCCATTTT	120
15	CAGCGGTAAT CATCATCTT TATGCATTAG ATTTAGTCAT CGCAACAGCT TTAAATCAAA	180
	TGTAGCGGAA GGAATTTTAA AATTATTCGA ACCATTATTT ACAGCAGCAG ATGGGATGGA	240
	TTGGTGTAC AATTATCCTT GGnGGCCTTT GCATATTCnG GGTGTAGGG AATCAGGTCC	300
20	GTCAATGTAG AGCCAGCAAT TGCAGCCATT ACATATGCGA TATCGGAGCG GACTTCAAGT	360
	TGCCTCAGCG GAGGACACGC	380

(2) INFORMATION FOR SEQ ID NO: 4316:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4316:

35	GCTCTAGGAT GACTGATTGA ATGTCCATGA ATGAACAACC CCTTTGTTTA ATATCGAGTT	60
	TGGCAAATTT ACGTTTATCA GCGTTTCTAT GATCAGTACT TCTACGGGTA GCGTTTCTAT	120
	GTAATTTACA TCATCTTAAC ATATAAATAC TTCGCTATTT AATTGAAAAC ATATCCTATT	180
40	ATTCTTTGTC CGTCTGACG TTTAATATCT AGCCTTAGGC ATTTCACTTG TTAATGAATT	240
	TAACTTTCTT CCACTAACCG TCCCTAAACC CAATCCCGCA ACAGTTTTTA ACTTTTTCGT	300
45	TGTTGTCTCTG ACATCTCATT AAGAAAGTTT ATTCTGCTTA AAACCTATAA TCCACACCCT	360
	GAGCAAACGn TnCTTATGAC AGAGTATTAA AATAAGCCGn	400

(2) INFORMATION FOR SEQ ID NO: 4317:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4317:

CCTTATTGAT AATGGTATGA GAATATTTGT TCGAGATGGA TGAAGGTAAT GAGTGAGAAA 60  
 5 CTGGATTTTT AAAGTATGAG ACAATATTTT AAAAAGTTCA ATTATTAACT TATAAGCAAA 120  
 TAATTGCTAT AAAAAAGTTT GGACGTGTAC AATTGCAATA TGAAGATTTT AAATTAATTG 180  
 TAAAGTATCG TGGAGTGGGT AACGTGTCAG AACATGTATA TAATCTTGTG AAAAAGCATC 240  
 10 ATTCTGTTAG AAAATTTAAG AATAAACCTT TAAGTGAAGA CGTTGTTAGG AAATTGGTAG 300  
 GAGCTGGGCA AAGCGCTTCG ACGTCAAGTT TCCTGCCAGC ATACTCCATT ATTGGTTCGG 360  
 15 CGGTGGGAGG TTAAnGGAAT TTACGGGGAG GTTCTGGGCA 400

## (2) INFORMATION FOR SEQ ID NO: 4318:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4318:

TAACTACGTC TCCTGTTTCT GGATTCTTAA TTCCTGGTTT ACCTGGAAC TCTCTTTCT 60  
 30 CTCCTGTTGG TAACTTCGGA TCAAATTCGT CTCGATGACC TGGTGTTATC GTTTCTGGTC 120  
 CGTATTCTGT TAATTCATTA ATCGGATCTn TTGTGATTTC TTCTTTTCGAT TCACCTGTAC 180  
 TAATAATTTT TCCAGTTAAT GGATTTTTTA GTGTTGGCGT CGTTATTGTC TTCTCACCTn 240  
 35 TTGTCTCTTC TCTTGTAAC TTTTCTGTCC CGGTGCTAAA TnCGGATTAA ATTACGGTCT 300  
 TTCTTGAAGG AATCTCTTC 319

## (2) INFORMATION FOR SEQ ID NO: 4319:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 368 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4319:

50 AGGTGCATTG AGAGAATTTG TAAATGACGT ATTAGGACCT CAAGACGATA TTAATAAATT 60  
 TGAATACTTA AAAAAATCTT CTCAAAATAC AGGTACTGTC AATTATTGGT ATTCAACTTA 120  
 AAGATCATGA TGATTTAATA CAACTCAAAC AACGTGTnAA ATCATTTCGA TCCTTCCAAT 180

ACAGTCATAA ATTGATTCT AATTGAAATC ATCTTATGAC TGCTTTTTAT TATACTTTAC 300  
 ATTTGCTCGT TCGTCAGAT TGCAAACGTT TTCACCTCGC CAAGCCCATC TTTcNTTGGn 360  
 5 GTTTGCCT 368

## (2) INFORMATION FOR SEQ ID NO: 4320:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4320:

TAAGTTAGCT ACCATCCTCG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60  
 20 TCCTCTCCTT CGGCTCTCGC TTAICTCAITT AGCTCTACTA AACTCGTTGC GCTCTTTTCT 120  
 CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT 180  
 TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTCACGGT CTCAACTTGC CTGGCAACGT 240  
 25 TCTACTCTAG CGGAANTAAA GTTGGnCTAC CATCGTCGCT AAAGACCTT CTTGACTTGT 300  
 GACAATCGCT TGCTTCTTTT CCTCTCCTnC GGCTCTCGGT TAACTCA 347

## (2) INFORMATION FOR SEQ ID NO: 4321:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4321:

GGGCAAGTTA CAGTGGTGCA TGGTTGTCGT CACTCGTGTC GTGAGATGTT GGGTTAAGTC 60  
 CCnCAACGAG CGGCAACCCT TAAGCTTAGT TGCCATCATT AAGTTGGGCA CTCTAAGTTG 120  
 ACTGCCGGTG ACAAACCGTA GGAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA 180  
 45 TTTGGcTACA CACGTGCTAC AATGGACAAT ACAAAGGGCA GCGAAACCGC GAGTCaAGCA 240  
 AATCCCATAA AGTTGTTCTC AGTTCGGATT GTAGTCTGCA ACTCGaCTaC ATGaAGCTGG 300  
 50 aATCGCTaGT aATCgTGGTC CAGCATGCTA CGGT 334

## (2) INFORMATION FOR SEQ ID NO: 4322:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4322:

CTGTTAAACG ACTACAGGAA GTATTTACAA TCAAAC TAAG CAAAAGTATT CAGATGCCTC 60  
AGATAAAGCT TGGGCGCATT CAAAATCTAT TTGGAGAGGC ACATCAAAAT GGTTTAGCAA 120  
CGATATAAAA GTGCAAAGGG TTGGCTAATA GATATGGCTA ATAAATCGCG CTCGAAATGG 180  
GATAATATTT CTAGTACAGC ATGGTGAAT GCAAATCCG TTTGGAANGG AGCATCGAAA 240  
TGGTTTAGTA nCTCATTACA AnTCTTTAAA GGGTTGGACT GGGGATATGT ATTCAGAGCC 300  
CACGATCGTT TTGATGCATT TCAGTTCGGC 330

(2) INFORMATION FOR SEQ ID NO: 4323:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 337 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4323:

CAATGATGCC ATGAGCAGTG CCTCCTTTAA TAGCATTMTA GCACTGTTTT GTCGTATTTT 60  
TAAATATAAA TTTGGAATGA ATAATAAAGT AGTGATTAAA TTAAGTTGTG TGATAGGAAA 120  
CTTGGACATC AATCAAAGTA ATAGGCACTA CAACGCTTAT TGGCGGGGCC CCAACAAAGA 180  
AGCTGACGAA AAGTCACTTG CAATAATGTG CAAGTChGGG ATGGGCCCCA ACATAGAGAA 240  
ATTGGGTCCG nAATTTCTAC AGACAATGCC AGTTGGCGGG GCCCCCACAT AGAGAATTTTC 300  
GAAAAGGAAT TCTACCAGCA ATGCCAGTTG GGGGANG 337

(2) INFORMATION FOR SEQ ID NO: 4324:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 330 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4324:

TTACTTACTA TCTAGTTTGT AATGTATAAA TTACATTCAT ATGTCTGGTG ACTATAGCAA 60  
GGAGGTCACA CCTGTTCCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG TCGATGGTAG 120

GCATTGAGAC CGCAAGnTCT TTTTTTTATG TCTAAAACGT CAAAATAAAA AGCAAACACA 240  
 AAGAAAAATG GCTTGGCGAA GTGAAAACGT TTGAATCTGC CGAACGAGAA AGAGCGnACC 300  
 5 GAGTTTAGTA GAnTAAATGA GTAAGCGAGA 330

(2) INFORMATION FOR SEQ ID NO: 4325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4325:

TTCATCCGCT CACTTTTCAA CGTAATCGGT TCGGTCCTCC ATTCAGTGTT ACCTGAACTT 60  
 20 CAACCTGACC AAGGGTAGAT CACCTGGTTT CnGGTCTACG ACAAATACTA AACGCCCTAT 120  
 TCAGACTCGC TTTCGCTACG GCTCCACATT TACTGCTTAA CTTTGACATC AAATCGTAAC 180  
 TCGCCGGTTC ATTCTACAAA AGGCACGCCA TCACCCATTA ACGGGCTCTG ACTACTTGTA 240  
 25 AGCACACGGT TTCAGGTTTCG ATTTCACTCC CCTTCCGGGG TGGCTTTTCA nCTTCCCTC 300  
 ACGGnACTGG TTCAC 315

(2) INFORMATION FOR SEQ ID NO: 4326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4326:

TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTTGCGGT TAnATGCGGC TCATCGCATC 60  
 CACTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGAACTAC CATCGACGCT 120  
 AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC TATAGTCACC 180  
 45 AGACATATGA ATGTAAATTA TACATTCAA ACTAGATAGT AAGTAAAAGT GTTTTGCTTC 240  
 GCAAAACCAT TTATTTTGAT TAAGTCTTCG ATCGnTTAGT ATTCGTCAAC TCCACATGTC 300  
 50 ACCATGCTT 309

(2) INFORMATION FOR SEQ ID NO: 4327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4327:

AAAGCTTATA AACGCTCATC TGACATTGTA GAATTCATGC TTTCAAAGA CGATATACTA 60  
CGACACTCCT ACGAACTTGT CCAAGGATTA CGAAAAGACC TAAGGTTATG TAATTnGCCT 120  
AAATTTATTA ATCGTTTAAA TTCAGTTAGT AAAAAGTCTG TGAGTAAGGG TGTATGGAAA 180  
GTGGTTAAAT ATTATAGAAA ACATCAAAGG ATGTTAAGAA ATACAATTTA TTACCCAGCA 240  
TTTAATAATG GTGCTATAGA AGGAATTAAT AATAAGATnA AATTAATCAA GTGAATTTCT 300  
TTTGTTnCA G 311

(2) INFORMATION FOR SEQ ID NO: 4328:

20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4328:

TAGCTTCTGC GAGCTAGCGG AATCGAAGCC CCAGTAAACG GCGGCCGTAA CTATAACGGT 60  
CCTAAGGTAG CGAAATTCCT TGTCGGGTAA GTTCCGACCC GCACGAAAGG CGTAACGATT 120  
TGGGCACTGT CTCAACGAGA GACTCGGTGA AATCATAGTA CCTGTGAAGA TGCAGGTTAC 180  
CCGCGACAGG ACGGAAAGAC CCCGTGGAGC TTTACTGTAG CCTGATATTG AAATTCGGCA 240  
CAGCTTGTTAC AGGATAGTAG GAGCTTTGAA ACGTGAGCGC TACTTACGTG GAGGCGCTGG 300  
TGGGATACTA CCCTAGCTGT TTTGGTnTCT nACCCGACCA 340

40

(2) INFORMATION FOR SEQ ID NO: 4329:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 325 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4329:

AATCCATAGC GAAATGTATA CCATCACCCA TCGTCCTTC TAAAGGTAAA TCTCTACCTT 60  
TTTGTGCACC AGTACATAAT ATAATGGCAT CATACTCAGA TTCTAACGTT GCTTTATCAA 120

55

TACGACGTCG AACCACATCT TTATCAAGTT TCATATTCGG AATACCATAC ATTAATAAAC 240  
 CGCCTGATTG TCTAGCACGT TCATAAATAG TTAAGTTCTT 300  
 5 CAGCAGCAGT AATCCTGnTG GACCG 325

(2) INFORMATION FOR SEQ ID NO: 4330:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4330:

CACTTCACCA CAGCCGCCAT GGCAGnGCA GTAGGAATCG AACCCACACC AAAGGTTTTG 60  
 20 GAGACCTCTA TTCTACCGTT GAACTATGCC CCTATTAAAA ATAATAAATG GAGGGGGGCA 120  
 GATTGAACT GCCGAACCCG AAGAGCGGAT TTACAGTCCG CCGCGTTTAA CCACTTCGCT 180  
 ACCCCTCCAT AAATGGTGCG GGCnGnAGG ACTTGAAACC CCCAACCTAC TGATTACAAG 240  
 25 TCAGTTGCTC TGACCAATTG AGCTAAGGCC GGCTAAGAAA TGTTCCAGG ACAGAGTCGA 300  
 AACTGCCGAC ACATGGGAGC TTTCAAT 327

(2) INFORMATION FOR SEQ ID NO: 4331:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4331:

GCATCATTTT CAGCTTCCCA CTTCCACATT TGGAAATTT CTCCAGTAAC AATGAAAGAC 60  
 CATATACTTT TTCCTACAAG AGCAGGACCC GGTAACAATA CAGGTTGGTA ATGCCCAATA 120  
 ATAATGACCA TTTCCTCAAAT GCCTAAGAAA ATAATAAATG TGATAATAGG TAATATAAAT 180  
 45 TTGTTATTTG TGGGACGTGT CATGAACGCG ATGCCTCCTT ATACAATGAC GGTTCACAA 240  
 AGTCATCATA TGCAGGTGGA TTAAACAAAT GATGTTGTTT TACCAATGTC GTAATTTCTT 300  
 GGATAGCCGG ATGnTTAAA TTGTTAAAAT CACCATAGGG TGTCCnGCC GTGGACTGTG 360  
 50 GTTAAAAACG TCACGGACTT TGTTTAAAAn GGTGCGTCAT 400

(2) INFORMATION FOR SEQ ID NO: 4332:

- (A) LENGTH: 366 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4332:

10 CTGGTATGCA GATTTACCAC CTGCCTCTCC ACAAnTnnGG GGAGAGCAAA CAGATGTGCC 60  
 TGAATCAAGT GACTGGTATA ACGCATCATA CATTATTATG TGGGGCTCTA ATGTACCTTT 120  
 AACACGTACT CCGGATGCAC ATTTTATGAC TGAAGTCCGC TATAAAGGTA CAAAAGTCAT 180  
 15 TTCAGTAGCA CCAGATTACG CAGAAAATGT GAAATTTGCA GATAACTGGC TAGCACCAGAA 240  
 TCCTGGTTCA GATGCTGCAA TTGCACAAGC AATGACGGCA TGTATTTTTA CAAGGAACAT 300  
 20 TATGTTAAAT CCAACCTGAA TGAACGGTTT TTATTAAATT ACGGTTAAAA CCATTATTAC 360  
 CAGGAT 366

## (2) INFORMATION FOR SEQ ID NO: 4333:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4333:

TATTATTTCA TTGAGCAGAA AGAAAATTAT GGCACCAAAC TTAAATATTT TTTTCAATGT 60  
 35 CATTCTTTTG AnGGGAGTGG GACAGAAATG ATATTTTCGC AAAATTTIATT TCGTCGTCCC 120  
 ACCCCAACCTT GCATTGTCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCATC 180  
 40 CCCAACTTGG CACATTATTG TGAAGCTGAC TTTTCGTCAC TTGCTGTGTT GGGGCCCTCA 240  
 CCCCAACTCG CATTGCCTGT AGAATTTCTT TTCGAAATTC TCTGTGTTGG GGCCCTGGA 300  
 CTGAGAATTG GAAAAAGCT TGTGACAAG CGChATTTTC GTTCCATGCA ACTGACTGCC 360  
 45 AAGAGAACnT CGTGAGAGCh ATGAAGAAGA TTGGATTGA 400

## (2) INFORMATION FOR SEQ ID NO: 4334:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

CGCCCTTAAT AACTTAATCT ATGTTTCCAT CCTACAGGAA ACGCGTTATT AATCTTGTGA 60  
 GTGTTCTTTC GAACnTATGC GATTATTTCT TATGAATTCA AGCTTATTTA AAACTCTTTA 120  
 5 TTCACTCGGT TTTGCTTGGT AAAATCTATA TnTTACTTAC TTATCTAGTT TTCAATGTAC 180  
 AATTTCTTTT TAGTCAAGCG CTCGCATAAG CAATATCACT TTAACCAAAA AATATTTGAA 240  
 10 TGTAAATAA ACATTCAAAA CTGAATACAA TATGTCACAT TATTCGCGCA TCTTCTGnAA 300  
 GAAGATGTT 309

## (2) INFORMATION FOR SEQ ID NO: 4335:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4335:

nAGGACTTTT CTCGGTCAGT GTGAAATCA ACGCACTCGT AnACACAATG TCTTCTCCCC 60  
 25 ATCAGAGCTC AGCCTTAACG AGTACCGGTA TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA 120  
 CGTGCAATCC AATCGCACGC TTCGCCTATC CTACTGCGTC CCCCCATCGA TTAAACGAT 180  
 30 TATAGGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT ACGCCTGTCG GnCTCAGCTT 240  
 AGGACCCGAC TAACCCAGAG CGGACGAGCC TTCCTCTGGA AACCTAGTC AATCGGTGGA 300  
 CGGGATTCTC ACCCGTCTTT CGCTACTCA 329

## (2) INFORMATION FOR SEQ ID NO: 4336:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4336:

CAAAGTGACA GGTGGTGAT GGTGTGCGTC AGCTCGTGTC GTGAGATGTT GGGTTAAGTC 60  
 CCGCAACGAG CGCAACCTT AAGCTTAGTT GCCATCATT AGTTGGGCAC TCTAAGTTGA 120  
 50 CTGCCGGTGA CAAACCGnnn GAAGGTGGGG ATGACGTCAA ATCATCATGC CCCTTATGCA 180  
 TTTGGGCTAC ACACGTGCTA CAATGGGACA ATACAAAGGG CAGCGAAACC GTGAGTGCAA 240  
 GCAAATCCCA TTAAAGTTGT TCTCAGTTCTG GATTGTAGTC TGCAACTCGG ACTACATGAA 300

## (2) INFORMATION FOR SEQ ID NO: 4337:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4337:

```

CCAGCACC GG GGCAGGCGTC ACCCTCATAC ATCACCTTAC GGTITAGCAG AGACCTGTGT      60
TTTTGATAAA CAGTCGCTTG GGCCTATTCA CTGCGGCTCT TCTGGGCGTT AACCTTAAAG      120
AGCACCCCTT CTCCCGAAGT TACGGGGTCA TTTTGCCGAG TTCCTTAACG AGAGTTCGCT      180
CGCTCACCTT AGAATTCTCA TCTTGACTAC CTGTGTCGGT TTGCGGTACG GGCATTATTT      240
TCTATCTAGA nGGCTTTCTC GGCAGTGTGA AATCAACGAC TCGAAGACAC AntGGCTnCT      300
CCCATCAGAG CTCAGCCTTA ACGA                                             324

```

## (2) INFORMATION FOR SEQ ID NO: 4338:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4338:

```

CGGACATCAA ACGGATGCTG CTCGATTGGC AAATGCATAT AACTAGTAAC ATGATCATCG      60
ACATCAAATT TAGATGATCA AATGTcCCCA ATcATTAAATT TGATTGGTT GTTTGCTCAA      120
TTGATTATAT GTTTTTCTTA GCACTTCATG CGGCACCATA TCTTTACCTA GTAGCCACAA      180
AGATAAGTCT AACAAGTGGC AACCATAATC GATTAACTA CCGCCACCTT GCAACGCTTT      240
ATTGGTAAAA ACACCCGAGC CAGGCACTTT ACGCCTACGC ATCGCTTGTA CACGTGCTAC      300
TAAAGGTTTA CCAACCACAC CTGATTCAAT TGCTTTTTTA GCAGTAATTG CCACATCTGT      360
GTGACGATAA TGATATGCGC CAGTAATAnt TTGTGnTTT                             399

```

## (2) INFORMATION FOR SEQ ID NO: 4339:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4339:

5 TGAGGCGATT ATTTCTTATG AATTCAAGCT TATTTAAAC TCTTTATTCA CTCGGTTTTG 60  
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGC 120  
 CTAAGTGGAC TCGAACCACC GACCTCACGC nTATCAGGCG TCGCTCTAA CCAGCTGAGC 180  
 10 TATAGGCCCA TTTnTTTGAA TGTAAATAA ACATTCAAAA CTGGAATACA ATATGTGCAC 240  
 GTTATTCCGC ATCTTCTGAA GAAGATGTTn CCGAATATAT CCTTAGAAAG GAGGTGATCC 300  
 AGCCGCACCT TCCGATACG GCT 323

## (2) INFORMATION FOR SEQ ID NO: 4340:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4340:

25 GGCTAGCCCT AAAGCTATTT CGGAGAGAAC CAGCTATTTT CAGGTTGAT TGAATTCT 60  
 CCGCTACCCT CAGTTCATCC GCTCACTTTT CAACGTAAGT CGGTTGCTC CTCCATTCAG 120  
 30 TGTACCTGA ACTTCAACCT GACCAAGGGT AGATCACCTG GTTTCGGGTC TACGACCAA 180  
 TACTAAACGC CCTATTGAGA CTCGCTTTTCG CTACGGCTCC ACATTTACTG CTTAACCTTG 240  
 CATCAAATCG TAACTCGCCG GTTCATTCTT ACAAAGGCA CGCCATCACC CATTACGGG 300  
 35 CTCTGAACTA ACTTGGTAAA GChCCGGTTT nChGGTCAA TTTT 344

## (2) INFORMATION FOR SEQ ID NO: 4341:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4341:

45 TGTACCACCT ATAATCGTTT TAATCGATGG GGGGACGCAT AGnGATAGGC GAACGTGCGA 60  
 50 TTGGATTGCA CGTCTAAGCA GTAAGGCTGA GTATTAGGCA AATCCGGTAC TCGTTAAGGC 120  
 TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TTCGAGTCGT TGATTTTACA CTGCCGAGAA 180  
 AAGCCTCTAG ATAGAAAATA GGTGCCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG 240

TTCnGGGAAA AAGGGnTCCC CTTTAAGGGT TAACCGCCCC AAAAAACCCC C

351

(2) INFORMATION FOR SEQ ID NO: 4342:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4342:

AATAATGACT CCTACGGGAC TCGAACCCGn GTTACCGCCG TGAAAGGGCG TGTACTTAAC	60
CGTATGACCA AGGAGCCATG GCTCACCAGG TAGGACTCGA ACCTACGACC GATCGGTTAA	120
CAGCCGATAG CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC	180
TCTAGCGGAA nTAAATTCGA ACTACCATCG ACGCTAAnGA GCTTAACTTC TGTGTTCCGC	240
ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT	300
TCAAAACTAG ATAGTAAGTA AAAGTGA	327

(2) INFORMATION FOR SEQ ID NO: 4343:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 360 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4343:

ACCGCTTGGG CTGACATTTT TGGCTTGTTA AGCAGCTTGC CTACTTTTTT GGCAATAGCA	60
CCATACGTTG TTAGAGTCCC ATAAGGAACC TGTCTTAATT CATTCCAAAC AACTGTTGA	120
AAATGACTAC CTGTTGGCTT TAAAGGTATT GTGATTTTCAG GATTGTCACC TTAAAATAC	180
GCGTCTAACC ACTGTGTCGC CTCTCTAAAT ATCGCTAAAG ACGTATTTTC TTCCCTAGTA	240
CCATCACCTT GTTGATTTTC AAACAAAACA GCGGTCAGAC TTACCCCATC ACTCAAAAGT	300
TCCAAnCGTC CTGACAGGCG AAnCAGAGTG AACGCTGAGA CTCCAGAAAA ATCCCCCTnT	360

(2) INFORMATION FOR SEQ ID NO: 4344:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 313 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4344:

ATTCCGACAT CTTCTGAAGA AGATGTTnCC GAATATATCC TTAGAAAGGA GGTGATCCAG 60  
 5 CCGCACCTTC CGATACGnCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC 120  
 GACGGCTAGC TCCTAAAAGG TTA CTCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT 180  
 10 GACGGGCGGT GTGTACAAGA CCCGGAACG TATTCACCGT AGCATGCTGA TCTACGATTA 240  
 CTAGCGATT CAGCTTCATG TAGTCGAGTT GCAGACTACA ATCCGAACTG AGAACAACCTT 300  
 TATGGGATTT GCT 313

## (2) INFORMATION FOR SEQ ID NO: 4345:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4345:

ATTTTATCGT AAGATTTTTT CGCAATGAGA TTTGGATCGT TTTTGTCCAC TACAATATCT 60  
 AATAGTTTTA CTTTAAGTCC AGCATTACACA AAAAGTGCTG CCAGTTGAGC GCCCATTGTG 120  
 30 CCTGCGCCAA GAACGGTTAC TTTATTAATT GTCATAGTGA TTCCTCCAAT TTAGTTGAGG 180  
 ATAAGATAAC CATTAGATA ATTGGAATAA CGTTGCTATT TTATAAAATT AATTAAGTAT 240  
 CTTTGACAGT CATCTTAGCC TCTTATTTAA GGnAAAAGCn TTATGCTTAA nATAAGTCTT 300  
 35 TTTTA 305

## (2) INFORMATION FOR SEQ ID NO: 4346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4346:

GTCAGTTATG GCAAGTGCAT CAACATTTTC AGACACAGCA AGTCTTACGG CATCTTCTAT 60  
 TTTTAAGCTT GAATTTAACA AATCATAAGC CGTATGAATA TTAAATATG CCACCATGAT 120  
 50 TGAATGGnCC CTTTCTATTA GTTAAGTTTG TCGTAAAGC TGTAGCAAGT TGCTCAAATT 180  
 CATCCCCAGC TGTCCACTGA AACTCCTGGA CGCATTCGGA TGAnCAACGC CAACCAAAT 240

AnTACCTTCA TCGACTGCAA ATACCCATAA TTTCCAGCCT TGATGTCAGC AATGTAATAA 360  
 CCAACTGAGA TGCTCATTGG CTGATACGAT GntCCATACA 400

(2) INFORMATION FOR SEQ ID NO: 4347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4347:

TCTGGGTTGA GTCGGGTCCT AAGCTGAGGC CGACACGTAG GCGATGGATA ACAGGTTGAT 60  
 ATTCCTGTAC CACCTATAAT CGTTTTAATC GATGGGGGGA CGCATAGGGA TAGGCGAnGT 120  
 GGCGATTGGA TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC GGTACTCGTT 180  
 AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCCA GTCGTTGATT TCACACTGGC 240  
 CGAGAAAAGC CTCTAGATAG AAATAnGTGC CCGTACCGCA ACCGACACAG GTAGTCCAAG 300  
 ATGAGATTCh TAAGGTGGAG CGACGAATCT CCGTTAA 337

(2) INFORMATION FOR SEQ ID NO: 4348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4348:

GTTAAGACAC CGCCCTTTCA CGGCGTAACA CGGGTTCGAG TCCCGTAGAG GTCACCATTT 60  
 TTTAGGTCTC GTAGTGTAGC GATTAACACG CCTGCCTGTC ACGCAGAGAT CGsGGGTTTCG 120  
 ATTCCCGTCG AGACCGTACA AATGCCTATC CAAGAGGATA GnatTTTTTTT TGC GTTTAAT 180  
 ATTATATTAA TAAAAGATAT ATGGACGAAT GATAATCATA TTGATTTATC TGTTCGTCCA 240  
 TTTTCTTTAA AATGTATGAA CCTCAAGTAA CTTAGTGGTT GGATATGAAA GATAAACGTh 300  
 GACAATAAAA TCTTTATT 318

(2) INFORMATION FOR SEQ ID NO: 4349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4349:

CTTTAAAGCA CGTATAATGA TGATTTTCAG CTTGTACAAA GGAGAAAAAA AGAAGACAAC 60  
 5 CAAGCCCAAT AATGGACTGG CCGCCTAATA ATAAAAGCTC TAAAAGTTGT ATTTTAAAAA 120  
 TAGTTCTTTA AATTATATAC CCACCACATT TGGTGnAGnA ACCTAAAAAA AnGCACCTCC 180  
 10 CAAAAATGGA AAGTGCAAGT AGTGAGCCAT AGAGGATTCG AACCTCTGAC CCTCTGATTA 240  
 AAAGTCAGAT GCTCTACCAA CTGAGCTAAA TGGCTCTAAA TGGCTGGGCT AGCTGGGATT 300  
 CGAACCAACG AGTGACGGA 319

## (2) INFORMATION FOR SEQ ID NO: 4350:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4350:

ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG 60  
 GGTTCGAACC GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GCTAATTCTC 120  
 CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT 180  
 30 AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACCGATCGGT 240  
 TAACAGCCGA TAGCTCTACC ACTGnAGCTA CTGTGGATTG AATCATTATG CCTGGCAACG 300  
 TTCTTACTAT AGCGGAAnGT CAAGTTCCGC ATnACCATAC GAAGCT 346

## (2) INFORMATION FOR SEQ ID NO: 4351:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4351:

ACGTCCTTCA TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT 60  
 ATGTTTCCAC CATTTTTATA AGTnAAACGT TAACATGAAG TTACGTTCTT TTATAAAAAG 120  
 50 ATTTAAACGC GTTATTAATC TTGTGAGTGT TCTTTCGAAC ACTAGCGATT ATTTCTTATG 180

ACTTACTTAT CTAGTTTTC AATGTACAAAT AATGGTGGGA GACTAGCGGG ATCGAACCGC 300  
TGACC 305

(2) INFORMATION FOR SEQ ID NO: 4352:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 302 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4352:

GTTTCATCAAT TGCTAATTCC AGTCCGCTA ACGGATCAAT TTCATCCGCA TGTATTTTCA 60  
CTTTAAACC TGGCTTCTTT GGCTTTTTC ATATAATGTT GCGATTGTTT TATTGTAAAT 120  
ACACCTGTTT CACAGAAAAT ATCCGCAAAG TCTGCATATT GTTTTACTTC CGGAAGTAAC 180  
GCAATCATTT CTCTAAAAA TGCCTCATTT GAACTGCTT CTTTAGGTAC AGCATGAGGC 240  
CCTAGGAAAG TATGTTTCAT GTCTAAATCA TATTCTCAG CTAAACGATT AGnCACTTTC 300  
AA 302

(2) INFORMATION FOR SEQ ID NO: 4353:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 411 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4353:

TCTACCGCTG AACTACTTCT GCGGGTGAAG GGAGTCGAAC CCCCACGCCG TAnnTGAGGA 60  
TCCTAAGTCT AGTGCGTCTG CCAATTCCGC CACACCCGCA AATGGTGAGC CATAGAGGAT 120  
TCGAACCTCT GACCTCTGA TTAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTT 180  
CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA 240  
CCAATTGAGC TAGGCCGGCA ATATGTAAGA ATAAATGGTG GAGAATGACG GGTTGGAACC 300  
GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GCTAATTCTC CGnTTTAAAA 360  
CTGCTGGCnA CGGTCTAnTC TAAGGGGACG TAAGGTCGAC TACCATCGAC G 411

(2) INFORMATION FOR SEQ ID NO: 4354:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 367 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4354:

	TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC TACCCAGCTA TGCCGTTGGA	60
10	CGACAACCTGG TACACCAGAG GTATGTCCAT CCCGGTCCTC TCGTACTAAG GACAGCTCCT	120
	CTCAAATTC CTACGACCAC GACGGATAGG GACCGAACTG TCTCAGACG TTCTGAACCC	180
	AGCTCGCGTa CCGCTTTAAT GGGCGAACAG ACAAGCCCTT GGGGACCGAC TACAGCCCCA	240
15	GGATGCGATG AGCCGACATC GAGGTGCCAA ACCTnCCCGT CGATGTGAAC TCTTGGGGGA	300
	GATAAGnCTG TTATCCCCGG GTAACTTTT ATCCGTTGAG CGATGGGCCC TTACCATGCG	360
	GAAACCA	367

20

(2) INFORMATION FOR SEQ ID NO: 4355:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 313 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4355:

	GTATTTTAAA TCATAGTGGT TTATGCGTCT TTTTCAAATT CTATAAAAAA TCGGATGACG	60
	TGTAATCTGC CATAGATTAA CACATTCATC CGATTTATAA TAATAAGATA GACTAACATT	120
35	TATTGAGAGC GGGACGGAAA TGATAAAGAA CGACTAATGA TTGATTATGT AGCGATTCTT	180
	TATCATTAGT CACAGCTAAT GTGTACTTAA AAATATGAAT GCATGAGTTA CACTCAnATT	240
	AGAGGAAATA CTAATTTCTA AAGAAAAAGT ATTTCTTTAT GTTGGGGnCC ACCCCAATT	300
40	GnCATTTGTCT GTT	313

(2) INFORMATION FOR SEQ ID NO: 4356:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 335 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4356:

	GGGCTGGGTT CAGAACGTCG AGGCAGTTCG yTCCCTATCC GTCGTGGGCG TAGGAAATTT	60
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55

TCGTGCCAnG CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AGATCCTGAA 180  
 GCATGAAGCC CCCCTCAAGA TGAGATTTC CAACTTCGGT TATAAGATCC CTCAAAGATG 240  
 5 ATGAGGTTAA TAGGTTTCGAG GTGnGAAGCA TGGTGACAGT GGnAGCTGAC GAATACTAAT 300  
 CGATCGAGGA CTTAATCAAA ATAAATGTTT TGCGA 335

## (2) INFORMATION FOR SEQ ID NO: 4357:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 304 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4357:

GCTCTAAAAG TTGTATTTTA AAAATAGTTC TTAAATTAT ATACCCACCA CATTGTTGn 60  
 nGAACCTAAA AAAAAGCACT TCCCAAAAT GGAAAGTGCA AGTAGTGAGC CATAGAGGAT 120  
 TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTA 180  
 25 ATGGCTGGGC TAGCTGGATT CGAACCAACG AGTGACGGAT nAAAGTCCGT TGCCTTACCG 240  
 CTTGGCTATA GCCCAATATA TAGATGGTGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA 300  
 AGAG 304

## (2) INFORMATION FOR SEQ ID NO: 4358:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 302 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4358:

ATAATGGTGA CGTTGATGAT GCATTAACAC AAGGTAAAGC AGCAATTGAT GCTATTCAAG 60  
 TAGATGCTAC TGTTAAACCT AAAGCGAACC AAGCTATTGA AGTTAAAGCA GAAGATACGA 120  
 45 AAGAATCTAT TGATCAAAGT GACCAGTTAA CTGCTGAAGA AAAAAGTGA GCATTAGCAA 180  
 TGATTAAACA AATTACAGAT CAAGCTAAAC AAGGTATTAC TGATGCAACA ACAACTGCTG 240  
 AAGTTGAAAA AGCGAACTC AAGGACTTGA AGCATTGAT AACATTCann TCGACTCAnC 300  
 50 AG 302

## (2) INFORMATION FOR SEQ ID NO: 4359:

(A) LENGTH: 350 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4359:

10 GGTGGGAAA TCATTGCATG AGAGTGTGAA AGGGCATAAG GGGAGCTTGG ACTGCGAGAC 60  
 CTACAAGTCG AGCAGGGTCG AAAGAGGACT TAGTGATCCG GTGGTTCCGC ATGGAAGGGC 120  
 CATCGCTCAA CGGATAAAAG CTACCCCGGG GATAACAGGC TTATCTCCCC CAAGAGTTCA 180  
 15 CATCGACGGG GAAGTTTGGC ACCTCGATGT CGGCTCATCG CATCTGGGG CTGTAGTCGG 240  
 TCCCAAGGGT TGGGCTGTTC GCCCATTAAG GCGGTACAG GCTGGGTTCA GAACGTCGTA 300  
 AGAAAGTTTC GTCCCTATCC GTCCTGGGGC GTAGGAAATT TnGAGAGGAG 350

20

## (2) INFORMATION FOR SEQ ID NO: 4360:

## (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 329 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4360:

AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG TGTGACGGGC 60  
 GGTGTGTACA AGACCCGGGA ACGTATTCAC CGTAGCATGC TGATCTACGA TTACTAGCGA 120  
 35 TTCCAGCTTC ATGTAGTCGA GTTGCACT CACAATCCGA ACTGAGAACA ACTTTATGGG 180  
 ATTTGCTTGC ACCTCGnGGT TTCGCTGTCC CTTTGTATTG TCCATTGTCA GCACGTGTGT 240  
 40 AGCCCAAATC ATAAGGGGCA TGATGATTTG GACGTTTCATC CCCAnCTTCC TCCGGnTTGT 300  
 ACACCGGCAG TTCAACTTAG AGTGCCCAA 329

40

## (2) INFORMATION FOR SEQ ID NO: 4361:

45

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 424 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4361:

55 AGACATAAAA AAAGAGACCT CACGGTCTCA ACTTGCCTGG CAACGTCTA CTCTAGCGGA 60

CTnTCCTCTC CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TGGCTCTTT 180  
 TCTCGTTTCG TCAGATTCAA ACGTTTTTCAC TnCGnCAAGC CATTTTTCTT TGTGTTTACT 240  
 5 TTTTATTTTG ACGTTTTTAGG CATAAAAAAA wGAGAcCTTG CGGTCTCAAT GCGGCTCATC 300  
 GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG GCTAACAACG 360  
 10 TCGCCAAAGA CCTTTCTTGA CTTGTGACAA TCGGCTTGCT TCTTTCCTCT CCTTCGGCTC 420  
 TCGC 424

## (2) INFORMATION FOR SEQ ID NO: 4362:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 316 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4362:

25 CACAACAAGT ATCTAAGATA CTGGCCGAAG ATTGTCACAG ACGGTAGGGG AAGGGGGTCA 60  
 CGGTACGAC CCAACATGTG GTTCCGGTTC ATnGTTGTTA CGTGTGGTA AAGAAACGCA 120  
 ATThAnTCGT TATTTTCGGAC AAGAACGTAA CAATACTACA TACAACTTAG CACCATGAAT 180  
 30 ATGTTATTAC ATGATGTGCG TTATGAGAAC TTCGAGATCC GTAATGATGA CACATTGGAA 240  
 AATCCAGCCT TTTTAGGCAA TACATTTGAT GCGGTTATTG CGAACCATAC AGTGCGAAAT 300  
 TGGACAGCAG ATTCCA 316

## (2) INFORMATION FOR SEQ ID NO: 4363:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 318 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4363:

45 GGGTACTAAG ATGTTTCAGT TCTCCGGGTG TGCCTTCTGA TATGCTATGT ATTCACATAT 60  
 CGATAACATG ACATAACTCA TGCTGGGTTT CCCCATTCCG AAATCTCTGG ATCAAAGCTT 120  
 50 ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA 180  
 AGGCATCCAC CGTGCGCCCT TGAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG 240  
 55 TTGATTAATC TTGTGGAGTG TTCTTTCGAA CATAGCGATT ATnTCTTATG GAATTCAAGC 300

## (2) INFORMATION FOR SEQ ID NO: 4364:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4364:

5	ntGCACTTAA GAACTTAGAC GATCGTGGTA TCGTTTATAT TGGTGCAGAA GTAAAAGATG	60
15	GAGATATTTT AGTTGGTAAA GTAACGCCTA AAGGTGTACT GCAGTTAACT GCCGAAGAnA	120
	GATTGTCACA TGCAATCTTT GGGTGAAAAA GCACGTGAAG TTAGAGnATA CTTCATTACG	180
	TGTACCTCAC GCGCTGGCG GGTATCGTTC TTGCATGTTA AAAGTATTCC AATCGTGCAA	240
20	GAAGGGCGAC GATACATTAT CCACCTGGTG TTAAACCAAT TTTAGTACGT GGTATATATC	300
	GTTCCAAAAA CGT	313

## (2) INFORMATION FOR SEQ ID NO: 4365:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4365:

35	AACCATTCCA TGCAATAGCG TCATTCTTGG ATATTAATCC CTAAATTGCC GTGATATCCC	60
	GCGTCTATCT TGGCCTGTTT CAATCACTAA ATGCGTTTTA CTACTTACAC CACTACGGGC	120
	TAGTTAATAG TCCGACATAG CCCTCTGGTA TGCTTACAGC TACATCTGTh TTAATCACTG	180
40	CCTTTTCTTG TGGCTCAAGT ACGACAGTTC AGCTGAGAAT ATGTCATAAC CTGCATCCGn	240
	CTTATGATTT CGTTCGGGCA TTCTAGCATT TTCTGATAAT AGCCTTACTT GTAATGTGTh	300
45	AGTCATTTTC	310

## (2) INFORMATION FOR SEQ ID NO: 4366:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AGTGGTACTT CTGTTAATTG GTGAATTTGG ATACTGGTTA TATTCAGCTG CACCGCAAGC 60  
 AACTTCTATT GATGGCCTAA CTGCCTTTTT ACCTCAAGCA ATGGGTATGG TAATTGTTGC 120  
 5 AGTCATTAT GGCTTTATGA ATATGAAAGC AGAGAATCCA TTCCGTAATA AAATTACGTG 180  
 GTTACAAATT ATTTCAAGTT TCTTCTTTGC ATTTGGTGCT TTAACATATC TTATTTCAAGC 240  
 10 ACAACCTAAT ATGAATGGTT TAGCACTGGA TTTATCCTTC TCAACATCCG TGGTGCTGCT 300  
 ACATTAAAGG TATTAATTCT TAAACCACAT AAACGTCAAA GAATGGTAAT ACAATCACGG 360  
 CTAGTACCAT TTAGTAGCCG CTCCGTACCG AATTATAAA 400

## (2) INFORMATION FOR SEQ ID NO: 4367:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4367:

CACCTGGACG AAACGGTTTT AGATCGTATT CAATTGAAAA GGCCGGTATT GAATGAATCA 60  
 CACTTAGCAG CGATTGATCA GGAACATTTT AAATTAAGTT ATTTATCAAC GGTATATGAA 120  
 30 GGGGATTTGG AAGATGCGTT AGAAGCATTG TGCCGAGAAG CAGTGAATGC TGTAACAAG 180  
 GCGCTCAAAT TCTAGTGTTA GATGATAGTG GATTAGTTGA TAGCAATGGC TTTGCAATGC 240  
 CGATGTTACT CGCATAAGT CATGTGCATC AATTACTTAT TAAAGCAGAT TACGnATGnC 300  
 35 TACAAATTTA ATCGCTAAAT CTGGTG 326

## (2) INFORMATION FOR SEQ ID NO: 4368:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4368:

ATTATAGCCG AAATGCCCAA AATAGATTTT GACGAATATT ACGAATGGTT GCTTTACTTG 60  
 50 CATAAATGGC TTTAGGAATA AGCATCAAGT CGCCACCAAG AATAGTAATA TCAGCTGCTT 120  
 CAATGGCAAC TTCTGTACCT GTAnCAATGG CGATACCGAT ATCAGCTTTA ACTAATGCAG 180  
 55 GTGCATCATT TACACCGTCA CCAAnCCATCG CAACCTTCTT ACCTTGTTGC TGTAGTTTCG 240

GTTTTGC

307

## (2) INFORMATION FOR SEQ ID NO: 4369:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 396 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4369:

TTCTTTCTCT TCCTCCGGGT ACTAAGATGT TTCAGTTCAC CGGGTGTGCC TTCTGATATG 60  
 CTATGTATTC ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT 120  
 CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA 180  
 TCGGCTTCTA GTGCCAAGgC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAT 240  
 CCTACAGGAA ACGCGTTATT AATCTTGTA GTGTTCTTTC GAACATAGC GATTATTTCT 300  
 TATGAATTCA AGCTTATTTA AAACCTCTTA TTCAATCGGT TTTGCTGGG TAAATCCTA 360  
 TATTTTACnT ACCnTATCGA GTTTTCAATG TAACAA 396

## (2) INFORMATION FOR SEQ ID NO: 4370:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4370:

CAGTAAGATA ATTTTCAATT AGAAAATATC TTAGTGCTGT TCTCTATTTA TACAATACTT 60  
 CGTATTGAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT 120  
 GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAACA TGTAATTTTA CTTTACATA 180  
 CTTTTAAAAA ATAAGACACT TTGCCAACT TGCACATAAA TGTTTAATTC AATAATTGA 240  
 ATTTTCTGTG TTGGGTCCCT TCGTATAATT TAATAAATAC CACTAACTA AATTATGAA 300  
 GTGCCTTATG TATAA 315

## (2) INFORMATION FOR SEQ ID NO: 4371:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4371:

5 GTCGTCAAAT GTACCTTCAC CAAGTAGTGA TGTACATATT TACCGCCTTG TTCAACAGCA 60  
 CGTGTGCGCG CACCTGTAAT CGCAATGACA GGTATGCGTT CAnATATGAA CCTGCGATAC 120  
 10 CGTTGACGGC ACTTAATTCG CCAACACCAA ATGTAGTAAC TAATGCAGCG AGTCCATTAA 180  
 GACGGGCATA ACCGTCCGCT GCGTAACTTG CGTTTAATTC ATTTGTATTT CCTACCCAAT 240  
 CTACAATGGG GTTGCTGATA ATATCGTCTA GAAAAGCGAG ATTAAATCA CCAGGGnCAC 300  
 15 CAAATTTTT ATCGACGGCn TG 322

## (2) INFORMATION FOR SEQ ID NO: 4372:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4372:

25 CCTAAGTCTA GTGCGTCTGC CAATTCGGCC ACACCGCAA ATGGTGAGCC ATAGAGGATT 60  
 30 CGAACCTCTG ACCCTCTGAT TAAAGTCAG ATGCTCTACC AACTGAGCnA ATGGCTCTTC 120  
 CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA GTTTGCTCTA 180  
 CCAATTGAGC TAGGCCGGCA ATATGTAAAG AATAAATGGT GGGAGAATGA CGGGTTCCGnA 240  
 35 ACGGCGGAAC CCTCTGCTTG TAAAGCAGAT GCTCTCCAGC TTGAGCTAAA TCTCCGATTT 300  
 AAAACTGCTG GGCAAGTTCT ACTCTAG 327

## (2) INFORMATION FOR SEQ ID NO: 4373:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4373:

50 CATTTTAATT TATTGTACAG AACGAAATGT GATGTTAGTA GATCATAGGG TTGATGATAA 60  
 TATTAAAGCT GAAAACGTTA TATTTATTGG CCTTTTGTGT AAACATGGAC ATTGGCATGC 120  
 AGTCATTAT GACATTGCTC AAGACAAAAC TGCCGAACTC GAAATTGAAA ATATTATAGA 180

TCAATTTTTA AACCCCATCG ATTCCTAAAA AACAGCAGTA AGATGATTTT CAATTAGAAA 300  
 ATATCTTGCT GCTGTTCTCT ATTTATACAA TACTTCGTAT TGAATGGCTC GCTTTCCCAG 360  
 5 GGnGCCGCTC AGCCTGGGCC TCGACTGGCA ATGCTCCCTC 400

## (2) INFORMATION FOR SEQ ID NO: 4374:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4374:

TAATGGATTT TTTAGTGTG GTGTCGTTAT TGTCTTCTCA CCTTTTGTG CTCTCTTGT 60  
 20 TACTTTTTCT GTCCCTGGTG CTAAATCAGG ATTAAATTIA CGTTCCTTCT CGAATGGAAT 120  
 CTCTTCTTTT TCTACAATCG AGTCTCCTTT TACAGGTCCA TATTTTGTTA CGCTATCGAC 180  
 CGGTGGTCTA ACTACATCTC CTGTTTCTGG ATTCTTAATT CCTGGTTTAC CTGGGAACCT 240  
 25 CCTCTTCTC TCCTGTTGGT AACTTCGGA TCAAATTCGT CTCGATGGAC CTGGTGTGA 300  
 nCGTTTCTGG GTCCGnAAGT CTGTnGAATT GCAG 334

## (2) INFORMATION FOR SEQ ID NO: 4375:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4375:

ATACATGCAA GTCGAGCGAA CGGACGAGAA GCTTGCTTnG TGAATGTTAG CGGCGGACGG 60  
 GTGAGTAACA CTGGATAACC TACCTATAAG ACTGGGATAA CTTGCGGAAA CCGnAGCTAA 120  
 TACCGGATAA TATTTTGAAC CGCATGGTnA AAGCTTGCAA AGACGGTCTT GCTGTCACTT 180  
 45 ATAGATGGAT CCGCGCTGCA TTAGCTAGTT GGTAAAGTAA CGGCTTACCA AGGCAACGAT 240  
 GCATAGCCGA CCTGAGAGGG TGATCGGCCA CACTGGAACCT GAGACACGGT CCAGACTCCT 300  
 50 ACGGG 305

## (2) INFORMATION FOR SEQ ID NO: 4376:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4376:

GATAAAGTGA AAGAACTCGG ACGTGACACC TATTGCACGA TTCGTTGGTT TTAAGGCAGT	60
AGGCGTTGAC CCGAAAATTA TGGGTATTGG GCCTGGCATA TGCGATTCTT GAAGTATTGT	120
CACTCAGCAA TCTATCTGTT GAAGACATTG ATTTGATCGA ATTGAACGAn CATTGCTCT	180
CAAACGATTG CATCTATTAA AGAAGTAGGT CTAGATATAT CACGTACGAA TGTGAATGnT	240
GGCGCTATTG CTTTAGGTCA TCCATTAGGT GCTACAGGCG CAATGTTAAC CGCGCGTTTA	300
CTTAA	305

(2) INFORMATION FOR SEQ ID NO: 4377:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4377:

AATGTCTTCT ACCCCATCAC AGCTCAGCCT TGAACGAGTA CCGGGTTTGn CCTAATACTC	60
AGACCTTGAC TGCTTAGACG TGACAATCCA ATACGACACG CTTGCGCTAT CCTACTGCGT	120
CCCCCATCG ATTAAAACGA TTATAGGTGG TACAGGAAAT ATCAACCTGT TATCCATCGC	180
CTACGCTGT CGGCCTCAGC TTAGGACCCG ACTAACCCAG AGCGGACGAG CCTTCCTCTG	240
GAAACCTTAG TCAATCGGTG GACGGGATTC TCACCCGTCT TCGCTACTC ACACCGGCAT	300
TCTCACTTCT AAGCGCTCCA CATG	324

(2) INFORMATION FOR SEQ ID NO: 4378:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4378:

CATCATGCTT AGAAAACGCT TAATTTAGGT TTTGACTTTT TAATCAGAGT ATATAAGCAA	60
AACTTATCAT ACAGGTAAGG TGTAATAAGT ATTTTTTATT AATTGAGAAT AATTATCAAT	120

TGGCACCAAAA CTTTAATATT TTTTCAATG TCATTCTTTT GATGGGAGTG GGACAGAAAT 240  
 GATATTTTCG CAAAATTTAT TTCGTCGTCC CACCCCAACT TGCATTGTCT GTAGAAATTG 300  
 5 GGGAAATCCA ATTCCTCCTT GGTGGGGGCC CATCCCCACC TTGCACATAA TGGnAGChGG 360  
 ACCTTTCCGC CGCTCCGGGG TGGGGGCCTC nACCCCAhTC 400

## (2) INFORMATION FOR SEQ ID NO: 4379:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4379:

20 ATAAATATA TCACTTGAAA AATTTCATGT AGAAAAGATG ATGGATAGGC TATAAAGTAA 60  
 TTGTGACTGA GATGAACTTT TATGTCTTAG ACACTACAAC ACTATATTGG CAGTAGTTGA 120  
 CTGCGGGGCC CCAACATAGA GCAAATTGGA TTCCCAATTT CTACAGACAA TGCAAGTTGG 180  
 25 GGTGGGCCCC AACATGAAAG AAATACTTTT TCTTTAGAAA TTAGTATTTT TTATGCATGA 240  
 GTGTACTCAT GTTGCGATTA TTTTnAGTA CACATTAGCT GTGGACTAAT GATAAAGGnn 300  
 30 TCGCTACATA ATCCATCCAT TAGGTCGTTT CTTGATTCAT TCCCT 345

## (2) INFORMATION FOR SEQ ID NO: 4380:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4380:

CTAAAGCTGn CATATGCGGC TTGCCGATGA AGCCAACCCT GCTGCTGTTG GTACAAAATT 60  
 45 GTCGCTTTCA ATTTCTGCAT ACCAATCGAT GCCAGCTCTA TTTCTGACAA TATCCATATA 120  
 TTTTGAAATT TTCTCTAATT CTTTGCCACT AACCTTTTCA CCATTCAACC AAAATTGATC 180  
 CTGTGTTAAC TGGTCGTTAA AAGTGACTTT CGTTTCAGTG TAAAATTTTT CTAATGTAAC 240  
 50 AGATATGCTA TTATTCATGG AAGATTAGTG CTTTCATCTTT TTTACCCCAA TATTTTATAA 300  
 GTGCAATATC GTAGTGCAAG CTTGCCACTT TAACACGCAT AACTCCTAAA TCTCAACCAG 360  
 ATn 363

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4381:

ACCTGAATGA	CTCAAAC	TTG ACTTTn	CGAC AATTG	ACTGT n	CATTTTGCA	TAGTTGTATG	60
nCTCCATTn	C GTAATT	TATTA GATTTG	TTTCG CTTAC	GTCTA TTGA	ATCATA CAGCTT	TATT	120
ATAGTTAGCG	TATTTGCACC	TTTGCACATT	AAACCATGTT	TAATAATCAT	TGAATCATT		180
TTAAGTAAAT	TAAGGAATCT	ATAATGTTTCG	TTAAATAAAA	CTGATCCCCT	TGTGGCTTCA		240
CACCCGATAG	ATAGGGATTT	ACAGATAAAT	TCAGGTCTCT	TCCACGTCCA	TATTTGGGAC		300
CCATCGAAAA	TCGGGTTCTC	AAATCATCGA	ACATAACAAA	AGAAGCTAAG	CAACAGTAGG		360
GCCGTTGTCA	CTTAACTTCT	GTTTTTCCGA	TGACAGCTTC				400

(2) INFORMATION FOR SEQ ID NO: 4382:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 304 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4382:

GnACTACAAA	GCAATGGGGT	TTGCCAGTTT	CTTTATTTAC	TGACGAATAC	TGGCAATGAC	60
ATCAGATACA	TGTGGCAnCA	CCAATCCATT	TCTTTTCACC	ATTGATAACC	CAAGTATCGC	120
CTTGGGTTGC	AGGGACTGTT	TCAAGACCTC	CCGCAACGTC	CGAACCGTGT	TCTGGTTTCAG	180
TTAAAGCAAA	GCATGTTACG	CnTTTCATGTG	AACTGTAAAT	TAGGTACATA	TTTCGCAATT	240
TGTTCTTTGC	TACCTCCGAA	ATAGAAAGTG	TTATGCCCTA	AACCTTGGTG	AACACCGAGT	300
AGGG						304

(2) INFORMATION FOR SEQ ID NO: 4383:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GTGCATTATT TTGGAGAATT AGCTCAGCTG GGAGAGCATC TGCCTTACAA GCAGAGGGTC 60  
 GGCGGTTTGA ACCCGTCATT CTCCACCATT TTGATTATTA AATTATATGA ATAAGCTGGA 120  
 5 GGGGTAGCGA ATGGCTAAAC GCGGCGGACT GTAAATCCGC TCCTTCGGGT TCGGCAGTTC 180  
 GAATCTGCCC CCCTCCACCA TCTATATATT GGGCTATAnC CAAGCGGTAA GGCAACGGAC 240  
 10 TTTGACTCCG TCACTCGTTG GTTCGAATCC AnCTAGCCCCA GCCATTAGAG nCATTAACTC 300  
 AGTTGGTA 308

## (2) INFORMATION FOR SEQ ID NO: 4384:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 309 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4384:

AATTTTGGCC AAAACACCCA TCCGCTGTAA CTTGAGAGTG TCATTGGCAT TTATTACACT 60  
 25 ATCTCCAACCT CCTAGTGGAA CAACCACATC TCGTCCTTGG GGTGCATGGA ATGTTCCGTC 120  
 AGCCCTGTGA ATTATTTCTT GAACTCCACC ACCTGGGGCG TTTCCAGAAC CTCTATCATT 180  
 30 TAATACAGCA AATGTCGGTT GCGTTAATGC TCCTGAATTA TCGGKAGCTA CACCCTTTCC 240  
 TGCTAAAGTA CCAGTAGACA ATGTAGGTAT TGGCTTGATG AGATTTtTAT CAGTAATGGC 300  
 TTTAGAnAT 309

## (2) INFORMATION FOR SEQ ID NO: 4385:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4385:

AAAGGTGAAA AGCACCCCGG AAGGnAGGTG AAATAGAACC TGAAACCGTG TGCTTACAAG 60  
 TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTTGTG GAATGAACCG GCGAGTTACG 120  
 50 ATTTGATGCA AGGTAAAGCA GTAAATGTGG AGCCGTAGCA nAACAGGTCT GAATAGGGCG 180  
 TTTAGTATTT GGTCGTAGCC GAnAACAGG TGATCTACCC TTGGTCAGGT TGAATTCAGT 240  
 AACACTGAAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA ACTGAAGGTA 300

## (2) INFORMATION FOR SEQ ID NO: 4386:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4386:

TAGAATCTTC ATCAATATGA TCTAACCAAT ATTGATAAAA CCTTGATGTG TTTCGTGTCA 60  
 ATGACATACC ATATCGACTA GGTACCTTTT TAGAATGTTG ATTAATCAnG GCAAATATCA 120  
 TGGCAAGGTC ATCTTCAAAA TGATTCGATT CAAGTGGAAG GCATATGACG TCTCATCACT 180  
 ATACCCTTTT TCCCATTCTG CAAATCCACC ATAAATACTA CGCGACGCGG AACCCGGACC 240  
 CATTCGCGGC AATCTCGGTn AATCCTTATC TGGACAGCTG GCATGTCTAG CGGCTGGATT 300  
 TACAAGCTGG CTGGCTAAAG CTGGCATATG CGCTTGCCGG TTGAAGCCCA ACCTGGCTGG 360  
 CTGGTGGGGn ACAAATTGGT CGCTTTTCAA TTTcNGGCAT 400

## (2) INFORMATION FOR SEQ ID NO: 4387:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4387:

TCAATTTATG GGGCATTATG ACTTTATATA CCTAAAATAC TATTAAGAAG TCCTGAAAAA 60  
 TTCACATTAG CAGTTGGATT GTTCAACTTT ATTAATGATA AGTATGCAA TAATTTCA 120  
 GTGTTTGCA GAGGGGCAAT TATGATTGCA GTACCTATAG CAATCGTATT CTTGTTCTTG 180  
 CAACGCTATT TAGTATCAGG TTTAACAACA GGTGCGACAA AAGGTTAGTT TGAAATTcNc 240  
 GnGTGGGGCA GAATTGATAA AGAACCACnA ATGACGATAA AGATTAAAAG GAGGACGTTA 300  
 TGGATGACGA 310

## (2) INFORMATION FOR SEQ ID NO: 4388:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4388:

AACATCATGC TGATGTTGTT GAATATGAAG AAGATACAAA CCCAGGTGGT GGTGAGGTTA 60  
 C TACTGAGTC TAACCTAGTT GAATTTGACG AGATTCTACA AAAGGTATTG TAACTGGTGC 120  
 TGTTAGCGAT nCATACAACA ATTGAAGATA CGAAAGAATA TACGACTGAA GTAATCTGAT 180  
 TGAAGTAGTA GATGAAGTAC CTGAGGAACA TGGTCAAGCG CAAGGACCCA TTCGAGGAAA 240  
 T TACTGGAAA ACATCATCAT ATTTCTCATC nGGTTTAGGn ACTGAAATGG TCACGGTAAT 300  
 TTTGGCGTGG 310

## (2) INFORMATION FOR SEQ ID NO: 4389:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4389:

TTTACCATAT CATCCACTAT TTATTAAACC TAATAAGAT GAATTAGAAG TGATGTTTAA 60  
 TACAACAGTG AACTCAGACA CAGATGTTAT TAAATATGGT CGTTTGTTAG TTGATAAAGG 120  
 T GCGCAATCT GTTATTGTCT CGCTGGCnG TGGATGGTGC TATTTATATT GATAAnGAAA 180  
 TCAGTATTAA AGCAGTTAAT CCACAAGGGA AAGTGGTTAA TACAGTTGGC TCTGGTGATA 240  
 GTACAGTTGC AGGCATGGTG GCTGGGAATT GCTTCAGTT TAACGnTTGA AAAGGCATTG 300  
 CA 302

## (2) INFORMATION FOR SEQ ID NO: 4390:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4390:

AAAGAGTGCG TAATAGCTCA CTAGTCGAGT GACACTGCCG CGAAAATGTA CCGGGGCTAA 60  
 ACATATTACC GAAGCTGTGG ATTGTCCTTT GGACAAATGGT AGGAGAGCGT TCTAAGGGCG 120  
 TTGAAGCATG ATCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG 180  
 CGAAAGACGG GTGAGAATCC CGTCCACCGA TTGACTAAGG TTTCCAGAGG AAGGCTCGTC 240

TnCCCTTACCA CCTATAATCG nTTAATCGTG GGG

333

## (2) INFORMATION FOR SEQ ID NO: 4391:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4391:

AGTGCGTTTG TGCACAnACT TGA CTGnAAC TTAGTGCCAT TGCAGCACCA GCAACCCATG	60
GCGCAATAAG CCCAATGCAG CTATAGGGAT ACCGnCAATA TTATAGCCGA ATGCCCAAAA	120
TAGATTTTGA CGAATATTAC GAATGGTTGC TTTACTTGCA TAAATGGCTT TAGGAATAAG	180
CATCAAGTCG CCACCAAGAA TAGTAATATC AGCTGCTTCA ATGGCAACTT CTGTACCTGT	240
ACCAATGGCG ATACCGATAT CAGCTTTAAC TAATGCAGGT GCATCATTTA CACCGTCACC	300
AACCAT	306

## (2) INFORMATION FOR SEQ ID NO: 4392:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4392:

TACGGTATGC ATATCTTTTA AAACCTATTC TTTTGTTATT AGGACATATA AATTCATCAT	60
TAAGTTCGTC ATATTTCCAA TTTTAAGTGT TGAAAATGTC ACTTTTAAAC TTTCTAGTTT	120
TATCTTTAAT AAACATGCCA TACGTAATAA GTGGCGTTTT ATTAAATCA TCTATAATAG	180
CCATATAGTT TTGCTCACTA CCATAACCTG CATCAGCTAC AATATACTCC GGTAAATAAC	240
CGAAGGGATT TTGAATCATT GTTAAAAATG GAATTAAAGT TCTAGTATCT GTTGGGTTTT	300
GAATAGGGTC ATGGGATAAA CCAAATGnGG AATTTGCCnC AATTnGTAAA TGGAA	355

## (2) INFORMATION FOR SEQ ID NO: 4393:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 364 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4393:

5 CATTCCGTAA TAAATTACG TGGTTACAAA TTATTCAGG TTTCTTCTTT GCATTTGGTG 60  
 CTTAACATA TCTTATTCA GCACAACCTA ATATGAATGG TTTAGCAACT GGATTTATTC 120  
 TTTCTCAAAC ATCCGTTGTG CTTGCTACAT TAACTGGTAT TTATTTCTTA AAACAACATA 180  
 10 AAACGTCAAA AGAAATGGTT ATTACAATCA TCGGCTTAGT ACTCATTTTA GTAGCCGCTT 240  
 CTGTTACAGT ATTTATAAAA TAAGGAGTGT AGATGTCATG AAAAAATCAG CGGTTTAAAT 300  
 GGAACCTATT CCAAAGCCAT CGCGACCAAT GGGTCATTG GATTANTAAC GATAATGGCG 360  
 15 nngg 364

## (2) INFORMATION FOR SEQ ID NO: 4394:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4394:

25 GATTAAAACG ATTATAGGTG GTACAGGAAT ATCAACCTGT TATCCATCGC CTACGCCTGT 60  
 CGGCCTCAGC TTAGGACCCG ACTAACCCAG GAnCGGACGA GCCTTCCTCT GGAAACCTTA 120  
 30 GTCAATCGGT GGACGGGATT CTCACCCGTC TTTCGCTACT CACACCGGCA TTCTCACTTC 180  
 TAAGCGCTCC ACATGTCCTT ACGATCATGC TTCAACGCCC TTAGAAGCT CTCCTAnCAT 240  
 35 TGTGCCAAAG GACATGCCAC AGCTTCGGTG AATATGTTTA GCCCCGGTAC ATTTTCGGCG 300  
 CATGTrCACT CGACT 315

## (2) INFORMATION FOR SEQ ID NO: 4395:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4395:

50 AGCCCCAAA TGGGTATTGA AATTGAATGG TGGGnCCtGA AnTGGACTCG AACCACCGAC 60  
 CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT AGGCCCATTA ATTTGAATGA 120  
 ACAAACATTC AAAACTGAAT ACAATATGTC ACGTTATTCC GCATCTTCTG AAGAAGATGT 180

TACGACTTCA CCCCAATCAT TTGTCCCACC TTCGACGGCT AGCTCCTAAA AGGTTACTCC 300  
 ACCGGCTTCG GGTGTTACAA AC 322

(2) INFORMATION FOR SEQ ID NO: 4396:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 303 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4396:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 60  
 AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTTG TGTTTACTTT TTATTTTGAC 120  
 GTTTTAGACA TAAAAAAGA nACCTCACGG TCCAAACTTG CCTGGCAACG TTCTACTCTA 180  
 GCGGAAnTGA ATTGGCTACC ATCGnCGCTA AAGACCTTTC TTGACTTGTG ACAATCGCTT 240  
 GCTTCTTTCC TCTCCTTCGG CTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT 300  
 CTT 303

(2) INFORMATION FOR SEQ ID NO: 4397:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4397:

TAAGAATATA AATGATTTTG AAAGCATTTG AAAGCTACAA CATTCTATA AAATTTTCA 60  
 ATAACAATTG CGCCACTAAA ACTCAAAATT TCCACCACCA ACATCCAAAT TATCAACATC 120  
 GCAACATAAC CAAATGTTAT AATAAATCTA TTACACAAAG AGATAAATTA CTTATGCAAA 180  
 GGCGGAGGAA TCACATGTCT ATTACTGAAA AACAACGTCA GCAACAAGCT GAATTACATA 240  
 AAAAATTATG GTCGATTGCG AATGATTTAA GAGGGACATG GATGCGAGTG AATCCGTAA 300  
 TTACATTTTA GGCTTGATTT TCCTATCGCn TCCTTATCTG GAAAAAnCCG ACCAGGATnT 360  
 GCAGATGCCT GGCCAGG 377

(2) INFORMATION FOR SEQ ID NO: 4398:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 313 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4398:

	TGCAATAACA GTATCTATGC CTACTTGTTT TGCAATGGCT TGAGCAGTGT TTTTATTATC	60
10	GCCAGTTAAC ATGGGCAACT TCAATGCCCA TATCATGGCA ATTGTTTTAT AGCATCTTTG	120
	GGCATGATnT TTGACAGTAT CTGCCACTGC GATGATACCA GTTAATGAAT AATTACAGC	180
	AATGAGCATA nCAGTTTTAC CATCTCGTTC ATAATGTGTT AAATCATCAG AAATATGCTT	240
15	AAGCAACTAA TATCATTGTC AACCATTAAAT TTACCGTTAC CAACCAATAT ATGGTGATGA	300
	TChATCCTTC CTC	313

(2) INFORMATION FOR SEQ ID NO: 4399:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4399:

30	TGGCTATGAT CATCCAAAT ATGGTGAATC AATTGCTGCA GCCATTATAC TTCGCGAAGA	60
	TGAACCTCAT TACGCTGAAA TTTTAAATCA ACATATGCGA AGTCGTTTAG CAGGTTATAA	120
	AGTCCCAAGA ATGTATGTAC CAGTGACACA TATGCCGTTA AACAGTACGC AGAAACCAGA	180
35	TAAACTTGCG ATTCGACAAA TGATGAATGA CAAAGTCTCG CAAACACTTT AAAGGTGATA	240
	AAAATTTTTG ACATTTAGTG TAAGCGTTTA CAAATAAAGC GTGTTGTTTT TGAATTAAAT	300
	GCATTTCACT TTAGTATTCA TATTATnTTT AGGAGGAATT TATATGACAT TTGAAAAAGA	360
40	ACGGGCTTAA AACATTATTC CTGAGATGTA CTAGTATGCT	400

(2) INFORMATION FOR SEQ ID NO: 4400:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 409 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4400:

	CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGT TTCGTCAGAT TCAAACGTTT	60
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55

AAAAGAGACC TCgtCTCAAC TTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAAGTTGGC 180  
TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT 240  
5 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC 300  
ArATTCAAAC GtTTTcAcTT CGGCCAAGGC ATTTTTCTTT GTGGTTACTT TTTAATTGG 360  
10 ACGGTTTTAG GCATAAAAAA AAAGGGGACC CTGCGGGCTC nAAAGGGG 409

## (2) INFORMATION FOR SEQ ID NO: 4401:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4401:

TCATGTAGAC TTCAAGAAT CGACACATGA AAATTCAAAA CATCATGCTG ATGTTGTTGA 60  
ATATGAAGAA GATACAAACC CAGGTGGTGG TCAGGTTACT ACTGAGTCTA ACCTAGTTGA 120  
25 ATTTGACGAA GATTCTACAA AAGGTATTGT AACTGGTGCT GTTAGCGATC ATACAACAAT 180  
TGAAGATACG AAAGAATATA CGACTGACAT nnATCTGATT GAACTAGTAG ATGAACTACC 240  
30 TGGAAGAACA TGGTCCAAGC GCAAGGnCCA ATCCGAGGAA ATTGACTGGA AAACAATCCA 300  
TCCATATTTTC C 311

## (2) INFORMATION FOR SEQ ID NO: 4402:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4402:

TTAACGGATT ATTTGGCAAT TCGGTTAGTT GTCGAACAAT TGCTAGTTGG TGATGAGTTT 60  
45 AAGTCAGTCG CTAAAGATTG TGAAAGTAGA TCGGAAAATT GGTTTAAGCA AACTGTTGCA 120  
TCATGGTGTT ACTACAGTGA TATGCCTAGC GATGTATTAC TACAACATGG ACGTCAATGT 180  
AAATTnCAAA CGTTTATTCA TTTTGGCAGC AACTATGGAA TAAAAATGTA TTTAAAAATT 240  
50 TATGGCTAAT TGCCTGGGGA AATGACATAC GAATCTCAGG TTAAAACAGA AAATTAAAGC 300  
AGGTCCATGT nAAGTGTTGG CGGGnCGCAT 330

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4403:

TGnTCACACA TAATTTGCGG CCATATGTTG TTGGCACTGG CCGTTTGGAT TATCTGGCAC 60  
 TTTGGGCCCA TATGTTGnCA AAATACGCGC CAATTGCTTC TTTATAAGTT GTTATTTTTT 120  
 TACTTTTTCC ATCGATAAGC CATACCTCTG GATGATACAT ATGATGCCCC ATCGCAGACC 180  
 AATAGCGAAA TTCACCCGTT AAAGTTTCGA GCTCTGATAA TTGTATAGAC CATTGATGAT 240  
 TTTGAGGTGG TACTTGATAT AAATTTTCTT CTCTAAAATA TTCATTTAAA ATGCGTTCGA 300  
 TAGCCGCATA CGCTGCCATG TTGTATTAAT CnTTAATTG 340

## (2) INFORMATION FOR SEQ ID NO: 4404:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4404:

TTAACATATA TTTTGGGACC TTAGCTGGTG GTCTGGGCTG TTTCCCTnA CGAACACGGA 60  
 CCTTATCACC CATGTTCTGA CTCCAAGTT AAATTAATTG GCATTGGAG TTTGTCTGAA 120  
 TTCGGTAACC CGAGAGGGGC CCTCGTGCC AACAGTGCT CTACCTCCA TAATCATCAC 180  
 TTGAGGCTAG CCTGAAAGC TATTTCGGGA GAGAACCAGC TGATTCCAG GTTCGATTGG 240  
 AATTTCTCCG CTACCCTCAG TTCATCCGCT CACTTTTCCA ACGTnAATCG GTTCGGTGCC 300  
 TGCCATT 307

## (2) INFORMATION FOR SEQ ID NO: 4405:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4405:

AnACTTGAGT GCAGAAGAGG AAAGTGGAAAT TCCATGTGTA GCGGTGAAAT GCGCAGAGAT 120  
 ATGGAGGAAC ACCAGTGGGC GAAGGCGACT TTCTGGTCTG TAACTGACGC TGATGTGCGA 180  
 AACGTGnGGG ATCAAACAGG ATTAGATACC CTGGTAGTCC ACGCCGTAAA CGATGAGTGC 240  
 TAAGTGTTAG GGGGTTTCCG CCCCTTGAGT GCTGnCAGCT AAACGCATTA AGCACTCCGC 300  
 CTGGGGGAGT GACGGACCGC AAG 323

(2) INFORMATION FOR SEQ ID NO: 4406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4406:

AATTATGGGA TGCAATGGGA TACGAACGTG TTAAACACG TATGGAAGAC GAACTTGGAG 60  
 ACTTACCACA ATGGATTAGT GATTTAGATG GTGGCTTTTA TAAACAAGAT GAGACCATTG 120  
 AATATGCAAC ACCTATTTCT CACTTCGTAA AAGATGAACT TTGGGATAAA GGTGATGCCA 180  
 AACTTTCCGT AACTCATGAT GATCAACTGT TACTGAAATT ACAAAGTAAA AATAATGTCA 240  
 TTACCGATGA ATTCAACGGT GCGTTAGTTG ATGCGATTGA TTTACTGGGA AATGACCCTT 300  
 ACnCnAGnAT GGGTA 315

(2) INFORMATION FOR SEQ ID NO: 4407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4407:

CACCACCTCC CTACCTACTC GCCCCCATC ATAAAATAGG TGGACAGGAA TATCAACCTG 60  
 TTATCCATCG CCTACCTGT CGCCTCAGCT TAGGACCCGA CTAACCCAGA GCGGACGAGC 120  
 CTCCTCTGG AAACCTTAnT CAATCGGTGG ACGGGATTCT CACCCGTCTT TCGCTACTCA 180  
 CACCGGCATT CTCATTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT 240  
 AGAACGCTCT CCTACCATTG TCCAAAGGAA TnCACAGCT TCGGTAATAT GTTTAGCCCC 300  
 GGTACATTTT CGGCGCATGT CACTCGACTA nTG 333

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 393 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4408:

ATTTAATGAA GTGCTTGTTA ATGAACCAAG CGCTAAAGAT ACTGTTGAAA TTTTAAAAGG 60  
 TATTCGCGAA AAATTCTGAAG AACACCATCA AGTAAAATTA CCAGATGACG TATTAAAAGC 120  
 ATGTGTTGAC TTATCAATTC AATATATTCC ACAACGATTA TTACCAGATA AAGCAATCGA 180  
 TGTGTTAGAT ATTACAGCAG CACATTTATC TGCGCAAAGT CCCAGCTGTC GATAAAGGTT 240  
 GAAACTGAAA AACGGATTTC TGGATTnGA AAATGATAAA CGTAAAGCAG TAAGTGCTTG 300  
 AAGGGATTTT AAAAAAGCTG ACGGACCATT CCAAAATTGG AATCCAAATC nnTTACCAGG 360  
 TTAAATTGG GAAAATGGTT AATTGGTGGG ACC 393

## (2) INFORMATION FOR SEQ ID NO: 4409:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4409:

GACTTGAGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTAGCTC 60  
 TACTAAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA 120  
 GCCATTTTTT TTTGTGTTTA CTTTTTATTT TGACGTTTTT GGCATAAAAA AAAGAGACCT 180  
 TGCAGTCTCA ATGCGGCTCA TCGCATCCAT TTTTTCCTG GCAACGTTCT ACTCTAGCGG 240  
 AAGTnAATTG GGCTACCATC GTCGCTAAAG ACCTTCTTGG ACTGTGGAC AATCGCTTGG 300  
 CnTCTnTCCT CTCCTTCGG 319

## (2) INFORMATION FOR SEQ ID NO: 4410:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AATTAAACAT TTCATTTTAA TCAATGAGAC TAAnATACGC CTAAC TTCGT TAACTTTTAA 60  
 AATGTATTAA AATTCTAAAG TTTCTTTTGC TTTTTCnATG ATGTCATTTT TGTTTGGTAA 120  
 5 CCAAACATTT TCAGCTTGAG TGAATGGATA AATTGTATCT GCCTGCCTGA ACTCTTCCAA 180  
 TAGGTGCTTC TAATGAAAGG ATTGCACGTC ACTTAATTCA GCTAACAACT GCTGCACCAA 240  
 CACCAGCTTG CnGTTGTGCT TCTTGACTAC AAACTGACGA CCAGTTTTTC AACTGAGCAC 300  
 10 AATTGTGCAC ATCGATTGGT GACAG 325

## (2) INFORMATION FOR SEQ ID NO: 4411:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4411:

GAGTTGGACA ATGCCGAAGC GTGAGCAAAG TTTTACCAT GCATGGTTGC ATTTAGCGCA 60  
 25 ACATGACCAT AGTTTTACTA AAGCACAGCG CCAAGTGATT AAAGGCTTAC CCAATGATCC 120  
 TGAAATGACG ATAGAGTCAG TATTAACTCA TTTTCAATA GATCAGGAAG ACTAnCAAGC 180  
 TTATGTTGAA GGACATCTTT TGGCGTTACC GGGTTnGGCA nGTATGTTGT ATTACCGTTC 240  
 30 ACCACAGCAT CACTTTGAAC CACCTTTGTT AACGGGTTAA TTGGCCATTC GGGTAAGTTG 300  
 TCCGACCATT GCCAAGTGGG TGATGAGTtn AGGCCAGTCC GCAAAAGATT GGGAAAGTAG 360  
 TCCGGAAAAT GGGTTAAGCC AACCTGTTGC CATCCAGGGG 400

## (2) INFORMATION FOR SEQ ID NO: 4412:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4412:

GATATATGGC AGCTCAAAGG AATGGGTTTC AGTTGAAGTG AAATTATCAC AGTCACTAGA 60  
 CCCGAGCACA TTATTTTCATC TCACTGACAA TGAGGCAGGA GATCGCTTTT ATATGCGTTT 120  
 50 GAATGATAAT CGAACGTCAT ATTTTGCTA CAAAGCAATT CAATTATTCA AAAATAATTC 180  
 TAAAAATAAA CAATCTATTT TAAAAGACTG GGGAAAATTA AACATAACCA TCACCATTTA 240

CCATAAATCA GATGATGAAT GGCGnGAGTT TGGCCTAAAn CATTGGAAT ACCCGGAGTT 360  
TTAATTCCA 369

5 (2) INFORMATION FOR SEQ ID NO: 4413:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 315 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4413:

TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT 60  
TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTGTTG CGCTCTTTTC TCGTTTCGTC 120  
20 AGATTCAAAC GTTTTCACCT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC 180  
GTTTtagaca TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG TTCnACTCTA 240  
GCGGAAGTAA GTGGGCTACC ATCGTCGCTA AAGACCTTTC TTGGACTTGT GGACAAnCGC 300  
25 TTGCGTCCTT nCCTC 315

(2) INFORMATION FOR SEQ ID NO: 4414:

- (i) SEQUENCE CHARACTERISTICS:  
30 (A) LENGTH: 309 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4414:

GACCATCTCC TAAGGCTAAA TACTCTCTAG TGACCGATAG TGAACCAGTA CCGTGAGGAA 60  
AGGTGAAAAG CACCCCGGAA GGAGGTGAAA TAGAACCTGC AAACCGTGTG CTTACAAGTA 120  
40 GTCAGAGCCC GTTAATGGGT GATGGCGTGC CTTTGTAGA ATGAACCGGC GAGTTACGAT 180  
TTGATGCAAG GTTAAGCAGT AAATGTGGAG CCGTAGCAGA ACAGGGTCTG GAATAGGGCG 240  
45 TTTAGTATTT GGTcGTAnCC GnAAACCAGG TGATCTACCC TTGGTCCAGT TGAAGTTCAG 300  
GTTnACACT 309

(2) INFORMATION FOR SEQ ID NO: 4415:

- 50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 300 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4415:

5 TTTATTATAC TTTACATTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA 60  
 TCTTTCTTTG TGTTCGCTTT TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTTGCGGT 120  
 CTCAAATGCG GTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAANTa 180  
 10 AGTTCGGACT ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG 240  
 TGACCTCCTT GGCTATAGTC ACCAGnACAT ATGAATGTGA AATTTATACA TTCAAAACTn 300

## (2) INFORMATION FOR SEQ ID NO: 4416:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 286 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4416:

25 AGAAAAATAA GCGAACTGna ATAAATAAAG ATTCAATTAA CGCATCAGTA TTAGGATTCA 60  
 CTCTAAAACG ATTAATAGTT TTATAAGAAG GTGTTTGATC TTGAGCTAAC CACATCATTC 120  
 GAATACTGTC ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT TGAGTATATG 180  
 30 CATATAAGAT GATTTTAAAC ATCATCTTTG GATGATAGGA TGTTCGCCCA CGATGATGTC 240  
 TGAATTCATC GAATTTGCTA TCAGGTATCG TTTCAACAAT TTCATT 286

## (2) INFORMATION FOR SEQ ID NO: 4417:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4417:

45 TTTGATAAAA ATGGGCCATC GTCACGAGCT TCAACAATTC GTTTCGCAAC GTTTTCGCCA 60  
 AGCCCAGCCT GATATATTAC ATGAGGAGCG GTGCAAATGT TGTTAGAAAT TAAAGATTTA 120  
 GTGTATAAAG CGAGCGATAG AATCATACTA GATCATATCA GTCTAAAAGT AGATAAAGGC 180  
 50 GAGAGTATTG CCATTATAGG TCCATCAGGT AGTGGTAAAA GTACATTTCa AAAGCAAATA 240  
 TGTAAATTTGT TTAGTCCAAC TAGTGGAGAA CTTTATTTTA AAGGTAAACC CTATAATGAT 300

55

GTTTGGTGGA ACGnATTGGA nGATAACCAT GGATAATTCC

400

## (2) INFORMATION FOR SEQ ID NO: 4418:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4418:

GTATTTACAA TCAAATAAG CAAAAGTATT CAGATGCCTC AGATAAAGCT TGGGCGCATT 60  
 CAAAATCTAT TTGGAGAGGC ACATCAAAAT GGTTTAGCAA CGCATATAAA AGTGCAAAGG 120  
 GTTGGCTAAT AGATATGGCT AATAAATCGC GCTCGAAATG GGATAATATT TCTAGTACAG 180  
 CATGGTCGAA TGCAAAATCC GTTTGGnAAA GGAnCATCGA AATGGTTTAG TAACTCATAC 240  
 AAATCTTTAA AAGGTTGGAC TGGGATATG TATTCAAGAG CCCACG 286

## (2) INFORMATION FOR SEQ ID NO: 4419:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4419:

CTCACTTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT AGAACGCTCT 60  
 CCTACCATTG TCCAAAGGnA TGCnCACAGC TTCGGTAATA TGTTTAGCCC CGGTACATTT 120  
 TCGGCGCATG TCACTCGACT AGTGAGCTAT TACGCACTCT TTAAATGATG GCTGCTTCTA 180  
 AGCCAACATC CTAGTTGTCT GGGCAACGCC ACATCCTTnT CCACTTAACA TATATTTTGG 240  
 GACCTTAGCT GGGTGGTCTG GGCTGTTTCC CTTTCGAACA CGGACCTTGA TCACCCCATG 300

## (2) INFORMATION FOR SEQ ID NO: 4420:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4420:

GGTGAGCGGA GCGAACTCnC GTTAAGGAAC TCGGCAAAAT GACCCCGTAA CTTCGGGAGA 120  
 AGGGGTGCTC TTTAGGTTAA CGCCCAGAAG AGCCGCAGTG AATAGGCCCA AGCGACTGTT 180  
 5 TATCAAAAAC ACAGGTCTCT GCTAAACCGT AAGTGATGTA TAGGGGCTGA CGCCTGCCCC 240  
 GTGCTGGAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAACT ACGAATCGAA GCCCCAGTAA 300  
 ACGGcGGCCG TAACTATAAC GGTCTAGACG ATCTGC 336

10 (2) INFORMATION FOR SEQ ID NO: 4421:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 297 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4421:

GGnCACCTC GTGCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG GCTAGCCCTA 60  
 AAGCTATTTT GGAGAGAACC AGCTATCTCC AGGTTTCGATT GGAATTTCTC CGCTACCCCTC 120  
 25 AGTTCATCCG CTCACTTTTC AACGTAATCG GTTCGGTCTC CCATTTCAGTG TTACCTGAAC 180  
 TTCAACCTGA CCAAGGTAGA TCACCTGGTT TCGGGTCTAC GACAAATACT AAACGCCCTA 240  
 TTCGACTCG CTTTCGCTAC GGCTCCACAT TTAGTGCTTA ACCTTGCATC AAATCGT 297

30 (2) INFORMATION FOR SEQ ID NO: 4422:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 35 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4422:

GTACATCGTC TAATAATAAG TTGACGATAT CTGCAATGC ATCTTTATCT AAATGTAAGA 60  
 ATTCAACGAT GCCGTTGAAG CGGTAAAGGA ATTCAGGGCG GAAGAATTTT TTCATTTTCGT 120  
 45 GCATAATATC TTTTCTTCA GCGTCATTGC CATTGCCAAA GCCAGCATTG GATGTACAAA 180  
 TAATAATTGT ATTTTAAAG TTGATGACAT TACCTTGACC ATCAGTCAAA TTACCATCAT 240  
 50 CCATTACTTG TAATAACAAT GTTAAATTG TGGATTGCTT TTCGATTCAa CAATAGAATG 300  
 ACTGAGAnGG GATACGGCGA CTTTTCAGTA AACGGATTGA ATGGCATCAT AnCCACATAC 360  
 CAGCGTGGAC CATCATTTTG GAACAGCGTG GGCACATATC 400

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4423:

AAGTTGAGTC GCATAGCTAG TATGAAACGT GGTGTGCGCA TGGGAACAT CAAGCTTTGA 60  
 AGATGTGGTA CTACATGCGT TGAATTAGGG ATCGGTACTT TATATGAAGA CGTGCTGCTT 120  
 CCATTAAATG AGTGATGCGA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT 180  
 AAAATTGCCT ATAAATTTTT AGCACATAAA ATAAGAnGnG CCAACCATTG TTAGACTATA 240  
 ACAACGGTTG GCTCTTTAAT TGTA AAAAGA AAACCATACG CTATGGTAGT T 291

## (2) INFORMATION FOR SEQ ID NO: 4424:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4424:

AACTGCCACC ACCTGGGGnG GTTCCAGAA CCTCTATGCA TTTCAATCAC AGnCAAATGT 60  
 GCGGTTGACG TTCAATGACT ACCTGCAATT CATCGGTCAG CTCACACCCT TTACCTGnCT 120  
 AAAGTACCAG TAGACAATGT AGGTATTGGA CTGTCATGAG CATTTTTATn CAGTAATGGG 180  
 CTTTAGATAT TTTATTAATA CCGGCCAATC ATGCTATTCA AACCGCCAAT AGCTTTATTA 240  
 GCAACATTTT TACCTAAATC AGCCGCAGCT CTTCCCATGT CTTTACCAAT ATCTCTAATC 300  
 CAATCATATG TTTTGCATA GCCATTTTCT AAAACCATTA AATACTGATT TAGCGTTAGA 360  
 CCATGCCGAA CTTGAAATTG CATCAAAACG ATCGTGGGCT 400

## (2) INFORMATION FOR SEQ ID NO: 4425:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4425:

AGATGATAAA AGCAACAGGT GGT TTTGCGA AAAGTGAAGT ATGGCGTCAA ATGATGTCAG 120  
 ATATATTTGA CACAGAGTTA GTGGTTCCTG AAAGTTATGA AAGTTCATGC TTAGGTGCCT 180  
 5 GCGTGCTCGG ACTTAAAGCT GTAGGTGACA TTGAAGATTT TTCAATCGTT TCATCGATGG 240  
 TCGGTGCCAC AAACAATCAT ACGCCGATTG AAGAAAATGC ACTGTTACCA AGANTCGAAT 300  
 10 CCATTnTTAT CATTAAAGCGT CTTAnCAGAG ATATGACAAT 340

## (2) INFORMATION FOR SEQ ID NO: 4426:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4426:

CTGAAGATGA TAAAGATGCA GATGGTGGCG AGTTCACGT AACAAATTACG GATCATGATG 60  
 ATTTCACTACT TGATAACGGA TACTTCGAnG AATTATCATC AGACAGCGAT TCAGACTCAG 120  
 25 ATAGTGACTC AGACAGCGAC TCAGACTCAG ACAGCGACTC AGACTCAGAC AGTGATTACG 180  
 ATTCAGACAG CGACTCAGAT TCAGATAGCG ACTCAGATTC GGACAGCGAT TCAGACTCAG 240  
 30 ATAGCGACTC AGATTACAGAT AGCGATTACG ACTCAGACAG CGACTCAGAT TC 292

## (2) INFORMATION FOR SEQ ID NO: 4427:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4427:

AACAGTGCTC TACCTCCAAT AATCATCACT TGAGGCTAGC CCTAAAGCTA TTTCGGAGAG 60  
 AACCAGCTAT TTCCAGGTTC GATTGGAATT TCTCCGCTAC CCTCAGTTCA TCCGCTCACT 120  
 45 TTTCAACGTA ATCGGTTCCG TCCTCCATTC AGTGTTACCT GAACTTCAAC CTGACCAGGG 180  
 TAGATCACCT GGTTCGGGT CTACGACAAA TACTAAACGG CCCTATTCAG ACTCGGCTTT 240  
 50 CGCTACGGTT CCCACATTTA CTGGCTAAAC CTTGCATCAA AATCGGTAAC TCGnCGGGTC 300  
 ATTCTAn 307

## (2) INFORMATION FOR SEQ ID NO: 4428:

(A) LENGTH: 354 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4428:

10 GACCATACAT CGTCATCGTT TGCACCGTCA AATACTGGTG ATGCAACGTG AATACCAAGA 60  
 TTTTtagcag CCATACCTAA GTGTAGCTCT AATACTTGTC CGATGTTTAT ACGAGATGGT 120  
 ACACCAAGAG GATTTAACAT GGATATCGAT CGGGACGTCC ATCTGGTGAA GTGAAGGCAT 180  
 15 ATCTTCTTCA GGGAACAATC TTGAGGAAAT GGACACCTTT GTTGACCATG TCGGACCACA 240  
 CATGCTTATG CACCAACATG GAATTTTACG TTTTGGAAa GATGATTATT ACACGTnACT 300  
 AATTGGTTTA CACCAGGTGG AnaATGTTAT CGTCGGCCTT GCTTCACGAT TGGA 354

20

(2) INFORMATION FOR SEQ ID NO: 4429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4429:

30

GTGnACTATC nGCTTGCTA TGATAATATT ATTCTTTGTA CTGTGTTAAA AGATATTAGA 60  
 CTAAAACTAA AAACAGCAGT AAGATGATTT ATGATTAAAA CTATCTTACT GCTGTTCACT 120  
 35 TTTTATAATA CTCTGAATG TCTCATTAT ACTTCTAGTC ACAGATTTAA ATAATCAAAA 180  
 GTGCACATTA TTAAATATC AATTTACAC TCAATGCGGC TCATCGCATT CATTTCTTGT 240  
 CTAGCAACGT TCTACTCTAG CGGAACGTAA GTAGCTACCA TCTCGCTAAG GAACTTTCTT 300  
 40 GACCTGGTGA CAACCGCTGC GnCTnTCTCT CTTCGGCTCT CGCTTACTCC ATTTAGCTCC 360  
 ACTAAACTCG TCGCGCCCTT CCCGTTCCGC AGATCCAACG 400

40

(2) INFORMATION FOR SEQ ID NO: 4430:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4430:

55

ACCATTACACA CCTTGACAGC CACATAACAT AACTAAGTTT AAGATnGGGG GATAAATCGT 120  
 ATCTGAGTTA AACCAATGGT TAATACCCGC ACCCATGATA ATCATTGAAC GCCCTTCAGT 180  
 5 ATCGATAGCG TTTTGCACAA ATTCTTTTCGC TACTTGAATG ACAACACTTT GTTTTACGCC 240  
 TGAAATGGCT TCTTGCCAAG CAGGTGTATA TTTTGATTCT GCATCGTCGT AA 292

(2) INFORMATION FOR SEQ ID NO: 4431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4431:

20 TGAGCCGnAC ATCGAGGTGC CAAACCTCCC CGTTCGATGT GAACTCTTGG GGGAGATAAG 60  
 CCTGTTATCC CCGGGGTAGC TTTTATCCGT TGAGCGATGG CCCTTCCATG CGGAACCACC 120  
 GGATCACTAA GTCCGTCTTT CGACCCTGCT CGACTTGTAG GTCTCGCATC AAGCTCCCTT 180  
 25 ATGCCTTTAC ACTCTATGAA TGATTCCAA CCATTCTGAG GGAACCTTGA GCGCCTCCGT 240  
 TACCTTTTAG GAGGCGACCG CCCAGTCAAA CTGCCCGCCT GACA 284

(2) INFORMATION FOR SEQ ID NO: 4432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4432:

40 TATCATTGTG GTACGATAAG GCATATGTTG TACCTATGnA TGGTGAAGA GCCTTCAGTT 60  
 GTCGCTGCAG CTAGTTATGG TGCAAAGCTA GTGAATCAGA CTGGCGGATT TAAAACGGTA 120  
 TCTTCTGAAC GTATTATGAT AGGTCAAATC GTCTTTGATG GCGTTGACGn TACTGGAAAA 180  
 45 TTATCAGCAG ACATTAAAGC TTTAGAAAAG CAAATTCATA AAATTGCGGn TGAGGCATAT 240  
 CCTTCTATTA AGCGCGTGTG GTGGTTACCA CGTATAGCGA TTGATACATT CCTGGCCACC 300  
 50 AGTTCTATCT TT 312

(2) INFORMATION FOR SEQ ID NO: 4433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4433:

CGGTACTCGT TAAGGCTGAG CTGTGATGGG GAGAAGACAT TGAGTCTTCG AGTCGTTGAT 60  
TTCACACTGC CGAGAAAAGC CTCTAGATAG AAAATAGGTG CCCGTACCGC AAACCGACAC 120  
AGGTAGTCAA GATGAGAATT CTAAGGTGAG CGAGCGAACT CTCGTTAAG AACTCGGCAA 180  
AATGACCCCG TAACTTCGGG AAAAAAGGTG CTCTTTAAGG TTAACGCCCA GAAGAGCCGC 240  
AGTGAATAAG CCCAAGCGAC TGTTTTATCC AAAACACAGG TCTCTGCT 288

(2) INFORMATION FOR SEQ ID NO: 4434:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4434:

GGACCGAACC GACTTACGTT GAAAAGTGAG CGGATGAACT GAGGGTAGCG GAGAAATTCC 60  
AATCGAACCT GGAGATAGCT GGTTCCTCTC nAAATAGCTT TAGGGCTAGC CTCAAGTGAT 120  
GATTATTGGA GGTAGAGCAC TGTTTGGACG AGGGGCCCCCT CTCGGGTAC CAATTTTCAGA 180  
CAAACCTCCGA ATGCCAATTA AATTAACTT GGGAATTCAG AACATGGGTG ATnAAGTCCG 240  
TGTTTCGAAA GGAAACAGCC CAGACCACCA GCCAAGTCCC AAAATATATG TTTAATGGGA 300  
AAAGGTGTGG CCTTTGCCCA GGACAACCAA GAAGTT 336

(2) INFORMATION FOR SEQ ID NO: 4435:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4435:

ATTGACGCCG CATTTTTACG GAATGGGAAT AAAGCGACAC AAACCGTCAC GTCnGTGTTG 60  
GTGTCATGAC AAGGTAATGC GAGTGATCTG ATGTATGGCT TATCATGGCA ATCTGTTATG 120  
GnCTGACTGA TCGGACGATG TATCATTCGC CAATTCGTTT ACTTGTCGTT ATTCAAGGCAC 180

55

AATCATTGGC TGC GTTTTAA TGAGCGTAAT GAGGAAGGGG CGTTTAAAAA GTTGGATTTA 300  
ACGA 304

(2) INFORMATION FOR SEQ ID NO: 4436:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 305 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4436:

AAATATACTCC GGTAATAAC CGAAGAGTTT TGAATCATTG TTAAAAATGG AATTAnAGTT 60  
CTAGTATCTG TTGGGTTTTG AAATAGGTCA TAGGATAAAA CAAATnGAGA ATTTGTCGCT 120  
ATTTGTAAAT TGTATCCTGG CTTAAGTTGG CCATTTTTCa TATGGTCTTC CTTCAATTCTC 180  
ATAAAAGTTG CATCATGGAT CAGTTTTAGA AAAGCTATTT CTATCTTTAA GAATCGATTT 240  
TTGTTCTTCA TATTTATTTT TTCTTTGCGA ATAATCATCA AATTTATnTT TGGAACCTTCT 300  
TAATC 305

(2) INFORMATION FOR SEQ ID NO: 4437:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 359 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4437:

ATCGTTTAAA TCAGTTAGTA AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAAATA 60  
TTATAGAAAA CATCAAAGGA TGTTAAGAAA TACAATTTAT TACCCAGCAT TTAATAATGG 120  
TGCTATAGAA GGAATTAATA ATAAGATAAA ATTAATCAAG TGAATTTCTT TTGGTTACAG 180  
AAATTTCAAC AACTTTAAAG CACGTATAAT GATGATTTTC AGCTTGTACA AGGGGGAnAA 240  
AAGGAnGnCA ACCAAGCCCA ATAATGGACT GGCCGCCTAA TATTAAAAAC TCTAAAGGTT 300  
GTATTTTAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGAGGA CCCGTTAAC 359

(2) INFORMATION FOR SEQ ID NO: 4438:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 286 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4438:

5 ACTTACAGTT ATTTTAACTT GGnCAGAATC CATCATCCAT AAGTTCGAAA TGTTGTAAAA 60  
 CATAAACCTT GnAAACGGCA ACATTTTTGG GTCCTTCTCC ATCATTTTAT TTAAAAGCGC 120  
 ATTATGATCA ATATCATGCC CAATTAACCTT TCCAGCAATT TCCATAGTAT GTTCTGAGGT 180  
 10 ATTGTTAAAA AGGAATCGCC CAGTATCACC GACGATACCA AGATATAAAA CGCTCGCGAT 240  
 ATCTTTATTA ACAATTGCTT CATCATTAAA ATGTGAGATT AAATCG 286

## (2) INFORMATION FOR SEQ ID NO: 4439:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4439:

25 TCGCTTGACT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAnCTCT ACTAAACTCG 60  
 TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTCGCCAAG CCATTTTTCT 120  
 TTGTGTTTAC TTTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180  
 30 TGCGGCTCAT CGCATCCATT TTTTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTG 240  
 GCTACCATCG ACGCTAAGAA CCTtTCITTGA CTTGTGACAA aTCGCTTGCT TCTTTCCTCh 300  
 TCTTCGGTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGCTCTTT TCTCGTTTCG 360  
 35 TCAGATTCAA CAGTTTTTCAT TCGCCAAGCC ATTT 394

## (2) INFORMATION FOR SEQ ID NO: 4440:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4440:

45 TAATAGGTTT GAGGTGGAAG CATGGTGACA TTGGCAGCTG ACGAATACTA ATCGATCGAA 60  
 GACTTAATCA AAATAAATGT TTTGCGACAA TGCAACTTTT ACTTACTATC TAGTTTTGAA 120  
 50 TGTATAAATT ACATTCATAT GTCTGGTGAC TATAGCAAGG AGGTCACACC TGTTCCCATG 180

TAGAACGTTG CCAGGCAAAA AATGGATGCG ATGACCGCAT TGAGACCGCA GCnTn

295

## (2) INFORMATION FOR SEQ ID NO: 4441:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 345 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4441:

TTTCATAAAA AGATTTCAAA CGCGTTCATC AAnCCTCGTC GCAGGTCTTT CGAACACTAG 60  
 CGATTATTTT tTATGAATTC AAGCTTATTT AAAACTCTTT ATTCaCTCGG TTTTGCTTGG 120  
 TAAATCTAT ATTTTACTTA CTTATCTAGT TTTCAATGTA CAATTTCTTT TTAGTCAAGC 180  
 GCTCGCATAC TGCTTTATTT TCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT 240  
 TAAATAAACA TTCAAACCTG AATACAATAT GTCACGTTAT TCCgCATCTT CTGAAGAAGA 300  
 TGTTCCGAAT ATATCCTTAG AAAGGAGGTG ATCCnGCCGn ACCTT 345

## (2) INFORMATION FOR SEQ ID NO: 4442:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4442:

AATCATTGTC AAAACTACGT TCTGGTAAAC AAGGACAACC CGTTTGAACC ATTGGCCCCAC 60  
 ACCATTTGAT AGGCAGnCAT GTGCGCAATG GACATCCACA TAGTTGCGTA ATGTTTCATA 120  
 CGTCATTGCT CAAATCATTG ATGACTAGCG CAACATGATT ACCTTGTCGT GnGCACCTTC 180  
 ATTAAAGnAA CTTATGATAG ATTTATTTCC CGGGACATTA AGCATTGCGA TCGTTAACAT 240  
 GCGTATTGCA CCCAATTTAG AAGTTCCTCC GTGCCGTTTG GTATATCACA AATTGTAGT 300  
 GTATCTTGGA TGC 313

## (2) INFORMATION FOR SEQ ID NO: 4443:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4443:

AGCATGGTGT TTCTCAGATT GTCGGATGTA TAAATGTGTA TGTTATGTTT TAATTTTTTCC 60  
 5 CAGTCTTTAA AAATAGATTG TTTATTTTTTA GAATTATTTT TGAATAATTG AATTGCTTTG 120  
 TAGCCAAAAT ATGACGTTTC ATTATCATTC AACGCATAT AAAGCGTATC TnCTGCCTCA 180  
 TTGTCAGTGA GATGAAATAA TGTGCTCGGG GTCTAGTGAC TGTGGATAAT TTCACTTCAA 240  
 10 CTGAAACCCC ATTCCTTTG AGCTGCCCAT ATATCTCTTT GGACAATATC GGTCCCTCTA 300  
 ATACGGnCCG TAGnCCATTC CATTTCAATT CTTTTT 336

## (2) INFORMATION FOR SEQ ID NO: 4444:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4444:

CAGACTGGGA TATTTATAAA ACGTTGGCAA AAGCATTTTC AGAAATGGCA AAAGACTATT 60  
 TACCTGGAAC GTTTAAAGAT GTTGTGACAA CTCCACTTAG TCATGATACA AAGCAAGAAA 120  
 TTTCAACACC ATACGGCGTA GTGAAAGATT GGTGGAAGGG TGAAATTGAA GCGGTACCTG 180  
 30 GACGTACAAT GCCTAACTTT GCAATTGTAG AACGCGACTA CACTAAAATT TACGACAAAT 240  
 ATGTCACGCT TGGGCCTGTA CTTGAAAAA GGGGAAATTT GGAGCACCTG GGGGTAAGTT 300  
 35 TCCGTGTCCA GTTGAACCAT TATGGAGGAn TnAAAAAGT ATGTTAAGGG ACCTGGGAGT 360  
 TGAATACCCA ATGGATnGAT TCCCGTGAAG AGCCGAATCC 400

## (2) INFORMATION FOR SEQ ID NO: 4445:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4445:

TACGCCCCAG ACGGATAGGG ACCGAACTGT CTCACGACGT TCTGAACCCA GCTCGCGTAC 60  
 50 CGCTTGTAAT GGGCGAACAG CnATCGCCTT GGGACCGACT ACAGCCCCAG GATGCGATGA 120  
 GCCGACATCG AGGTGCCAAA CCTCCCCGTC GATGTGAACT CTTGGGGGAG ATAAGCCTGT 180

CACTAAGTCC GTGCTTTTGA CCCTGACTAC GGACTTGThA GGTCTGCGGC ATTCAAGCTT 300  
 CCCTTGATGG CCTTTGACAC TGCTTATGGA ATGnATTG 339

(2) INFORMATION FOR SEQ ID NO: 4446:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 318 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4446:

CAATTTTAAG TGTTGAAAAT GTCACTTTTA AACTTTCTAG TTTTATCTTT AATAAACATG 60  
 CCATnCGTAA TAAGTGGCGT TTTATTAAAA TCATCTATAA TAGCCATATA GTTTTGCTCA 120  
 CTACCATAAC CTGCATCAGC TACAATATAC TCCGGTAAAT AACCGAAGGA TnTTTGGAAT 180  
 CATTGTAAAA AATGGAATTG AAAGTTCTAG TATCTGTTGG GTTTTGAAAT AGGTCATAGG 240  
 ATAAAACAGG GTGAGAAATT GTCGCTATTT GTAAATTGTA TCCTGGCTTA AGTTGGCCAT 300  
 TTTTnCATAG GTCTTCCT 318

(2) INFORMATION FOR SEQ ID NO: 4447:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 279 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4447:

TTTTGAAATT CTCTATGTTG GGGCCCGGAC TATAATTGAA AAATGCTTGT TACAAGTGCA 60  
 TTTTATTTCA GTCAACTACT AACAAATATAA CATTGTGGAG CCCAGAnCTT TGATTAATGT 120  
 ATATGAAAAT CAAAGTAATG CTTATGTATG ATTATTTCAA ATATTTTACA TACATGAACT 180  
 TTTCCAATGT ACGATACTAT TATTATAAAG CGCTCGCTAA GATTTTACGA TGATTAGAGG 240  
 GTAAAAAATG AACGATCAAT GGTnTAACCA TTTAATTGG 279

(2) INFORMATION FOR SEQ ID NO: 4448:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 302 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4448:

GACACCGGCA TTCTCACTTT CTAAGCGCTC CACATGTCCT TACGATCATG CTTCAACGCC 60  
 5 CTTAGAACGC TCTCCTACCA TTGTCCAAAG GACAATCCAC AGCTTCGGTA ATATGTTTAG 120  
 CCCC GGTTACA TTTTCGGCGC AGTGTCACTC GACTAGTGAG CTATTACGCA CTCTTTAAAT 180  
 GATGGCTGCT TCTAAGCCAA CATCCTAGTT GTCTGGGGCA ACGnCACATC CTTTTCCTACT 240  
 10 TAACATATAT TTTGGGACCT TTAGCTGGTG GTCTnGGGCT GTTTTCTGnA TTGAACACGG 300  
 GA 302

## (2) INFORMATION FOR SEQ ID NO: 4449:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4449:

CGTTGGTATA TAGAGGGCAA CCGTCACCTG ATAAATGTG GACACAGTTT TTACAAGAGG 60  
 TTAAGGAAAT GAGTTTGGAG GCATACGAGC ATCAAGAATA CCCATTGAA TGTTTAGTAA 120  
 ATGACTTAGA TCAATCACAT GATGCCTCAC GGAATCCATT ATTTGATGTC ATGTTAGTAC 180  
 30 TACAAAACAA TGAnACGAAA TCATGCTCAT TTTGGGCATA GTAAATTTAA CACACATTCA 240  
 ACCCCAAATC AGTGACGGGC GGAAATTTGG ATTTnTCCTT TTCCATCATT GGAAGAAGGA 300  
 TCGCGGATGA CCTAATAnCA ATCCAATTAT CGGGGTATAA ATACCGGATT TTATAACCA 359

## (2) INFORMATION FOR SEQ ID NO: 4450:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4450:

GATGACAAAA TTTGCTTGAA AACCGAAATG GATGGTCATC ATTGACTGnA TCAAGGTACA 60  
 TCATTCTTTG GTGCTTATGC ATTTAGACAT TATACAAAA CAATACTTTT ATAGGGCAAC 120  
 50 CTTATGGGGT TCTATCGGCT ATACATTACC TGCAACATTA GGTTCACAAT TAGCAGACAA 180  
 AGATCGTCGn TAACTTATTA TTAATTGGTG ATGGCTCATT GCCAACTAAC TGTTCAGCT 240

GCTATACGGT AGAACGACTT ATTCCC

326

(2) INFORMATION FOR SEQ ID NO: 4451:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 381 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4451:

5	AAAAACATCA AAGGATGTTA AGAAATACAA TTTATTACCC AGCATTTAAT AATGGTGCTA	60
15	TAGAAGGAAT TAATAATAAG ATAAAATTAA TCAAGTGAAT TTCTTTTGGT TACAGAAATT	120
	TCAACAACTT TAAAGCACGT ATAATGATGA TTTTCAGCTT GTACAAAGGA GAnAAAAAGA	180
20	AGACAACCAA GCCCAATAAT GGACTGGCCG CCTAATAATA AAAACTCTAA AAGTTGTATT	240
	TTAAAAATAG GTCTTTAAAT TATATACCCC CCCCATTTGG GTGGAGAACC GGTAACCAT	300
	GCCTAGGTGC CTAACCTCCh ATAATGGnAC CCCTCCTTAC CATTTGGGCC ATGGGGCCAA	360
25	TAAAGCGGGG GGCAATTGGG G	381

(2) INFORMATION FOR SEQ ID NO: 4452:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 276 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4452:

35	TTAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG TTATTAATCT TGTGAGTGT	60
40	CTTTCGAACA CTAGCGATTA TTTCTTATGA ATTCAAGCTT ATTTAAACT CTTTATTCAC	120
	TCGGTTTTGC TTGGTAAAT CTATATTTTA CTTACTTATC TAGTTTTCAA TGTACAATTT	180
	CTTTTTAGTC AAGCGCTCGC ATAAGCAATA TCACTTTAAAC CAAAAATAT TTGAATGTTA	240
45	AATAACATT CAAAACTGAA TACAATATGT CACATn	276

(2) INFORMATION FOR SEQ ID NO: 4453:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 341 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4453:

GGCGAAACCG CGTAGCGTTT TTAAAGTCTG ATGTGAAAGC CCACGGTCAA CCGGGAGGGT 60  
 5 CATTGGAAAC TGGAAAACCT GAGTGCAGAA GAGGAAAGTG GAATTCCATG TGTAGCGGTG 120  
 AAATGCGCAG AGATATGGAG GAACACCAGT GAGCGAAGCG ACTTTCTGGT CTGTAAGTGA 180  
 CGCTGATGTG CGAAACGTGG GGGATCAAAC AGGATTAGAT ACCCTGGTGA GTCCACGCCG 240  
 10 TAAACGATGA nTGCTAAATG TTAGGGGGTT TCCGCCCCCT AGTGGCTGCC AGCTAnACGC 300  
 ATTGAAGCAC TGCCGCCTGG GGAGTGACGA CCGCAAnTTG A 341

## (2) INFORMATION FOR SEQ ID NO: 4454:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4454:

ACnCTCCCCA AAGTCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA GTGnCCAAGG 60  
 CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA CCATTTTTAT AAGTCAAACG 120  
 CTCACATACG GCTTCGTTTT CATTATTTTA AATGCTCATT TACATAAGTA AACTCTGCTT 180  
 30 TAAATAATT TAACTCATTG TCTGCTAAAC GTTTTCTTTT ATAAAAAGAT TTAACGCGT 240  
 TATTAATCTT GTGAGTGTTT TTTGGAACAC TAGCGATTAT G 281

## (2) INFORMATION FOR SEQ ID NO: 4455:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4455:

ATGTCCTCAC TTATACTTCT AGTCACAGAT TTAATAATC AAAAGTGCAC ATTATTAAAA 60  
 TATCAATTTC AACTCAATG CGGCTCATCG CATTCAITTC TTGTCTAGCA ACGTTCTACT 120  
 CTAGCGGAAC GTAAGTTAGC TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC 180  
 50 GCTTGCnTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG 240  
 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCnGT 279

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4456:

ATTTTGACGT TTTAGGCATA AAAAAAAGAG ACCTTGCGGT CTCAATGCGG CTCATCGCAT 60  
 CCATTTTTTG CTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT 120  
 AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT 180  
 ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TnTCGTCAGA TTCAAACGTT 240  
 nTCACTTCGC CAAGCCATT TTCTTGTTGTT TACTT 275

## (2) INFORMATION FOR SEQ ID NO: 4457:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4457:

ATCCGATTCA CAAAGCACAT CATCATATAC AAGTCAGTCA ACAAGCCAAA GTGAATCCAC 60  
 ATCGACATCA ACGTCACTAA GCGATTCAAC AAGTATATCT AAAAGTACGA GTCAATCAGG 120  
 TTCGGTAAGC ACATCAGCGT CATTAAAGTGG TTCAGAGAGT GAATCTGATT CACAAAGTAT 180  
 CTCAACAAGT GCAAGTGAGT CAACATCAGA AAGTGCCTCA ACATCACTCA GTGACTCAAC 240  
 AAGTACAAGT AACTCAGGAT CAGCAAGTAC GTCAACATCG CTCAGTAACT CAGCAAGCGC 300  
 AnTGGAAATCC GATTGTGCGT CAACATCTTT AAGTGGATTG AACATCTGCG TCnATGCCAA 360  
 AGnnGTGAAT CCGATTCACA AAGCACATCA GCATCCTTAA 400

## (2) INFORMATION FOR SEQ ID NO: 4458:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4458:

AGTCGCTGTC TGAATCTGAA TCACTGTCTG AATCCGAATC GCTATCTGAT TCTGAGTCGC 120  
 TATCTGAACC TGAGTCGCTG TCTGAGCCTG AGTCACTGTC TGAATCCGAA TCCGGATCCG 180  
 5 GGTCTGGGGn TGTTCCGGT TCTGGGTCTG GGA CTGGATTCTGG CGTTGGTTCT 240  
 GGGTCTGGGG TCTGGACTGG TTCTGGGGTC AAACGGCGGC CCTGGAGTGG GGTCTTTTCGG 300  
 10 AATnAACGGC GGAATCACCA TCAAGCAACT TnCAACAACC ATAACGAAAA A 351

## (2) INFORMATION FOR SEQ ID NO: 4459:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4459:

ATCCTGCAGT TGATCAGTAT GGTGATATTA ATTTAGTTAA TACGAACGCG TCATCTACAA 60  
 GTGAAATCAT TTACGATTTA ATCTCACATT TTAATGATGA AGCAATTGTT AATAAAGATA 120  
 25 TCGCGAGCGT TTTATATCTT GGTATCGTCG GTGATACTGG GCGATTCCTT TTTnACAATA 180  
 CCTCAGAACA TACTATGGAA ATTGCTGGAA AGTTAATTGG GCATGATATT GATCATAATG 240  
 30 CGCTTTTAAA TAAAATGATG GAGAAGGnCC C 271

## (2) INFORMATION FOR SEQ ID NO: 4460:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4460:

ACTGTGGATT AATATTATGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTTCGACTAC 60  
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 120  
 45 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAGATAGT AAGTAAAAGT 180  
 GATTTTGCTT CGCAnAACAT TTATTTTGAT TAAGTCTTCG ATCGATTAGT ATTCGTCAGC 240  
 50 GCCACATGTC ACCATGCTTC CACCTCGAAC CTATnAACCT CAG 283

## (2) INFORMATION FOR SEQ ID NO: 4461:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4461:

CTTCTACAAG TCCTGAATAT ACTTATGAAT CTCTTCTTTC GTGTATGCAA ACTGACGTTG	60
TAATTTAAAT AACGTCTCAT CTTTCCATTG CGAATCTTGA TATTGTATAT TTTCAAAATC	120
AAAGTCAACT TTATGGTTAT CAATCCACGC TTTATATGGT AATTCTCCAG CAATCGCACC	180
TTTTAAATCA TTATTTTCAA TGACTTTATT CTGTTAAAT CAACAACAT AACTTTCnG	240
GATTCAATTG ACCTTTAAAA GCAACATTAC TTCC	274

(2) INFORMATION FOR SEQ ID NO: 4462:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 271 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4462:

GGCTGCTAAA AATCTTGGA TTCACGTTGC ATCACCAGTA TTTGACGGTG CAAACGATGA	60
CGATGTATGG TCAACAATTG AAGAAGCTGG TATGGCTCGT GATGGTAAAA CTGTACTTTA	120
TGATGGACGT ACAGGTGAAC CATTGATAA CCGTATTTCA GTAGGTGTAA TGTACATGTT	180
GAAACTTGCG CACATGGTTG ATGATAAATT ACATGCGCGT TCAACAGGAC CATATTCACT	240
TGnTACACAA CAACCACTTG GCGGTnAAGC G	271

(2) INFORMATION FOR SEQ ID NO: 4463:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 300 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4463:

GCGGCTCATC GCATTCATTT CTGTCTAGC AACGTTCTAC TCTAGCGGAA CGTAATTAGC	60
TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT	120
TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACGCTTG CGCTCTTTTC TCGTTTCGTC	180
AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTAnTTTGAC	240

55

## (2) INFORMATION FOR SEQ ID NO: 4464:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 bas pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4464:

TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCCTAA GGTAGCGAAA 60  
 TTCCTTGTCG GGTAAGTTCC GACCCGCACG AAAGGCGTAA CGATTGGGC ACTGTCTCAA 120  
 CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG GACAGGACGG 180  
 GAAAGACCCC GTGGGAGCTT TTACTGGTTA GCCTGGATAT TGGAAATTCG GGCACACTTG 240  
 GTTACAGGAT AGGTAAGGAG CCTTTTGGAA ACGTTGAGCG CTACTTTAnG TTGGGAGGCG 300  
 CTGGTnGGGA TACTTACCCT AACTGTGTTT GGCTTTTCTn AACCGGCACC ACTTATCCTG 360  
 G 361

## (2) INFORMATION FOR SEQ ID NO: 4465:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4465:

CTGTATGTAC ACCACCAATC GGTTTAGGTT TAGCAACGTT TGTTCAAAAG TATAAATTCA 60  
 ATCATTCCGA AAGAGAAATG GGTAAGGCTT CCTTCACTAT GGGACTATTT GGTATTACTG 120  
 AAGGTGCTAT TCCTTCGCA GCCCAAGATC CATTGCGCAT TATACCTGCA AACATCATTG 180  
 GTGCAATGAT TGCATCAGTC ATTGCAGCCA TTGGTGGTGT CGGCGATAGA GTCGCACATG 240  
 GnGGTCCCAA TCGTGGCTGT ATTAGGTGGG TTTTGT TTTTnTTTT TT 292

## (2) INFORMATION FOR SEQ ID NO: 4466:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GCAAACAAAA CAGTATTAGT AGATTATGAA AAATATGGTA AGTTTTATAA CTTATCTATT 60  
 AAAGGTACAA TTGACCAAAT CGATAAAACA AATAATACGT ATCGTCAGAC AATTTATGTC 120  
 5 AATCCAAGTG GAGATAACGT TATTGCGCCG GTTTTAACAG GTAATTTAAA ACCAAATACG 180  
 GATAGTAATG CATTAAAGA TCAGCAAAAT ACAAGTATTA AAGTATATAA AAGTAGATAA 240  
 TGCCnCTGAT TTATCTGAAA GTTACTTTGT GGAATCCCGG AAACCTTGAG GGTGGCCCCCT 300  
 10 AATAnTGG 308

## (2) INFORMATION FOR SEQ ID NO: 4467:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4467:

AAGCAGGCGC TCTCCAGCT GAGCTAAGCC CCCATAATAA TTACAGTATA TCGGGAAGAC 60  
 25 AGGATTCGAA CCTGnGACCC CTTGGTCCCA AACCAAGTGC TCTACCAAGC TGAGCTACTT 120  
 CCCGTATAAT TAAnGCGCCC GATAGGAGTC GAACCCATAA CCTCTTGATC CGTAGTCAAA 180  
 CGCTCTATCC AATTGAGCTA CGGGCGCATA TGTTTTTATT GAAAATAGTG CCGAGGACCG 240  
 30 GAATCGAACC GGTACGTGAT CACTCACCGC A 271

## (2) INFORMATION FOR SEQ ID NO: 4468:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4468:

TGTGTTAGGT ATTACATCAT CACATTTATC TCGCTCAAAG TCCAGCTGTC GATAAAGTTG 60  
 45 TAAACTGTAA AAACGCAATT TCTGAATTAG AAAATGATAA ACGTAAAGCA GTAAGTGCTG 120  
 AAGAnTATAA AAAAGCTGAC GACATTCAAA ATGAAATCAA ATCATTACAA GATAAATTAG 180  
 AAAATAGTAA TGGTGAACAT ACTGCTGTTG CTACAGTTCA TGATATTTCA GATACTATTC 240  
 50 AACGATTAAC TGGTATTCCA GTTTCTCAAA TnGATGATAA CGnTATTGAA CGTTTAAAAA 300  
 ATATTT 306

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 329 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4469:

10	GGTTTATTAA CAGCATTCTT ATCAGCATTT GTAACGTGTA TTGTTTATAA CTTCTGTGTG	60
	AAGCGCAATA TTACAATTAA AATGCCGAAA GAAGTACCGC CGAATATTTT ACAAGTATTT	120
	AAGGACTTAA TTCCATTTTC AGCGGTAATC ATCATTCTTT ATGCATTAGA TTTAGTCATT	180
15	CGCAACAGCT TTAAATCAAA TGTAGCGGAA GGTATTTTAA AATTATTCGA ACCATTATTT	240
	ACAGCAGCAG ATGGATGGGT TGGTGGTCAC CATTTAACnT TGGGnGCnTT TGCATTAATC	300
20	CTGGGTTTGT AGGGTAATCC ATGGGTCCG	329

(2) INFORMATION FOR SEQ ID NO: 4470:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4470:

30	AACTGGGTGA TAAGGTCCTG TTCGAAAGGA AACAGCCCAG ACCACCAGCT AAGGTCCCAA	60
	AATATATGTT AAGTGGAAAA GGATGTGGCG TTGCCCAGAC AACTAGGATG TTGGCTTAGA	120
35	AGCAGCCATC ATTTAAAGAG TGCCTAATAG CTCACTAGTC GAGTGACACT GCGCCGAAAA	180
	TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTGGACAAT GGTAGGAGAG	240
40	CTTCTAAGGA CTTGAAGCTG ATCGTAAGAC TGTGGAGCGn TAGAATGAGA TGCCGTGTGA	300
	TAGnAAAGAC GGTGAGATCC CTCCACCGTT GACTAAGTTC CAGAGGAAGC TCTCCGTCGG	360
	GTTATCCGGT CCTAAGnGAG GCCGACAGCT AGGCATGGnT	400

(2) INFORMATION FOR SEQ ID NO: 4471:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TCATTTTtag AAATATTATC TTTTCCACAA ATCATTtGAT ATAAAGTGCG ATCATTtGCC 60  
 GCGAGTGCTG CCATTGACAC TAGCTGTTGC GTATCATTtT TGGCTAGCAC TTCGGGATAC 120  
 5 TTTCTTAGCT GAACAGTTAG ATGACCTAAT TGATCTTtGA AAATATCATT ATCTTGACCC 180  
 ATATATGACC ACCAAGCTGT TTCATCACAA ACCATGACAT ACTTAGCTAG TGCTTCATCT 240  
 TTTTCTATAA GCTGACGTAA TAATTGTCTG CTTGTCTCCTCC GTTTtTnCATG TACCGCGAGG 300  
 10 CGTAAnCTTA AAGGGCCCAA GGnCG 325

## (2) INFORMATION FOR SEQ ID NO: 4472:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4472:

CCCGTCTTTC GCTACTCACA CCGGCATTCT CACTTCTAAG CGCTCCACAT GTCCTTACGA 60  
 25 TCATGCTTCA ACGCCCTTAG AACGCTCTCC TACCATTGTC CAAAGGACAA TCCACAGCTT 120  
 CGGTAATATG TTTAGCCCGG TACATTTTCG GGGGCAGTGT CACTCGACTA GTGAGCTATT 180  
 ACGCACTCTT TAAATGATGG GCTGCTTCTA AGnCAACATC CTAGTTGGTC TGGGGCAACG 240  
 30 CCACATCCTT TTTCCACTTT AACAnATATT TTGGGA 276

## (2) INFORMATION FOR SEQ ID NO: 4473:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4473:

AATTTnCCAA AAAATTCAAA TGGCTCATTt ACCAAAAGGT AAACCTCCGC CTTTAAnTTT 60  
 45 CTTaATGCAT kGTCTAACAA cCGCTTTCTT TAAAAGaATA GATTGTCAAG CGCTCGCATA 120  
 AGCAATATCA CTTTAACCAA AAAATATTtG AATGTtAAAT AAACATTCAA AACTGAATAC 180  
 AATATGTCAC GTTATTCCGC ATCTTCTGAA GAAGATGTTT CGAATATATC CTTAGAAAGG 240  
 50 AGGTGATCCA GCCGCACCTT CCGATACGGC TACCTtGTTA CGACTTCACC CCAATnCATt 300  
 TGTCCCACCT TCGACGGGCT AGCTCCGAAA AGG 333

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4474:

TATAAAATAG CAACGTTATT CCAATTATCT TAATGGTTAT CTTATCCTCA ACTAAATTGG 60  
 AGGAATCACT ATGACAATTA ATAAAGTAAC CGTTCCTGGC GCAGGCACAA TGGGCGCTCA 120  
 ACTGGCAGCA CTTTTTGTGA ATGCTGGACT TAAAGTAANA CTATTAGATA TTGTAGTGGA 180  
 CAAAAACGAT CCnAATCTCA TTGCGAAAAA ATCTTACGGT TAAATTACAG GTAAGAAACG 240  
 GCCGCTACTA TTCGnCTTAA ATCTAGCGGT CATTTACCAT ATGGTATTTT GATGTGCTTG 300  
 GTAAATGTGT GCTGTTTGAT ATCGA 325

## (2) INFORMATION FOR SEQ ID NO: 4475:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4475:

TAACTGCGGC AACATTTGCT TGTTTTGGTT ATGGTTGGCA CATTGATGTC GGCATTTCATA 60  
 CAATACATCT AGTATTATCT GGTATTTTTG ATCGTTATCC AAAGTTAAAT AATGATTATT 120  
 GGACATTGGG GTGAGTTTAT CCCATTCTTC TTAGAAACGT ATGGATGAAG CTTATTCGCT 180  
 GACATTTnAC CACCCTGTAA GCTATACTTT AAAAATAATT TTTAATCACA CCGAGTGGCA 240  
 TGTTAACGAG CCACAGTTTG ATTTAGTCAA GAAGnAGAGG TATTGTAGAn TCTTATGCGC 300  
 TGATATCC 308

## (2) INFORMATION FOR SEQ ID NO: 4476:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4476:

CCTACCTATC CTGTACAAGC TGTGCCGAAT TnCAATATCA GGCTACAGTA AAGCTCCACG 120  
 GGGTCTTTCC GTTCCTGTCG CGGGTAACCT GCATCTTCAC AGGTACTATG ATTTACCCGA 180  
 GTCTCTCGTT GAGACAGTGC CCAAATCGTT ACGCCTTTCG TCGGGGTCGG AACTTACnCG 240  
 ACAAGGAATT TCGCTACCTT TAGGACCGTT ATAGTTACGG 280

(2) INFORMATION FOR SEQ ID NO: 4477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4477:

GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG 60  
 CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC 120  
 GTTTTCACCTT CGCCAAGCCA TTTTCTTTTG TGTTTACTTT TTATTTTGAC GTTTTAGACA 180  
 TAAAAAAGA GACCTCACGG nCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA 240  
 ATTGGGCTAC CATCGnCGCT AAAGACCTTT CTTGACTTG 279

(2) INFORMATION FOR SEQ ID NO: 4478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4478:

GAGGATCCCG GAATGTTGAA CCCATCACTG ATTCTGGTTC ATAATTATCC ATCATCCATA 60  
 ACGTTAAATC TAAAGCGTGT GTACCGATAT CGATTAAATGG TCCTCCACCT TGAGCTTCTT 120  
 CGTCTAGAAA GACACCCCAT GTTGGnACTG CTCGACGACG AATGGCATGT GCCTTTCCGA 180  
 AGTAAATGTC TCCTAAGTCG CCACGTTGCG CTGCTTGATG TAAAAATTGA CTATCTGCTC 240  
 GGAaACGATT TTGATAACCT ATTGTTAATT TT 272

(2) INFORMATION FOR SEQ ID NO: 4479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4479:

GAAATTGGGA ATCCAATTTT nCTTTGTTGG GGCCCATCCC CAACTTGCAC ATTATTGTAA 60  
 5 GCTGACTTTT CGTCnCTTAC TGTGTTGGGG CCCTCACCCC AACTCGCATT GCCTGGTAGA 120  
 ATTTCTTTTC GAAATTCTCT GTGTGGGGC CCCTGACTAG AATTGAAAAA AGCTTGTTAC 180  
 10 AAGCGCATT TCGTTTCAGTC AACTACTGCC AATATAACTT CGTAGAGCAT AGAATATTGA 240  
 TTTATGTCCC AGCCTGAGTT AATTT 265

## (2) INFORMATION FOR SEQ ID NO: 4480:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4480:

ACATAGAAAT GCCACTTTTA CAAACAAATG AATATTCGTC TTTTACATC ATTACGCATA 60  
 25 ATAAAAGAAG CTAAGCAACA TGTAACCGT TGTCACCTAA CTTCTTGTTT TTCCGATGAC 120  
 AGCTTCTATT TAGAGAATGT CATGATTATT TTATATTCAC TTCAATGTTA TCAATATTAG 180  
 30 TGCCATCTAT GACGTCTGCC ATACGATGCT CTGGCAGTTT TTTGGTGGTA ATTCAAACGT 240  
 ATATTCCCAC CGTTTTTATT TAATAACGTT GTCCnGGACC CATGTACCGT AAGATATGTT 300  
 TTCATAGTGG TTCCAATTAA ACCAnTCTTC AGGAACCTCn TAG 343

## (2) INFORMATION FOR SEQ ID NO: 4481:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4481:

ACTGCGGCAA TAGCAGCAGC ACCACAAACG GCCTGTGTCC GGACACCTAG GTAATAATGC 60  
 GCATGTTTTT GTCACCATGC CAACAGTTTG TTGACAAAGA GCATCATTAC AATACTGGAA 120  
 50 AATAACGACA CCTACATCGA TGGCTAATAG TTTACTACCT TGACCGATAA TATCGAATAT 180  
 ATTGAGTTTA AGTCCATATA GGATGATTGC AAATCTTAAT AAATATTTAG ATGAAAACGT 240

## (2) INFORMATION FOR SEQ ID NO: 4482:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4482:

GAGGCATCCC CGGGCCTTCC TTCCAACAG TCGCTTCAAA GTTTGGTGGT AAACCTGnTA 60  
 CATCAAATTA TCGGTGCTAC TGnAGGTAC GTGTAATCTT CGCTATTTTA TTAGCCGTAT 120  
 CACATCAAGT GGCTTCCCTA CTGGAACCAA TTTGCTATTC GCCTTATTAT CAGGTGCAGG 180  
 ATGGGGATTC GGACAAATCA TTACATTTAA AGCGTTCGAA TTAGTCGGCT CATCTCGTGG 240  
 CCATGCCAGT CACAACAGCA TTCCAATTAT TAGGCGCATC TTTATGGGG 289

## (2) INFORMATION FOR SEQ ID NO: 4483:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4483:

AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC ATCGCATTCA 60  
 TTTCTTGTCT AGCAACGTTT TACTCTAGCG GAACGTAAGT TAGCTACCAT CCTCGCTAAG 120  
 AACCTTTCTT GACTTGTGAC AATCGCTTGC TTCTTTCTC TCCTTCGGCT CTCGCTTACT 180  
 CATTTAGCTC TACTAAACTC GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTnC 240  
 ACTTCGCCAA GnCATTITTTT TTTG 264

## (2) INFORMATION FOR SEQ ID NO: 4484:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4484:

CTGTACCACC TATAATCGTT TTAATCGATT GGGGGACGCA TAGGATAGGC GAnGTGGCGA 60

TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TCGAGTCGT TGATTTCACA CTGCCGAGAA 180  
 nAAGCCTCTA GATAGAAAAA GGTGCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG 240  
 AATTCTAAGG TGAGCGAGCG A 261

## (2) INFORMATION FOR SEQ ID NO: 4485:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4485:

ATGCAGCTAT TATTTTTGAC AGATTCCATA TCGTTCAACA TTAAATAGA GAACTTAATA 60  
 AGTATCGTGT ACAAGTTATG AATGAATACC GTAATAAAAA AGGACCTGAT TATACAATTT 120  
 TTAAGAATAA CTGGAAAGTC CTATTGATGG ATACTAGTAA AACCATATTT AGTAAATACA 180  
 GATGGANTAA ATCTTTTAAAG GCTTATAAAC GCTCATCTGA CATTGTAGAN GTCATGCTTT 240  
 CAAAAGACGA TATACTACGA C 261

## (2) INFORMATION FOR SEQ ID NO: 4486:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4486:

AGCAACATGA TGCACTTCTC GTGTCTCACC AGATTTAGCG ACTAAACTTG TAGACATACC 60  
 TAAATCTGCT TTAATAAGTA ATTAATGCAC ATGACTTATT GCGAGTAACA TCGGCATTGC 120  
 AAAGCCATTG CTATCAACTA ATCCACTATC ATCTAACACT AGANTTTGAG CGCCTTGCTT 180  
 TACAGCATTG ACTGCTTCTC GGCCTAATGC TTCTAACGCA TCTTCCAAAT CCCCTTCATA 240  
 TACCGTTGAT AAATAAGTTA 260

## (2) INFORMATION FOR SEQ ID NO: 4487:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4487:

5 ATGAGGTGCA TAGGGATAAA ACAGnAGCA GCAATTTGTC GCTATTTGTA AATTGTATCC 60  
 TGGCTTAAGT TGGCCATTTT TCATATGGTC TTCCTTCATT CTCATAAAAG TTGCATCATG 120  
 ATCAGTTTFA GAAAAGCTAT TTCTATCTTT AAGAATCGAT TTTTGTCTT CATATTTATT 180  
 10 TTTCTTTTCG GAATAATCAT CAAATTTATT TTGAACTTC TTAATCTTAG TTCTTTTTTA 240  
 CGGGTCTGTT TTCCAATTTG AGTACTATCC TCGTCCCCA ATAGAATGAA TTAAACCTT 300  
 CCGATTTCTT TTAAnC 316

## (2) INFORMATION FOR SEQ ID NO: 4488:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4488:

25 CACTTTTACT GCTAAAACGT CAATTGTTGA TGAGTCGTGT TTTATCTCAA GATGTGTTAC 60  
 TCAAAAAGTT ATAGAAGAAG CTAATAAAGT TAAAACAGAG ATTGATACTG CCAGAAGATA 120  
 30 ACTGTATCTC TCCATCTACT GTAAGTCCGT ATTAGAACTA AAGCGGCTAA TTCATTACGA 180  
 ATTAAACCCT TTAATTGTTT GCCAGACACA TCGCTATGGA TGAATTTAAA GCGTnAAAAT 240  
 GTACTGGATC ATGAGTTCAT TTTTATAGnT ATGTACnCAT GTGTATAGTA TTTAGAAATA 300  
 35 GACTCAA 307

## (2) INFORMATION FOR SEQ ID NO: 4489:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4489:

TTGGCAAATG TCATATAACT AGTAACATGA TCATCGACAT CAAATTTAGT ATGATCAAAT 60  
 50 GTTCCCCAAT CATTAAATTG ATTCGGTTGT TTGCTCAATT GATTATATGT TTTCTTAGC 120  
 ACTTCATGCG GCACCATATC TTTACCTAGT AGCCCCACAA AGATAAGTCT AACAAAGTGGC 180  
 55 ACCATAATCG ATAAACTACC GCCACCTGCA CGCTTATGGT AAAACACCCA GCCAGCACTT 240

TAGCAGTATG CCACnCCGGn GACGATATGG TAGCGACGTA AnAA

344

## (2) INFORMATION FOR SEQ ID NO: 4490:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4490:

CCCAACCGGC ACATTGTTGT AAGCTGACTA TATGTCACCT CnTGTGTTGG GGCCCCCTGTC 60  
 TTCGACTGGC ACTGCTCCCT CAGGAGTCTC GCCATTATA CTACGTATTA ACATGTAATT 120  
 TTACTTTTAA ATACTTTAAA AAAATAAGAC ACTTTGGTCC AACTTAAGCC AGGGATACAA 180  
 TTTACAAATA GCGACAAATT CTCAATTTGT nTTATCCTAT GGACCTATTT CAAAACCCAA 240  
 CAGGTACTTA GTAACCTTGA ATTCCATTTT TTAACAATGG ATTGCAAAAT GACCTTACGG 300  
 TTCATTTGAC CGG 313

## (2) INFORMATION FOR SEQ ID NO: 4491:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4491:

AGGTC TGACT CTAGAGGATC CCCGATGAGT TTAAAGAAAA ATATCAAACA CCTGAATTAT 60  
 ATTTTAAAGC TTGGCAAGGT TTTTACCACG AGGTTACAA TGAGCCAGAA CGTGATGAAG 120  
 TAATGCGTTA TATTCTGACT TTCTTAAATA ACAGCGTCAA TACAATGGGC TTTATTGTTG 180  
 AAGATGACGA AATTGTAGAA ATTTAATATT CTAAAAAGGT TGGGACATAA ATCCCTAAAA 240  
 AACAGCAGTA AGATAATTTT CCATTAGAAA ATATCTTACT GCTGTGCnCh A 291

## (2) INFORMATION FOR SEQ ID NO: 4492:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GCCGTCTCAG CCTTGGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC CATTAACTACT 60  
 ACGTATTAAC ATGTAATTTT ACTTTGAAAT ACTTAAAAAA ATAAAACACT TTGCCCAACT 120  
 5 TACACTACCA ATAGAACTG CTGTTAGAAT TCCTCAAAT GATATTTTCGC GATATGTTAA 180  
 TGAAATTGTT AAAAAGATAG CTGATAGCGA GATTCGATGG AATTCAGACA TCATCGTGGG 240  
 10 CGCAACATCC TATCATCTAA AAATGATGTT AAAAATCACC TGCATATTGC ATATACTGCA 300  
 ATCTGGAATT TTCTGGGCCG TGAGAATGAG AAAAATnGAC nTCATGAACA GTGATTGCGA 360  
 ATGGATGTGG GTTAAGCTnC AAGATTCAAA CACCTTGCTnT 400

(2) INFORMATION FOR SEQ ID NO: 4493:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 265 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4493:

TGATCCAGAG ATTTCCGAAT GGGGAAACCC AGCATGAGTT ATGTCATGTT ATCGATATGT 60  
 GAATACATAG CATATCAGAA GGCACACCCG GTAGAACTGA AACATCTTAG TACCCGGAGG 120  
 30 AAGAGAAAGA AAATTCGnTT CCCTTAGTAG CGGCGAGCGA AACGGGAAGA GCCCAAACCA 180  
 ACAAGCTTGC TTGTGGGGT TGTAGGACAC TCTATACGGA GTTACAAAGG AnGACATTAG 240  
 ACGAATCATC TGGAAAGGTG AATCA 265

(2) INFORMATION FOR SEQ ID NO: 4494:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 293 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4494:

CATTACTAAA AAAGATAATC AAGGTATGAT TTCACGCGAT GTTTCAGAAT ACATGATTAC 60  
 TAAGGAAGAG ATTTCCCTGA AAGAGCTTGA TTTTAAATTG AGAAAACAAC TTATTGAAAA 120  
 50 ACATAATCTT TACGGTAACA TGGGTTGAGG AACAAATCGTT ATTAAATGA AAAACGGTGG 180  
 GAAATATACG TTTGAATTAC ACAAAAAACT GCAnGAGCAT CGTATGGGCA GACGTCATAG 240  
 ATGGGCCCTA TATTGATACC ATTGGAGGTG AATnTAAATA ACCATGCACT CTC 293

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 256 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4495:

ACTTACAAAG TTCTGTGAAC CAAGTACCAT CAACTGCTGG TATGACGCAA CAAAGTATTG 60  
 ATAACTATAA TCGGAAGAAG CGTGAAGCAG AAAGTAAAT AACTGCAGCT CAACGTGTTA 120  
 TTGACAATGG CGATGCAACT GCACAACAAA TTTCAGATGA AAAACATCGT GTGCGATAAC 180  
 GCATTTAACA GCATTAAAC CAAGCGAAAC ATGANTTTAA CTGCAGATTA CACATGCCTT 240  
 AGGAGCAAGC AGTGCA 256

(2) INFORMATION FOR SEQ ID NO: 4496:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 254 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4496:

GTCAATCAGAA ACCCTGTGCA CACAAGGCTT GTATTTTTTA TACTTATTTT TTAAATTAAA 60  
 TTCATCATT TCTAATTAA AACAAATATAC TAAACGTTTC ATAATTATCG CCTGTACAAT 120  
 ACGCACAAA ACATGTCTTG AAACGCCTTT CATTACTCTA AATACCCAA TATACTTTTT 180  
 ATATCGTTTCG GATTCTGAGT ATTTTCAGACG ATTTTCTGCA TAAAAATAAA CGTGTTTCAA 240  
 GGCAATATAT TGCA 254

(2) INFORMATION FOR SEQ ID NO: 4497:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 269 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4497:

AATCGGCTGT CTGATTCTGA ATCGCTATCT GAGTCCGAAT CGATATCTGA ATCCGAGTCG 60  
 CTATCCGAGT CTGAGTCGCT ATCTGAATCC GAGTCACTGT CGGAGTCGGA ATCACTATCT 120

GAGTCACTGT CGGAATCTGA ATCGCTATCT GAATCCGAAG TCACTGGTCG GGAATCTGAG 240  
TCACTGTnGG AATCTGAATC GCTATCTGA 269

(2) INFORMATION FOR SEQ ID NO: 4498:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 273 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4498:

CACCCCGGCA CTATAAAAT GGAGCAGAAG ACGGGATTCTG AACCCGCGAC CCCAACCTTG 60  
GCAAGGTTGT ATTCTACCGC TGAAGTACTT CTGCATATGC GGGTGAAGGG AGTCGAACCC 120  
CCACGCCGTA AGCTTAGnAT ACCTCAAGTC TAGTGCCTCT GCCAATTCCG CCACACCCGC 180  
AAATGGTGAG CCATAGAGGA TTCGAACCTC TGACCCTCTG ATTAAAAGTC AGATGCTCTA 240  
CCAAGTGAGC TAAATGGCTC TnncAGGTGC CGG 273

(2) INFORMATION FOR SEQ ID NO: 4499:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 314 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4499:

GTAGTAAAC GCATTTAGTG ATTGAAACAG GCAAGATAGA CGCGGGATAT CACGGCAATT 60  
TAGGGATTAA TATCAAGAAT GACGCTATTG CATCGAATGG TTATATCACA CCAGGTGTTT 120  
TTGAATATTA AAAGGAGAAT CGATTTGAAG TGCnnCATAA GACAATACGG ACTTATCAAA 180  
TCAACGAAGG AGACAACTA GCTCAATTGG TTATCGTGCC TATATGGACA CCTGAACTAA 240  
AGCAAGTGGA GGAATTCGAA GTTGTTCAnA CGTGGAGAAA AGGCTCGGAG AGCGGGTGAA 300  
AGCATCTTAG TCGA 314

(2) INFORMATION FOR SEQ ID NO: 4500:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 304 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4500:

ATTGTAAGGC TATCATGTCA AAGATTATAA CAATAAATCT GGTGAGATT TGGTGGCGGG 60  
 5 GCGATGGAAG CTATCTATTT GACCATCCAT TTGGCAAAGG TTTGGGAGTT ACACAGGTGG 120  
 ACTTAACTTT AATGGCGGTC GTCATATGG TATCGACTTT GGTATGCCTA CAGGAACGAA 180  
 CCATTTATGC TGTAAAAGG CGGTATAGCT GATAAAGTAT GGnCTGATTa CGGTGGCGGT 240  
 10 AATTCTATAC AAATTAGGAC CGGTGCTAAC GAATGGAnCT GGTATATGCA TTTATCTAnG 300  
 CATT 304

## (2) INFORMATION FOR SEQ ID NO: 4501:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4501:

25 TTCCTTCATT CTCATAAAG TTGCATCATG ATCAGATCAG TTTTAGAAAA ACTATTTCTA 60  
 TCTTTAAGAA TCGATTTTTG TTCTTCATAT TTATTTTTTC TTTCCGnATA ATCATCAAT 120  
 TTCTTTTTGA ACTTCTTAAT CTCAGTTATT TTTTACGGG TCTGTTTTCT AATTTGAGCA 180  
 30 CAATCTTCGT TCTCAATAAG AATGATTTAA ATCTnCGATT TCTTTATCTA AATGGACTAC 240  
 CAATTAAATC TAT 253

## (2) INFORMATION FOR SEQ ID NO: 4502:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4502:

45 AGTTCGGTCC CTATCCGTCG TGGGCGTAGG AAATTTnGA GGAGCTGTCC TTAGTACGAG 60  
 AGGACCGGGA TGGACATACC TCTGGTGAC CAGTTGTCGT GCCAAnGCAT AGCTGGGTAG 120  
 CTATGTGTGG ACGGGATAAG TGCTGAAGAT GCTTAAGCAT GAAGCCCCC CAAGATGAGA 180  
 50 TTTCCCAACT TCGGTTATAA GATCCCTCAA AGATGATGAG GTTAATAGGT TCGAGGTGGA 240  
 AGCATGGTGA CATGTGG 257

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4503:

ATACGTTTAA TACACAAAA ACTGCAAAGC ATCGATGGCA GACGTCATAG ATGGCACTAA 60  
 TATTGATAAC ATTGAAGTGA ATATANAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA 120  
 TCGGAAAAAC AAGAAGTTAA GTGACAAGnT TTACATGTTG CTTAGCTTCT TTTATTATGC 180  
 GTAATGATGT AAAAAGACGA ATATTCATTT GTTTGTAAAA GTGGCATTTC TATGTCTTAA 240  
 AAGTGACGAA ACTTCAAATG TGCCAAGTGT 270

## (2) INFORMATION FOR SEQ ID NO: 4504:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4504:

TACCTTGACC GAAGTTCTTA CCTACATCAC CTAAATTAAT GACATGTCCA CCAGTCATAT 60  
 ACTCTAATCC ATGGTCGCCG ATACCTTCAA CGACAACATC TACACCACTA TTTCTAATAC 120  
 AGAATCTTTC TCCTGCACTA CCGTTAATAA ATGCCTTACC ACTTGTCGCA CCATAGAATG 180  
 AGACGTTACC AGCAATAATT TCATTTTGTC GTTCTTCAAA AGGTGCTTTG ACAATGACCG 240  
 TACCACCGn T 251

## (2) INFORMATION FOR SEQ ID NO: 4505:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4505:

AGAAGTTAAG CTCCTTAGCG TCGATGGTAG TCGAACTTAC GTTCCCGCTA GAGTAGAACG 60  
 TTGCCAGGCA AATGACAAAT CGGAGAATTA GCTCAGCTGG GAGAGCATCT GCCTTACAAG 120

TAGCTCAATT GGTAGAnCAC TGA~~CT~~TGTAA TCAGTAGGTT GGGGGGTCAG TCCTCTGGCC 240

GGCACCATCT TTTGnCCATA 260

(2) INFORMATION FOR SEQ ID NO: 4506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4506:

TTCTTTAGTA GATACTAAGG CGTTATTAGA CGCATTAGAC AATGGTGTGA TTAAAGGTGC 60

AGCACTTGAT ACGTATGAAT TTGAACGCAA ACTTTTCCCA AGTGATCAAA GGGGCAAAAC 120

ACTGAACGAT CCATTGTTAG AATCGTTGAT TGACAGGGAA GATGTCATAT TAACACCACA 180

TATTGCGTTT TATACTGAAG CTGCAGTTAA AAATCTATTG TCGTGCAATTA GGTGCAACAT 240

TAGGTGTATT GCAGCTTGGG GAACTTnGnt ACGGGTAAAT TTAAATCGG CTGTGGGTAT 300

TTTGnTTTT GGG 313

(2) INFORMATION FOR SEQ ID NO: 4507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4507:

GnCAATACGG CCAATTCCTA AGATTGCTAC TTCTGGGTGG ATTGATAACT GGAGTGAACC 60

ATTGTCCACC AGCTGnAACC GATATTACTG ATTGTGCATG TAGCACCTTT CATTTTCATCG 120

GCTGTTAATT TACCATCACG TGGCTTTAAC AGCTAATTCA TTAATTTTCAT CTGAAATTTG 180

GGAAAATAGA CTTACGGATC AGCATGTTTA ACAACAGGTA CTAATAATCC TCTATCAGTG 240

TCTGCTGCAA TT 252

(2) INFORMATION FOR SEQ ID NO: 4508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4508:

CATCGAACCA GATGTA<sup>5</sup>CTCG CACTTGT<sup>10</sup>TGA GTCTGATGTT GAATCACTAA CACTATCAGA 60  
 TAATGACGTT GAATCACTCA TACTTGT<sup>15</sup>TGA TGTACTTGTC GAAAGCGACA TACTTTGTGA 120  
 ATCACTAGTA CTTGTACGCA TCGAAGTACT AGTTGAAGCT GATGTACTAC GAGAGTCACT 180  
 TGTGATGTT GATGTACTTG CTGATCCTGA TGCATTGTA CTTCTTGATG TGCTTTGTGA 240  
 ATCGGATTTT GCTCGTGChT GGTACTnG 268

## (2) INFORMATION FOR SEQ ID NO: 4509:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4509:

CGAGAGTGCG TTAATTCGGT TACTGCTATC AcgTAAGGGG CGGAAACCCC CTAACACTTA 60  
 GCACTCATCG TTTACGGCGT rGACTACCAG GGTATCTAAT CCTGTTTGAT CCCACGCTT 120  
 TCGCACATCA GCGTCAGTTA CAGACCAGAA AGTCGCCTTC GCCACTGGTG TTCCTCCATA 180  
 TCTCTGCGCA TkTCACCGCT ACACATGGAA TTCCACTTTC CTCTGCTGGC ACTCAAGTTT 240  
 TCCAGTGTCC AATGACCCTC CACGGTTGAG CCGTGGGCTT nCACATCACA CTTAnA 296

## (2) INFORMATION FOR SEQ ID NO: 4510:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4510:

TTACTACTTA CTGAGTGACC TGTACCTGCT TTCGGAGTAA TTGTGATTGA TGAATTTGGT 60  
 TTTATAGTAT TGGCATTGAA CGTCACTTTA CCAGTTTGTG CATCTAACGT TACATAGTCA 120  
 GGCTTATTCG CAATTGTCCA TTGnTTATTT TGACCACGAA CAACATTAAT TGTCTTACTA 180  
 TGTTGCTGCA CCATTACCCA CTTnTTCAGT GTAAGCAATA TCCATTGCTT GAGTTGGGAT 240  
 TAATTAAATG GTCCTGA 257

## (2) INFORMATION FOR SEQ ID NO: 4511:

(A) LENGTH: 250 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: doubl  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4511:

AAAATCACAT CAGCCTGCAT TAACGACGTC GTTAATTTAT ATACATCTCC TG TAGTATCT 60  
 AGATAATTCT TTCCAACGCT AAATTCTAAT TCAAGTTCTC GTAAATCCAT CAACTCTATT 120  
 TGATGTCCCT CATTGATGAC TTCTAGTTCA TTTTTTAAAT CATCCATAGC AATTCTCGTT 180  
 TTAGAACCTA CTGTGGAACC TGACAATAAT ACAATATTCA nGAnGACGCC CCTCCTATTT 240  
 TGATAAATGC 250

## (2) INFORMATION FOR SEQ ID NO: 4512:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4512:

AGCTGGnTTC GAACCAACGA GTGACGGAGT nAAAGTCCGT TGCCTTACCG CTGGGCTATA 60  
 GCCCAATATA TAGATGGTGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA AGAGCGGATT 120  
 TACAGTCCGC CGCGTTTAGC CACTTCGCTA CCCCTCCAGC TTATTTCATAT AATTTAATAA 180  
 TCAAAATGGT GGAAGAATGA CGGGTTCGAA ACCGCCGACC CTCTGCTTGT AAGGCAGATG 240  
 CTCTCCCCAG CTG 253

## (2) INFORMATION FOR SEQ ID NO: 4513:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4513:

GnCGACCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA CGTTAACATG 60  
 nAAGTTACGT TCTTTTATAA AAAGATTTAA ACGCGTTATT AATCTTGTGC AGTGTTCCTT 120  
 CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT AAAACTCTTT ATTCACTCGG 180

GTGGAGACTA GC

252

## (2) INFORMATION FOR SEQ ID NO: 4514:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 244 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4514:

GTCATTGAAT ATGGAAACTT TAGAATTACA AGGCGCTAAA TTACGATACC ACCAAGTCGG	60
ACAAGGACCC GTGCTCATCT TTATTCCTGG TGCAAACGGT ACCGGAGACA TTTTCTGCC	120
TCTTGCAGAA CAGTTAAAAG ACCATTTTAC TGTTGTAGCC GTTGATCGTC GTGATTATGG	180
AGAAAGCGAG TTAAGTGAAC CACTCCCTGA TTCCGCTTCA AACCCTGACA GTGATTATCG	240
TGTC	244

## (2) INFORMATION FOR SEQ ID NO: 4515:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 243 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4515:

TATTAGGCAA ATCCGGTACT CGTTAAGGCT GAGCTGTGAT GGGGAGAAGA CATTGTGTCT	60
TCGAGTCGTT GATTTACAC TGCCGAGAAA AGCCTCTAGA TAGAAAATAG GTGCCCCGTAC	120
CGCAAACCGA CACAGGTAGT CAAGATGAGA ATTCTAAGGT GAGCGAGCGA ACTCTCGTTA	180
AGGAACTCGG CAAAATGACC CCGTAACTTC GGGAGAAGGG GTGCTCTTTA GGGTTAACGC	240
CCA	243

## (2) INFORMATION FOR SEQ ID NO: 4516:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 267 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4516:

GATTGTCCTT TGGACAATGG TAGGAGAGCG TTCTAAGGGC GTTGAAGCAT GATCGTAAGG 120  
 ACATGTGGAG CGCTTAGAAG TGAGAATGCC GGTGTGAGTA GCGAAAGACG GGTGAGAATC 180  
 5 CCGTCCACCG ATTGACTAAG GTTCCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT 240  
 CCCTAACCT GAGGCCGCAA nngTAGG 267

## (2) INFORMATION FOR SEQ ID NO: 4517:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4517:

20 TTGAATCTGA CGAAACGAGA AAAGAGCGCA ACGAGTTTAG TAGAGCTAAA TGAGTAAGCG 60  
 AGAGCCGAAG AGAGGAAAGA AGCAAGCGAT TGTCACAAGT CAAGAAAGGT CTTTAGCGAC 120  
 GATGGTAGCC AACTTACGTT CCGCTAGAGT AGAACGTTGC CAGGCAAAAA ATGGGATGCG 180  
 25 ATGAGCCGCA TTGGAGACCG CAGTCCTnTn TnTTTTTTTA TGGCCTTAAA ACGTCAAAAT 240  
 TAAAAAGTTA AACACAAAGA AAATGGGCTT TGGCGAGTGG AAACGTTTTG AATCTGGACG 300  
 GAACGAGAAA GAGCGCACG 319

## (2) INFORMATION FOR SEQ ID NO: 4518:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 259 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4518:

40 GGTATAATAG ATGACTATGT ACTATTCCG GTACATCCTT GGCAATATCA GCATATTCTG 60  
 CCGAACGTCT TTGCGAAAGA GATTAGTGAA AAGTTGGTTG TACTATTACC GTTAAAATTT 120  
 45 GGAGATTATC TGTCGTCTTC AAGTATGCGT TCATTAATTG ATATTGGCGC ACCGTATAAC 180  
 CATGTCAAnG TACCATTTCG AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GnCTACGGTT 240  
 ACATGAAAAA CGGGGAACA 259

## (2) INFORMATION FOR SEQ ID NO: 4519:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 253 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4519:

ATAGGGTGTT GCTGAATAGG GCGTTTAGTA TTTGGTCGTA CCGnnAACCA GGTGATCTAC	60
10 CCTTGGTCAG GTTGAAGTTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA	120
AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGG AGATAGCTGG	180
TTCTCTCCGA AATAGCTTTA GGGCTAGCCT CAAGTGATGA TTATTGGAGG TAGAGCACTG	240
15 TTTGGACGAG GGG	253

(2) INFORMATION FOR SEQ ID NO: 4520:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4520:

AACTCGTTGC GCTCTTTTCT CGTTTCGTC AATTCAAACG TTTTCACTTC GCCAAGCCAT	60
30 TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTCACGGT	120
CTCAACTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTTGGCnACC ATCGTCGCTA	180
AAGACCTTTC TTGACTnGTG ACAATCGCTT GCTTCTGTCC TCTCCTTCGG CTCTCGCTTA	240
35 CTCAT	245

(2) INFORMATION FOR SEQ ID NO: 4521:

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4521:

GGGCCTAAGT GGA CTGGAAC CACCGACCTC ACGCTTATCA GGC GTGCGCT CTAACCAGCT	60
50 GAGCTATAGG CCCATTAATT TGAATGAACA AACATTCAA ACTGAATACA ATATGTCACG	120
TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG	180
55 CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TnCCACCTT	240

## (2) INFORMATION FOR SEQ ID NO: 4522:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4522:

nATAGAACCT GAAACCGTGT GCTTACAAGT AGTCAGAGCC CGTTAATGGT TGATGGCGTG 60  
 CCTTTTGTAG AATGAACCGG CGAGTTACGA TTTGATGCAA GGTTAAGCAG TAAATGTGGA 120  
 GCCGTAGCGA AACGATGTCT GAATAGGGCG TTTAGTATTT GTCGTAGAC CGAAACCTGG 180  
 TGATCTACCC TTGGTCaGT TGAAGTTCAG GTAACACTGA ATGGAGGACC GAACCGACTT 240  
 ACGTTTGAA 249

## (2) INFORMATION FOR SEQ ID NO: 4523:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4523:

TCCCTATCCG TCGTGGGCGT AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG 60  
 GGATGGACAT ACCTCTGGTG TACCAATTGT CGTGCCAaG CATAGCTGGG TAGCTATGTG 120  
 TGGACGGGAT AAGTGCTGAA GATCTnaAGC ATGAAGCCCC CCTCAAGATG AGATTTCCCA 180  
 CTTCCGTTAT AAGATCCCTC AAAGATGATG AGGTTAATAG GTTCGAGGTG GAAGCATGGT 240  
 GACAGTGG 248

## (2) INFORMATION FOR SEQ ID NO: 4524:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4524:

AACGTTAAGA TCCCTATTAA ATTATCTTAG GAATCATCAT GGCATTAT GATGTCTTAA 60

AAATTAGTAA TCTGAATCTG CTTCTAAACC TTGTCATAAT TTGA<sub>n</sub>CGGCT GTGGCTCG<sub>n</sub>A 180  
 CCAATACGGG TCGGACCTGC TT<sub>n</sub>AACCATT TTATTGGAAA TCTTCTAAAT TACGGACGGC 240  
 5 ACCCGGATGC TTTTACTTCT ATATCAGCAC CTACTGTATC TTTCATTAAT TTAACGGCTT 300  
 CTGCAGTCGG ACCGGCAACT GCAAAA 326

## (2) INFORMATION FOR SEQ ID NO: 4525:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 301 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4525:

AAGAGCACCC TTCTCCGAGT TACGGGGTCA TTGCCGGTT CCTTAACGAG AGTCGCTCGT 60  
 CACCTTAGAT TCTCATCTTG ACTACCTTGT CGGTTTGCGG TA<sub>n</sub>GGCACCT ATTTTCTATC 120  
 TAGAGGTTTT CTCGGCATGT GAAATCAACG ACTCGAGACA CAATGTC<sub>TT</sub>C TCCCATCACA 180  
 25 GTCAGCCTTA ACGAGTACCG GATTTGCCTA ATACTCAGCC TACTGCTTAG nGGCATCCAT 240  
 CGCAGTT<sub>n</sub>GC TATCCACTGG TCCCCCTCGA TTAAACGATT ATAGGTGGTA CAGATATCAA 300  
 C 301

## (2) INFORMATION FOR SEQ ID NO: 4526:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 241 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4526:

TGATATTATG AGCTGTGTTT TTAGCTTTAG AACCGAAGTC CCCTGCTTTT TTACCAAGAT 60  
 TTTAGTAAC TTGT<sub>n</sub>CCATC CATTTTTTCT TTTTCGTACC ACCATGGAAT TTTGGCAAAA 120  
 45 CACCCATCCG CTGTAACTTC AGAGTGTCAT TGGCATTTAT TACACTATCT CCAACTCCTA 180  
 GTGGAACAAC CACATCTCGT CCTTGGGGTG CATGGAATGT nCCGTCAGCC CTGTGAATTA 240  
 T 241

## (2) INFORMATION FOR SEQ ID NO: 4527:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 316 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4527:

CGATCACACT CTTCGTCGT CATCGCCATT GGCTTTTCAC ACAATACATG GACACCATGG	60
10 TGTCAATGCT TCTATAGAAA GATCAGCATG GAATTTATTA GGTGTACAAA TGACCACCGC	120
ATCAACAAGT TTAAACAGCT CGCTAGGTGT CTCAACTGCA TGAGGTATAT TGAAAGCGCT	180
TCGCAACCAT nCAATCATCT GGCAGTGTTA TTGAATATCT TGTGACTGGC AACTTAATGA	240
15 GnACTGTGTC TTTTGGAGTT TCCAGnCAAT GCCGGGAATT ATGGACGGGT CTTGGTGGCA	300
ATACCACCCA ACACCT	316

(2) INFORMATION FOR SEQ ID NO: 4528:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4528:

30 GTCCCAAGGG TTGGGCTGTT CGCCATTAA AGCGGTACCG ACGACTGGGT TCAGAACGTC	60
GTGAGACAGT TCGGTCCCTA TCCGTCGTGG GCGTAGAAAT TTGAGAGGAG CTGTCTTAG	120
TACGAGGAGG AnCGGGATGG ACATACCTCT GGTGnACCAG TTGTCGTGCC AACGGCATAG	180
35 CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAAGCAT CTAAGCATGA AGCCCCCCTC	240
AAGATGAGAT T	251

(2) INFORMATION FOR SEQ ID NO: 4529:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4529:

50 AGTACGTGAC GTTCACTACT CTCACTATGG CCGTATGTGT CCAATTGAAA CACCTGAGGG	60
ACCAAACATT GGATTGATTA ACTCATTATC AAGTTATGCA CGTGTAATG AATTCGGCTT	120
TATTGAAACA CCATATCGTA AAGTTGATTT AGGATACACA TGCTATCACT GATCAAATGA	180

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ATGGTCGTTT AGGTGATGAG TGTATGCGTT CGGGnACnAT CAGTATGCAA GAAAAGGTTT 300  
GTGACGCGAC AGTGTcNA 318

(2) INFORMATION FOR SEQ ID NO: 4530:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 240 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4530:

TAGCTGTGTG ATAAATTGCA AGTGCGGCAC CACATAAGCC GAACATCATC GTAATAAAAC 60  
GGCCTGACAT ACACGCTGAC ACACCTGAAT AATACTTCGT CACATCTGGA TCACCAAGTT 120  
GAGCAAAGAn GATGTTCTnC GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC 180  
CAAGTGCCGT CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT GGACCTAACA 240

(2) INFORMATION FOR SEQ ID NO: 4531:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 254 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4531:

CGGCTCTTCT GGGACGTAA CCCTAAAGTG CACCCCTTCT CCCGAATTAC GGGGTCATTT 60  
TGCCGAGTTC CTTAACGAGA TTCGACTCGn TCACCTTAGA ATTCTCATCT TGACTACCTG 120  
TGATCGGTTT GCGGTTAGGG GCACCTATTT TCTATCTAGA GGCTTTTCTC GGCAGTGTGA 180  
AATCAACGAC TCGAAGACAC AATGTCTTCT CCCCATCACA GChCAGCCTT AACGAGTACC 240  
GGATTTGCCT AATA 254

(2) INFORMATION FOR SEQ ID NO: 4532:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 238 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4532:

TGAATAAACC GAATGTGGCT AAAGTCGTTA ACGCAAATA TGACGTCATC TATAACGGAC 120  
 ATACTTTTGC AACATCTTTA CCAGCGnAAT TTGTAGTAAA AGATGTGCAA CCAGCGAnAC 180  
 5 CAACTGTGAC TGAACAGCG GCAGGAGCGA TTACAATTGC ACCTGGAGCA AACCAAAC 238

## (2) INFORMATION FOR SEQ ID NO: 4533:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4533:

GGTCATTAAT AAAATATCTA AAGCCATTAC TGCATAAAAA TCTCATCAAG CCAATACCTA 60  
 20 CATTGTACTA CTGGnCACTT TAGACAGGnC AAGGGTGTAG CTACCGATAA TTCAGGAGCA 120  
 TTAACGCAAC CGACATTTGA CTGTATTAAA TGATAGAGGT TCTGGAAAAC GCCCCAGGTG 180  
 GTGGAGTTCA AGAAATAATT CACAGGGCTG ACGGAACATT CCTGCACCCC AAGGACGAGA 240  
 25 TGTGTTTGT CCAC TAGGAG TTGGAA 266

## (2) INFORMATION FOR SEQ ID NO: 4534:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4534:

TACTCAGAGG ATACCCCGAC GTAATGCATT CAATTCAATT TTAAACGTA TTATTTCAAT 60  
 40 GAGCAGAAAG AAAATTATGG CACCAACTT TAATATTTTT TTCAATGTCA TTCTTTTGAh 120  
 GGGAGTGGGA CAGAAATGAT ATTTTCGCAA AATTTATTTT C TCGTCCCAC CCCAACTTGG 180  
 CATTGTCTGT AGAAATTGGG AATCCAATTT CTCTTTGTnG GGGCCCATCC CCAACTTGCA 240  
 45 CATTATTGTA AGCTGACTTT TCGT 264

## (2) INFORMATION FOR SEQ ID NO: 4535:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4535:

GCGAATGGAT AACAGTTGAT ATTCCTGTAC CACCTGATAA ATCGTTTTAA TCGATGGGGG 60  
 5 GACGCATAGG NATAGGCGAC TGCCGATTGG ATTGCACTCT AAGCAGTAAG GCTGAGTATT 120  
 AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCGA 180  
 GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AAATAGGTGC CCCGTACnGC 240  
 10 AAACCGACAC 250

## (2) INFORMATION FOR SEQ ID NO: 4536:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4536:

AATGACGGGT TCGAACCGCC GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT 60  
 25 AATTCTCCGA TTAAAACTG CCTGGCAACG TTCTACTCTA GCGGAANTAA TTCGAACCTAC 120  
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 180  
 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAnATAGT AAGTA 235

## (2) INFORMATION FOR SEQ ID NO: 4537:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4537:

TGCATCTTCA CAGGTACTAT GATTTACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 60  
 TACGCCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT 120  
 45 ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAG CTAACCACTC 180  
 CTCTTAACCT TCCAGCACCG GGCAGGCGTC AGCCCTATAC ATCACCTTAC GGTT 234

## (2) INFORMATION FOR SEQ ID NO: 4538:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4538:

5 ACCCTCTGCT TGThAGGCAG ATGCTCTCCC AGCTGAGCTA ATTCTCCGAT TTAAAACTGC 60  
 CTGGCAACGT TCTACTCTAG CGGAACGTAA GThGACTACC ATCGACGCTA AGGAGCTTAA 120  
 CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA 180  
 10 TGTAATTTAT ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTTGCTTC GCAAACCATT 240  
 TA 242

## (2) INFORMATION FOR SEQ ID NO: 4539:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4539:

25 TCATTAACAC CATCACCATA AATAAACCT TCCATATCTG TTCCTGTGCC AATAAGCCA 60  
 TATTGCGTTT GThCTGTCTG GCCAGTGCAA GATTTC AAC GATAATTTCT AGGCGTCACT 120  
 GCTGGCGAAC CATCTAATGG ATAATCATAA TCCATCGTGC GTCCAAGAAG TACTTThTTT 180  
 30 ATTTAAAGTT TGTATTGTGG AATCCTGTGC ACATGTTCTC ACTCCTCTGT ACCT 234

## (2) INFORMATION FOR SEQ ID NO: 4540:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4540:

ACACAAAGAA AAATGGCTTG GCGAAGTGAA AThGTTGAA TCTGACGAAA CGAGAAAAGA 60  
 45 GCGCAACGAG TTTAGTAGAG CTAAATGAGT AAGCGAGACC GAAGAGAGGA AAGAAGThAG 120  
 CGATTGTCAC AAGTCAAGAA AGGTTCTTAG CGAGGATGGT AGCTAACTTA CGTTCCGCTA 180  
 GAGTAGAACG TTGCTAGACA AGAAATGAAT GCGATGAGCC GCATTGAGTG TGAAATTGAT 240  
 50 AT 242

## (2) INFORMATION FOR SEQ ID NO: 4541:

(A) LENGTH: 240 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4541:

10 GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATATA GTCAAACGCT CACATACGGC 60  
 TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA 120  
 ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT AAACGCGTTA TTAATCTTGT 180  
 15 GnAGTGTCTTCT TTCGAACATA GGCGATTATn TCTTATGAAT TCAAGCTTAT TTA AAAACTCT 240

## (2) INFORMATION FOR SEQ ID NO: 4542:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 242 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4542:

AAGCTAGCAA TGATGTCAAG CAATGGCAAC ATGTGCTCAn TTAGCTAATA TGCAAGCACA 60  
 30 TGGTGAATAT GACGAGGTTG CAACTTCAAC GGCGAGGnTG ATGAATGCCT TACGTTTGCG 120  
 TGAGACAGTA GCTATGGGCC GCGGTATTAC AGGTGGTAAT GGCATACTGA GCTGACGATT 180  
 ATGATATTGT CACGTTTTCT TCTCTGTATG CAGAAGCGAT TTACACGTAC GAGGTACACA 240  
 35 TG 242

## (2) INFORMATION FOR SEQ ID NO: 4543:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 239 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4543:

TGGTGAGCCA TAGAGGATTC GAACCTCTGA CCCTCTGATT AAAAGTCAGA TGCTCTACCA 60  
 50 ACTGAGCTAA TGGCTCTTCC ATGGTGCCGG CCAGAGGACT TGAACCCCCA ACCTACTGAT 120  
 TACAAGTCAG TTGCTCTACC AATTGAGCTA GGCCGGCAAT ATGTAAGATT AAATGGTGGA 180  
 55 GAnTGACGGG TTCGAACCGC CGACCTCTG CTTGTAAGGC AGATGCTCTn CCAGCTGAG 239

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4544:

ATAGAGGATT CGAACCTCTG ACCCTCTGAT TAAAGTCAG ATGCTCTACC AACTGAGCTA 60  
 ATGGCTCTTC CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA 120  
 GTTGCTCTAC CAATTGAGCT AGGCCGGCAA TATGTAAGAA TAAATGGTGG AGAATGACGG 180  
 GTTCGAACCG nCGACCCTCT GCTTGTAAAG CAGATGCTCT nCCAGCTGAG CTAAATTCT 239

## (2) INFORMATION FOR SEQ ID NO: 4545:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4545:

AATTCATGCT TTCAAAAGAC GATATACTAC GAACTTCTA CGAACTTGTC CAAGGATTAC 60  
 GAAAAGACCT AAGGTTATGT AATTGGCTA AATTATTAA TCGTTTAAAT TCAGTTAGTA 120  
 AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAATA TTATAGAAA CATCAAAGGA 180  
 TGTTAAGAAA TACnATTTAT TACCCAGCAT TTAATAATGG TGCTATAGAA GGA 233

## (2) INFORMATION FOR SEQ ID NO: 4546:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4546:

ACTTTGTTGT CTTCCATCAA CTGAGACTT CATAACGTTT TGCATCTTCG CCACCTTCAC 60  
 CACTATTACT CTTTCCACCT AATTGGTTCA TGGCTTGTGC TAnTTTTTCA TGTGCTCCG 120  
 CTGAAATCGA TCCATAACTC ATCGCCCTG TATTAAAGCG TTTGACAATG TCACTTACCG 180  
 GTTCAACTTG GnCGATGTCA ATCGGTGTAC ATGCTTTAAA TTCAAGTAA TGTCTAATGT 240

## (2) INFORMATION FOR SEQ ID NO: 4547:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4547:

GAGGAAATTA CTGAAAACAA TCATCATATT TCTCATTCTG GTTTAGGAAC TGAAAATGGT 60  
 CACGGTAATT ATGGCGTGAT TGAAGAAATC GAAGAAAATA GCCACGTGGA TATTAAGAGT 120  
 GAATTAGGTT ACGAAGGTGG CAAAATAGC GGTAATCCAG TGCATTGAG GAAGACACAG 180  
 AAGAAGTTTA AACCGAAATA TGAACCAAG GTGGGCATTA TCGTTGGTTA TCGATTTTCG 240  
 ATAGTGTACC TCAAATTICA TGGGTCCAAA TTAATGGTTA ACCCATCCAT TCGAnGnAGG 300

## (2) INFORMATION FOR SEQ ID NO: 4548:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4548:

TTGCTATAGT CACCAGACAT ATGAATGTAA ATTATACATT CAAAACTAGA TAGTAAGTCA 60  
 AAGTGATTTT GCTTCGCAAA CATTTATTTT GATTAAGTCT TCGATCGATT AGTATTCGTC 120  
 AGCTCCACAT GTCACCATGC TTCCACCTCG AACCTATTAA CCTCATCATC TTTGAGGGGA 180  
 TCTTGATAAA CCGnAAGTTG GGGAAATCTC ATCTTTACGG GGGGGCTTCA TGCTTAGGAT 240  
 GGCTTTnCAG CACTTTATGC CCGGTnCCAC ACATTAGGCT TACCCAGCCT ATGCCCGTTT 300  
 GGCACG 306

## (2) INFORMATION FOR SEQ ID NO: 4549:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4549:

CTTCTACTTT TGTACCATCA ATAAGATTTT GCTTTAAACA TTGACTATGA AACTGGATAA 120  
 ATAAAGATTC AATTAACGCA TCAGTATTAG GATTCACTCT AATACGATTA ATAGTTTAT 180  
 5 AAGAAGGTGn TTGATTTTGA GCTAACCACA TCATTGGAAT ACTGTCATGn AG 232

## (2) INFORMATION FOR SEQ ID NO: 4550:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4550:

CTGGGTTTCAG AACGTCGTAT GnAGTTCGGA TCCCTATCCG TCGTGGGCGT AGGAAATTTG 60  
 20 AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG TACCACTTGT 120  
 CGTGCCAANG CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AACATTCTTA 180  
 AGCATGAAGC CCCCCTCAAG ATGAGATTTC CCAACTTCGG TTATAAGATC CCTCAAAGAT 240  
 25 GATGAAGTTA ATAAGTTC 258

## (2) INFORMATION FOR SEQ ID NO: 4551:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4551:

TTACAGGCAT GCGAGTTGGG GTGAGGGCCC ACACAGAAGC TGACGAAAAG TCATGACAAT 60  
 40 AATGTGCAAG TTGGGGATGG GCCCACAAAG AGAAATTGGA TTCCCAATTT TACAGACAAT 120  
 GCAAGTTGGG TGGGACGACG AAATAAATTT GCGAAAATAT CATTTCTGTn CCCTCCCTCA 180  
 AAAGATGACA TTGAAAAAAT ATTAAAGTTG GTGCCATATT TTCTTCTGCT CATGAATATA 240  
 45 CGTTAAATTT GATTGATCAT CGCGAATTGA TATTATTCTC ATTATAAAAA TACTTATTAC 300  
 ACTTACCGTA TGATAGTTTG nTATATACTC TGATAAAGTC AAACCTAATA GCGTTTCTAG 360  
 50 CTGTGnGTGT TTCATAATTA TATACATTAT CAGGCTTTAA 400

## (2) INFORMATION FOR SEQ ID NO: 4552:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4552:

	ATAGGAAACT GCCAATTGGA CGGTTGCCGC ATTCAAACCC AGCACGATTA CGGCGAATTG	60
10	CACGTGAAnC ATTTCTACAG CTTGATCTTG ACCTATGATT TTA CTCTTA AACGATTAGA	120
	AATATTTTTT AAACGTTCAA TATCGTTATC ATCCATTGG AGAACTGGG AATACCATTG	180
	AATCGTTGnA ATAGTATCTG GAAATATCAT GGAAGTGTAG CAACAGCAGT GTGTTGCACC	240
15	ATTnACTGAT TTGCTAATT TATCTTGGTG AATGGATTTG GATTTCATT TTGGAATGTG	300
	CGTGCAGCTT TT	312

(2) INFORMATION FOR SEQ ID NO: 4553:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 254 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4553:

30	AGCAGCGATC AAAAATAATC CGCAATACGC TGGCAAACCTA CCAATACCAA ACCATAGAAC	60
	AACAAATGGT GCCCATGCTA TCGGAGATAT CGGCCTAATC AATTGAAATA GCGGTTGAT	120
	AGCGTTGTAT AGCCAACGAT TCCTTCCAAG CAAGAAGCCC AATGGAATAG CAACCAACAA	180
35	TGCGACAACA AAGnCCGCTA CAAATCTCCA TGAATAATT GCTAAATGTG GnGAATTTCT	240
	CCAGTAACAA TGGA	254

(2) INFORMATION FOR SEQ ID NO: 4554:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4554:

50	GGTCTGAATC GCTATCTGAG TCTGAATCGC TATCTGAGTC TGAATCACTG TCTGAGTCCn	60
	AGTCACTGTC TGAATCTGAC TCACTATCTG ATTCTGAGTC GCTATCTGAT TCTGAGTCGC	120
	TGCTCTGGAAT CTGAATCACT GTCTGGAATC CGAATCGCTA TCTGGATCTG AGTCGCTATC	180

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CTGGGGCTTG G

251

## (2) INFORMATION FOR SEQ ID NO: 4555:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4555:

TACACAAAGA GATAAATTAC TTATGCAAAG GCGGAGGAAT CACATGTCTA TTACTGAAAA 60  
 ACAACGTCAG CAACAAGCTG AATTACATAA AAAATTATGG TCGATTGCCA ATGATTTAAG 120  
 AGGGAACATG GATGCGAGTG AATTCGGTAA TTACATTTTA GGCTTGATTT CTATCGCTTC 180  
 CTATCTGAAA AAGCCChACC AGAATATGCA GTGCCCTGTC AAGnGAAGAC ATCACGTTCC 240  
 AGAAGCATGG C 251

## (2) INFORMATION FOR SEQ ID NO: 4556:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4556:

AGCTACCCCG GGGATAACAG GCTTATCTCC CCCAAGAnTT CGCATCGACG GGGAGGTTTG 60  
 GCACCTCGAT GTCGGCTCAT CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT 120  
 TCGCCCATTA AAGCGGTACG GAGGCTGGGT TCCGAACGTC GTGAGnCCGT TCGGTCCCTA 180  
 TCCGTCGTGG GCGTAGGAAT TTGAGAGGAG CTGTCCTTAG TACGAGAGGA CCGGGTGGAC 240  
 ATA 243

## (2) INFORMATION FOR SEQ ID NO: 4557:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4557:

TCATTATTTT AAATGCTCAT TTACATAAGT AAACCTCTGCT TTAAAATAAT TTAACTCATT 120

GTCTGCTAAA CGTTTTCTTT TATAAAAAGA TTTAAACGCG TTATTAATCT TGTGAGTGTT 180

5 CTTTCGAACA CTAGnCGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTG 235

(2) INFORMATION FOR SEQ ID NO: 4558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4558:

CCGTTAAGCA CTAAATCCGC TTAATAACGG CTTTCTATCG CGCGCAACAT CTCGTTTGAC 60

20 TGCTTTTTCT TTCAAAGCTT GACGTTATCA TATTTTTTCT TACCTCGTGC ACACCAAGTA 120

ATACTTTACA ATGTCCATGC TTCAAATAAA GCTTTAACGG ACAATCGAAT AACCAAnCTC 180

ACGTGTTTGA TCACCCAATT TAATGATTTT ACGCTTGTGC AATAATnATT TTCGAGACGA 240

25 GAGGATCGGA TTAAACGAT CCCCTCCTCG TATGG 275

(2) INFORMATION FOR SEQ ID NO: 4559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4559:

TTATATGGAT GTATCGCCGA AGCAAGTTGT TTCAGCAGCG ACAnATGTAT TCCGATGACT 60

40 CAAACCGTGC ATTGATGGGT GCGAACATGC AACGTCAAGC AGTGCCTTTG GATGAATCCA 120

GAAGCACCAT TTGTTGGTAC AGGTATGGAA CACGTTGCAG CACGTGTATT CTGnGTGCGG 180

CTATTACAGC TAAAGCACAG AGGTCGTGTT GAACATGTTG GAATCTAATG AAAT 234

45 (2) INFORMATION FOR SEQ ID NO: 4560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG 60  
 TTCTACTCTA GCGGAAnTAA nTGGCTACCA TCGTCGCTAA AGACCTTTCT TGACTTGTGA 120  
 5 CAATCGCTTG CTTCCTTCCT CTCCTTCGGC TCTCGCTTAC TCATTTAGCT CTACTAACT 180  
 CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA AG 232

## (2) INFORMATION FOR SEQ ID NO: 4561:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4561:

20 TCAAAGGACG CATACCATTA CGGGTCTGCT ACTTGTAAGC ACACGGTTTC AGGTTCTATT 60  
 TCACTCCCCT TCCGGGGTGC TTTTnACCTT TCCCTCACGG TACTGGTTCA CTATCGGTCA 120  
 CTAGAGAGTA TTTAGCCTTA GGAGATGGTC CTCCAGATT CCGACGGAAT TTCACGTGCT 180  
 25 CCGTCGTACT CAGGATCCAn TCAAGAGAGA CAACATTTTC GACTACAGGA TTATTACCTT 240  
 CTTTGATTCA TCTTGTC 257

## (2) INFORMATION FOR SEQ ID NO: 4562:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4562:

40 TACCTAATAA GTTGTGAATT TGAACAGCGG CTGCTTTACA nTGGAAGTGC TGATTTCAGTT 60  
 GCCACAATTA CCATACCAAT TTTCTTTTTG TCTTCGTCTG TnATAATGTC CTTAGCAGCG 120  
 TTAGCTCCGA TTGAAACGAT GTCTTGTTTT ACAGGACTAA CAGCCATTTT AGTTTGACCA 180  
 45 ATTCCAATTA AAAATTTGTT TGGGTCTACT TGGCGTGGCT TCCTGCTGAA TTTAGCCATG 240

## (2) INFORMATION FOR SEQ ID NO: 4563:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4563:

CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC 60  
 TAGTGCCAAG GCATCCACCG TCGGCCCTTA ATAACCTAAT CTATGTTTCC ACCATTTTTA 120  
 TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTATTTT AnATGCTCAT TTACATAAGT 180  
 nGACTCTGCT TAAAATAAT TTAACTCATT GTCTGCTAAA CGTTT 225

## (2) INFORMATION FOR SEQ ID NO: 4564:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4564:

TGTTAATTGG nGAATTTGGA TACTGGTTAT ATTCAGCTGC ACCGCAAGCA ACTTCTATTG 60  
 ATGGCCTAAC TGCCTTTTTA CCTCAAGCAA TGGGTATGGT AATTGTTGCA GTCATTTATG 120  
 GCTTATGAA TATGAAAGCA GAGGAATCCC ATTCCCGTAA TAAAATTACG GTGGTTACAA 180  
 AATTATTICA GGTTTCTTTC TTTTGCATTT GGGTGCTTTA ACCATATCTT nTT 233

## (2) INFORMATION FOR SEQ ID NO: 4565:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4565:

AGCTCAGATA GCGCTCAGAC TCAGACAGCG ACTCAGATTC AGATAGCGAT TCAGACTCAG 60  
 ACAGCGACTC AGACTCAGAC AGCGACTCAG ACTCAGATAG CGACTCAGAT TCAGATAGCG 120  
 ATTCAGACTC AGACAGCGAC TCAGATTCAG ATnGCGATTC GGAnTCAGAC AGCGATTTCAG 180  
 ATTCAGACAG CGACTCAGAC TCGGATAGCG ATTCAGATTC AGATA 225

## (2) INFORMATION FOR SEQ ID NO: 4566:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4566:

CCAAGTGGAG CTAATGGCTC TTCCATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC 60  
 5 TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCGG CAATATGTAA GAATAAATGG 120  
 TGGAGAnTGA CGGGTTCGAA CCGCCGAnCC TCTGCTGTG AAGGCAGATG CTCTCCCAGC 180  
 10 TGAGCTAATT CTCCGATTTA AAAGTGGCCT GGGCAACGTT CTACTCTAGC GGGAAGT 237

## (2) INFORMATION FOR SEQ ID NO: 4567:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4567:

GTTGGAGATA GTGTAATAAT GCCAATGAGC CACTCTGAAG TTACAGCGGA TGGGTGTTTT 60  
 GCCAAAATTC CATGGTGGTA CGAAAAAGAA AAAATGGATG GAAACAAGTT ACTGAAAATC 120  
 25 TTGGTAAAAA AGCAGGGGAC TTCGGTTCTA AAGCTAAAAC ACAGCTCATA ATATCAAAAA 180  
 GGTGCAGAGG AAATGGTTGA nngGCAGCGG ATAAATCAAG ATGGTGCACT TGGTTAGCGT 240  
 30 TAAATCGCGA TGTGTGGGTT AnTACACATC CGGGAAGTAG TAATAAGTAT GTCAGTTTAA 300

## (2) INFORMATION FOR SEQ ID NO: 4568:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4568:

ATCCCGTGGG GGTTCAGTC CTCTCGGCCG CATCAAAATT CTTAATTTAA ATAAGCGGGT 60  
 GTAGTTTAAT GGCAAAACCT CAGCCTTCCA AGCTGATGTT GTGGGTTCGA TTCCCATCAC 120  
 45 CCGCTCCATA GATAATTTTA ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT 180  
 TCCAAAAACG TAACTATAAG TTACAAACAT TnATTTTAgT ATTTGATGGA GCCTnAATCC 240  
 50 AAACATTCCA 250

## (2) INFORMATION FOR SEQ ID NO: 4569:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4569:

GATCCCCTAG CTTTACGTTT AACTTTATAT GGGTATAACT CGAATATAAT TTGGCGCTCT 60  
10 ATGTCATGGG ACAACGAGTA GACATTTAAT AACGGATCAG GTTCTGGTGA CGGTATCGAT 120  
AAACCAGTTG TTCCTGAACA ACCTGGTGAG CCTGGTGAAA TTGAACCAAT TCCAGAGGnT 180  
TCAGATTCTG ACCCAGGTTT AGATTCTGGG CAGCGnTTCT AATTCAGATA GCGGT 235

15

(2) INFORMATION FOR SEQ ID NO: 4570:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4570:

AATCTATTTC TTCTATTGTT AAATCGCTAT CTCCATCTTC TTTTATCTCT GGTATTATTT 60  
TTTCTTCAAC TAAGTCACGA TATAATGTTT TTGAATTTTC GTTCAATTTT GATTCGTGAT 120  
30 TTTGAATACT TTTCTTCCAC ACAAATGTAT ACCTATTGGC ATTAGCnTCT ACTTTTGTAC 180  
CAnCAATAAG ATTTTGCTTT AAACATTGAC TATGAAACTG GGA 223

(2) INFORMATION FOR SEQ ID NO: 4571:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4571:

CATGATATTT TGAACCGCAT GGTTAAAGTT GCAAAGACGG TCTTGCTGTC ACTTATAGAT 60  
45 GGATCCGCGC TGCATTAGCT AGTTCGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATAG 120  
CCGACCTTAG AGGGTGATCG GCCACACTGG nACTAAGACA CGGTCCAGAC TCCTACGGGA 180  
50 GGCAGCAGTA GGGAATTTTC CGCAATGGGC GAAAGCTGTA CGGCGCAACG TCGTGTGnAG 240  
TGCTGCAGGT TCTTCGGATC GTAAAAT 267

(2) INFORMATION FOR SEQ ID NO: 4572:

55

(A) LENGTH: 221 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4572:

10 AATnCAACTT TTACTIONACTA TCTAGTTTTG AATGTATAAA TTACATTCAT ATGTCTGGTG 60  
 ACTATAGCAA GGNGGTCACA CCTGTTCCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG 120  
 TCGATGGTAG TCGAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAT AATATTAATC 180  
 15 CACAGTAGCT CAGTGGTAGA GCTATCGGCT GTTAACCGAT C 221

## (2) INFORMATION FOR SEQ ID NO: 4573:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 230 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4573:

GCAGAAATGC CAGCCGCATT GAGTGAACAC AGAGTTACAG GGTATTCTGT AGCCGAACCA 60  
 30 TTCGGTGCAa TGGGGGAAAA GTTAGGCAAA GGTAAGACTT TGAAACATGG TGATGACGTT 120  
 ATACCTGATG CGTATTGCTG TGTGCTAGTA CTnAGAGGGG AATTGCTTGA TCAACACAAG 180  
 GATGTAGCGC AAGATTTGTA CAAGTTATA AAAAGTCTGG CTTTAAAATG 230

35

## (2) INFORMATION FOR SEQ ID NO: 4574:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 230 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4574:

TCACATATCG ATAACATGAC ATAACTCATG CTGGGTTTCC CCATTCCGAA ATCTCTGGAT 60  
 CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC 120  
 50 TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACTTAAT CnATGTTTCC ACCATTTTAA 180  
 TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTAnTTT AAATGGCTCA 230

## (2) INFORMATION FOR SEQ ID NO: 4575:

55

(A) LENGTH: 309 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4575:

10 CTTACAATAG TGTGCAAGTT GGGGTGGAGC CCCGACACAG AGAAATTAGC TCCTCAATTT 60  
 CTACAGACAA TGCAAGTTGG CGGGGCCCCA ACACAGAAGC TGGCGAAAAG TCAGCTTACA 120  
 ATAGTGTGCA AGTTGGGGTG GGACGACGAA ATAAATTTTG CGAAATATC ATTTCTGTCC 180  
 15 CACTCCCAAA AAGACCGCAG TAGGATAATT CCATTGGAAT ATACCTTACT GCCnGTTTTT 240  
 AAAGTAATAG CnAATATTTT GGAATTAnGT TTCCTAGTTA ACCATACCAA CTAATGGCCT 300  
 CCTTAAATT 309

20

(2) INFORMATION FOR SEQ ID NO: 4576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4576:

30

TGATTCTAGG AATTCAAGCT TATTTAAAC TCTTTATTCA CTCGGTTTTG CTTGGGTAAA 60  
 ATCTATATTT TACTTACTTA TCTAGTTTTT AATGTACAAA TAATGGTGGG CCTAAGTGGA 120  
 35 CTCGAACCAC CGACCTCAG CTTATCAGGC GTGCGCTCTA ACCAGCTGAG CTATAGGCCC 180  
 ATTTTTTTGA ATGTTAAATA AACATCnAAA CTGGnATACC ATATGTCACG GTAATCCGCA 240

(2) INFORMATION FOR SEQ ID NO: 4577:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4577:

50 CTTCGTGTTA AAATTTGATG CACAATGGTC ATCATTTTTA TCTTTCCAAT AAGTACTGTC 60  
 TGGGTAAAAA TnTATTAATT GGGTGGTTCG TGAAATGCAA TCTTTTAAAC GACTTCAGGG 120  
 TAATCTTTTA ACACATGCAT CGCAACGATT GAACCTnAAC TTGAACCTAA TATATAGACA 180

55

## (2) INFORMATION FOR SEQ ID NO: 4578:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4578:

5	TAGGCATACC AAAGTCGATA CCATAGTGAC GACCGCCATT AAAGTTAAGT CCACCTGTGT	60
10		
15	AACTCCCAA CCTTTGCCAA ATTGGATGGT CAAATAGATA GCTTCCATCG CCTCCGCCAC	120
	CAAAATCTTC AAACCACGAT TTACTTTGnC TACTAATTTT TTTTGTAGCA ATGAGTACGC	180
	GCCTTAGCAA TTTTAnTAG CGTAGTCCGC TCCAAAATAA TATTAACTG ACATACTTAT	240
20	TACnAGTTCC CTGGATGTGT ACATAATCCA CACATCGCA TTTATCGCTA ACAGAGCACA	300
	CTTGATTACG CGCGCTCAAC ATTC	324

## (2) INFORMATION FOR SEQ ID NO: 4579:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4579:

35	AATGTAAAA CTGATTTCTA TTAATTATTT GATAGAAATC ACTTTTTTGT ATTTTATAAT	60
	GTACAGCTCG TTGCATTCAT ATAGCTTGAA GTCACGTTA AAACCATATC TATCATTATG	120
	GTATGCATAT CGTTTAAAC CTATTCTTTT GTTAnTAGGA CATATAAATT CATCATTAAAT	180
40	TCGTCAATATT TCCAATTTTG AGTGThAAAA ATGTCACTTT TAAACTTTC	229

## (2) INFORMATION FOR SEQ ID NO: 4580:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4580:

55	CGGGGACTCn AACCCGTGTT GACCGCCGTG GAAAGGGCGG TGTCTTAACC GCTTGnACCA	60
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CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA 180  
 CGTAAGTTCG ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTCCGC ATGGGAACA 239

(2) INFORMATION FOR SEQ ID NO: 4581:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4581:

CCGnACGAAT TTACACGTGT TCCGTCGTAC TCAGGATCCA CTCAAGAGAG ACAACATTTT 60  
 CGACTACAGG ATTATTACCT TCTTTGATTTC ATCTTTCCAG ATGATTCGTC TAATGTCGTC 120  
 CTTTGTAACCT CCGTATAGAG TGTCTACAA CCCCAACAAG CAAGCTTGTT GTnTTGGGCT 180  
 CTTCCCGTTT CGCTCGCCGC TACTAAGGGA ATCGAATTTT CTTTCTCTTC CTC 233

(2) INFORMATION FOR SEQ ID NO: 4582:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 218 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4582:

TTAGTAAAAA GTCTGTGAGT AAGGGTGTAT GGAAAGTGGT TAAATATTAT AGAAAACATC 60  
 AAAGGATGTT AAGAAATACA ATTTATTACC CAGCATTTAA TAATGGTGCT ATAGAAGGAA 120  
 TTAATAATAA GATAAAATTA ATCAAGTGAA TTTCTTTTGG TTACAGAAAT TTCAnCAnCT 180  
 TTAAAGCACG TATAATGATG GATTTTCAGC TTGTACAA 218

(2) INFORMATION FOR SEQ ID NO: 4583:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4583:

TAATAAACAT GCCATACGTA ATAAGTGGCG TTGTATTAAA ATCATCTATA ATAGCCATAT 60

ATTTTGAAT CATTGTAAA AATGGAATTA AAGTTCTAGT GATCTGTTGG GTTTTGGAAA 180  
 TAGGTCATAG GGTAAAAACn TTTTGGAGAA TTTGTCGCTA TTTGTAAAT TGTATCCCGG 240  
 5 CTTGAAGTTG G 251

## (2) INFORMATION FOR SEQ ID NO: 4584:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4584:

TTTAGGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTGTA GCTTCGCAGA 60  
 20 nTAACCCACT CCTCTTAACC TTCCAGCACC GGGGCAGGCG TCACCCCTAT ACATCACCTT 120  
 ACGGTTAGCA GAGACTGTGT TTTTGATAAA CAGTCGCTnG GCCTATTCAA TGGGGGCTCT 180  
 TCTGGGGGTT AAACCTAAAG AGCAACCCTT CTCCCGAAGT TACGGGGTC 229

## (2) INFORMATION FOR SEQ ID NO: 4585:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4585:

TTATAAAAAG ATTTAAACGC GTTATTAATC TTGTGAGTGT TCTTTCGAAC ATAGCGATT 60  
 TTTCTTATGA ATTCAAGCTT ATTTAAACT CTTTATTCAC TCGGTTTTGC TTGGTAAAT 120  
 40 CTATATTTAC TTACTTATCT AGTTTTCAAT GTACAATTnC TTTTGTAGCA AGCGCTCGCA 180  
 TACTGCTnTA TTTTCAAAAA ATCAAATGCT CATTTACA 218

## (2) INFORMATION FOR SEQ ID NO: 4586:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4586:

GGAATTCCAC TTTCTCTTC TGCACTCAAG TTTTCCAGTT TCCAATGACC CTCCACGGTT 120  
 GAnCCGGGGC TTTTCACATC AGACTTAAAA AACCGCCTAC GCGCGCTTGT ACGCCCAATA 180  
 5 ATTCCGGATA ACGCTTGCCA CCTACGTATT TACCGCGGGC TGCTGGCAGC TATThAGCCG 240  
 T 241

(2) INFORMATION FOR SEQ ID NO: 4587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4587:

20 CAGCCACCTG TTGCCACCAG CTACACTTGC ATTGTTTGCT ACGACACGCC CAAACAATGC 60  
 TGAAGTGAAT AAGAAATCAA TCATTTGCTC TTCTGTAA TCAATGTGTTT TTTCTAATTT 120  
 25 AAAAAGTGCA CCGGGAATGG TACCCGAGGA ACCAGCTGTT GCGGTTGCAC AAATAATACC 180  
 CATCGCAGCA TTGACTTCAT TGTTGCAAGG CACChTTGAC TGCGGCAATC ATTCATATCC 240  
 GACnAAGCAG ATG 253

(2) INFORMATION FOR SEQ ID NO: 4588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4588:

40 ATGAACGGGT GGTAGCGAGT GGACGAAAAA CATCAATGAA AAGCTAGCTG TAGTTGCAAG 60  
 AGAAACTGGC TTACGATGGC ATTGGATCAA CACATGCGGC ATTGAGAAAT CCACGCATGG 120  
 45 CTGAGACGTT TACGATTGCG CGAAAAATGA ATCCTGAAGG CATTTTAGCA ATGTTGGTGC 180  
 GGACGTACCA GTAGAAAAGG CTTTGGAAGC AGTTGAAT 218

(2) INFORMATION FOR SEQ ID NO: 4589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 55 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4589:

GCCATGGCTC CACAGGTAGG ACTCGAACCT ACGACCGATC GGTAAACAGC CGATAGCTCT 60  
 5 ACCACTGAGC TACTGTGGAT TAATATTATG CCTGGCAACG TTCTACTCTA nCGGAACGTA 120  
 AGTTGACTA CCATCGACGC TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT 180  
 10 GACCTCCTTG CTATAGTCAC CAGACATATG nATGTA 216

## (2) INFORMATION FOR SEQ ID NO: 4590:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4590:

AGATTAAAT AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC 60  
 ATCnCATTCa TTTCTTGTCT AGCAACGTTT TACTCTAGCG GAACGTAAGT TAGCTACCAT 120  
 25 CCTCGGCTAA GAACCTTTCT TGACTTGTGA CAATCGGCTT GCTTCTTTCC TCTCCTTCGG 180  
 CTCTCGCTAC TCAATTAGC TCTACTAAAC TCGGTTGCGG CTCTTTTCTn GTTT 234

## (2) INFORMATION FOR SEQ ID NO: 4591:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4591:

AATTGACTGA CTTCTGTTTA CCGCGTGTTT AATATTGTTA TACATATATT CTAATTGCAC 60  
 ATTTAAACTT CGTAAATGCC AATGTGnGTG GGACAGAAAT GATATTTTCG CAAAATTTAT 120  
 TTCGTCTGCC CACCCCAACT TnCACATTA TTGTAACCTG ACTTTCCGCC AGCTTCTATG 180  
 45 TTGGGGCCCC GCCAACTTGC ACATTATTGT AAGCTG 216

## (2) INFORMATION FOR SEQ ID NO: 4592:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4592:

ATTCCGGATA ACGCTTGCCA CCTACGTATT ACCGCGGCTG CTGGCACGTh TTAGCCGTGG 60  
 5 CTTTCTGATT AGGTACCGTC AAGATGTGCA CAGTTACTTA CACATATGTT CTTCCCTAAT 120  
 AACAGAGTTT TACGATCCGA AGACCTTCAT CACTCACGCG GCGnTGCTCC GTCAGGCTTT 180  
 10 CGCCATTGCG GAAGATTCCC TACTGCTGCC TCCCCG 216

## (2) INFORMATION FOR SEQ ID NO: 4593:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4593:

TTGGACTAGA ACCAATGAAG GACGTTACTA ACGACGATAT GCTTAAAGGA GCTGTAAGTA 60  
 AGCTTTGATC CAGAGATTTC CGAATGGGGA AACCAGCAT GAGTTATGTC ATGTTATCGA 120  
 25 TAGTGAATA CATAGCATAT CAGAnGGCAC ACCCGGAGAA CTGAAACATC TTAGTACCCn 180  
 GTGGAAGAGA AAGAAAATTC GATTCCCTTA GTAGCGGCGA GCAGAACG 228

## (2) INFORMATION FOR SEQ ID NO: 4594:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4594:

CAATCGTTGA AGGAAATGTA CCAGCAGCAA TCAAAGACAA AGAAATTATT TCTGTAGACA 60  
 TTTCATCATT AGAAGCTGGA ACGCAATATC GTGGTGCTTT TGAAGAAAAT ATTCAAAAAT 120  
 45 TAATCGAAGG TGTAAATCT TCACAAAATG CCGTACTATT CTTTGATGAA ATCCATCAAA 180  
 TTATCGGTTT AGGTGCCACA GnaAGTGGAT TCCAGGTTAG CCAAAGGGGT TAATCTGGAT 240  
 TAATTTTTTT Th 252

## (2) INFORMATION FOR SEQ ID NO: 4595:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4595:

5 ACTCTCTAGT GACCGATAGT GAACCACTAC CGTGAGGAGA AGGTGAAAAG CACCCCGGAA 60  
 GGAGnTGAAA TAGAACCTGA AACCGTGTGC TTACAAGTAG TCAGAGCCCG TTAATGGGTG 120  
 10 ATGGCGTGCC TTTTGTAGAA TGAACCGGCG AGTTACGATT TGATGCAAGG TTAAGCAGTA 180  
 AATGTGGAGC CGTAGCAGAA GCACGGTTCT GGAATAGGGG CGTTTTAGTT ATTTTGGGTC 240  
 GTTACCCGGG AGnAAAGG 258

## (2) INFORMATION FOR SEQ ID NO: 4596:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4596:

25 CCTACCGCTG CAGCCGCTGG ATCTGCTGGA GTTGCACTAG GATCTGCCGG TGCCGCACGT 60  
 CTACTTCTCT TTTTCGGTCT ATTAGATGCT GGTTCAAGAA TTGCAACTAG CTCTGGTTTA 120  
 30 TTTGAAGAAT GACGAACATC TTCTGAATT TCCTTTAAAG TAGATGTCCT CCTGAACCAT 180  
 TnCATGTGTT AGTTGGGTAC ATTAATGCnG TATTATCGAC ACTACATCA 229

## (2) INFORMATION FOR SEQ ID NO: 4597:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4597:

45 GCTCACCTTA GAATTCTCAT CTTGCACTCA CCTGGTGGTC GGTTTGGCGG GTAGGGTCAC 60  
 CTATTTTCTA TCTAGCAGGC TTTTCTCGGC AGTGTGAAAT CAACGACTCG AAGnCACAAAT 120  
 GGTCTTCTCC CCATCACAGC TCAGCCTTAA CGAGTACCGG ATTTGCCTAA TACTCAGCCT 180  
 50 TACTGCTTAG ACGTGCAATC CAATCGCAGC CTTGCGCTAT CCTACTGnGG TCCCCCATC 240  
 GATTAA 246

## (2) INFORMATION FOR SEQ ID NO: 4598:

(A) LENGTH: 223 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4598:

AAGAAAATAA AGAATGCTAC AATTACGATT GCAATCAAAC CAAAGAACCA TAATGATGTG 60  
 TACCAAGTGC TGCACCTTTA GTAATGACAA CGTTTAAACT TAGCAACATA ACTACTAGAA 120  
 CAATTAGCCC TGCAACGTCA AATTTATGTG TATTGGTAAT TTCTGATTTC GTTTCAGGCG 180  
 TCCCTTTGAT GAGTAGCATT GAAAGTACGG nAACGATGnG TTG 223

## (2) INFORMATION FOR SEQ ID NO: 4599:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4599:

nTnTCACTGT TTGACCCGGT ACCGTGTCAG ATAATCCCGC ACGCAATGCA ATCGTTCGTG 60  
 CAATGTTTTG GCCTTGTAAT CCTTCTGGAA AAGCCGTACC AACAAATGACA TCTTCAATCA 120  
 TATTCTTATT GAATTTCCG TCAATACGTT TCAATACGCC TTGTAATACT TTGGCTGCGA 180  
 CATCATCAGG TCTTTCGTGG AATAATGCGC CTGCTTTGCG 219

## (2) INFORMATION FOR SEQ ID NO: 4600:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4600:

AAGGTTAAGA GGAGTGGTTA GCTTCTGCGA ATACCGAATC GAAKCCCCAG TAAACGGCGG 60  
 CCGTAACATAT AACGGTCCTA AGGTAGCGAA ATTCCTTGTC GGGTAAGTTC CGACCCGCAC 120  
 GAAAGGCGTA ACGATTTGGG CACTGTCTCA ACGAGAGACT CGGTGAAAAT CATAGTACCT 180  
 GTGAAGATGC AGGTTACCCG CGGACAGG 208

## (2) INFORMATION FOR SEQ ID NO: 4601:

(A) LENGTH: 286 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4601:

10 AGTGCCAGTG ATTAAGTGCA TTTTCAATA GATCAGGGAA GACTACCAAG CTTATGTTGA 60  
 AGGACATCTT TTGGCGTTAC CGGTGGGCA GGTATGTTGT ATTACCGTTC ACAACAGCAT 120  
 CACTTGAACA ACATTGTGTA ACGGATTATT TGGCAATTCG TTATTGTCGA ACAnTGcNAG 180  
 15 TTGGTGAGAT TTAATCATCG CTAAAGATGT GAAATAGATC GAAAATGGTT TAAGCAAACG 240  
 TTGCTCAGGT GTTACTACGT GATATGCCTA GCGAGTATAC TACAAC 286

## (2) INFORMATION FOR SEQ ID NO: 4602:

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## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4602:

30 ATATGGCTAT GGTATTCACA TATCGATnAA CATGGACATA ACTCATGCTG GGTTCCTCCA 60  
 TTCGGGAAAT CTCGGGATC AAAGCTTACT TACAGCTCCC CAAAGCATAT CGTCGTTAGT 120  
 AACGTCCTTC ATGGCTTCTA GTGCCAGGCA TCCACCGTGC GGCCTTAATA ACTTAATCTA 180  
 35 TGGTTCCACC CATTTTATA GGTCAAACGG TAACATGAGG TAGGGTCTTT TATAAAAAGG 240  
 nTTAAACGGG GTATTAATCT TGTG 264

## (2) INFORMATION FOR SEQ ID NO: 4603:

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## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4603:

50 GAAACGTTAG CACAAGCCAT GAACCAATTA GGTGGAAAGA GTAATAGTGG TGAAGGTGGC 60  
 GAAGATGCAA AACCGTTATG AAGTACAAGT TGATGGAAGC AACAAAGTAA GTGCGATTAA 120  
 ACAAGTTGCT TCTGGGCGTT TTGGTGTAnC TAGTGATTAT TTACAACATG CCAAAGAATT 180

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TATCCn

246

## (2) INFORMATION FOR SEQ ID NO: 4604:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 248 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4604:

ATTAAC TAAC ATGGGCATCT ACGATGGAAA CAGACGTGGT ATCCTCGCTA TTATCCAGCT 60  
 AnCGCCATGC TGGCTCGTTT TTCAAATCAA GCCATTTTAA ATTTTGAAA GGTGTATGGA 120  
 CCAAGCCCTA TGACATTGCA TTCACCGATT GAACACGATG TTATCGCCAT GTCTCATGGA 180  
 GAAAATCAAG AGCATCATTG AGCAGTATCG CGATGCTACA TTACGCGCGA TTAAAGCAGn 240  
 TTTGATGG 248

## (2) INFORMATION FOR SEQ ID NO: 4605:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 246 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4605:

CAAGTTTTCC AGTTTCCAAT GACCCTCCAC GGTGAGCCG GGACTTnTCA CATCAGACTT 60  
 AAAAAACCGC CTACGCGCGC TTTACGCCCA ATAATCCGG ATAACGCTTG CCACCTACGT 120  
 ATTACCGCGG CTGCTGGCAC GTATTAGCCG TGGCTTTCTG ATTAGGTACC GTCAAGATGT 180  
 GCACAGTTAC TTAACACATG ATGTTCTTCC CCTAAATGAA CAGAGTTTTG TTTTGTTTTn 240  
 TGGGTT 246

## (2) INFORMATION FOR SEQ ID NO: 4606:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4606:

TGTATCTGCA GTTAAATCAT GTnTCGCTTG GTTTAATGCT GTTAATGCGT TATCGACACG 120  
 ATGTTTTTCA TCTGAAATTT GTTGTGCACT TGCATCGCCA TTGTCAATAA CACGTTGAGC 180  
 5 TGCAGTTATT TCAGTTTCTG CTTCACGCTn CT 212

## (2) INFORMATION FOR SEQ ID NO: 4607:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4607:

TAGTCAAGAT GAGAATTCTA AGGTGAGCGA GCGAACTCTC GTTAAGGAAC TCGGCAAAAT 60  
 20 GACCCCGTAA CTTCGGGAGA GGGGTGCTCT TTAGGGTTAA CGCCCAGAAG AGCCGCATGA 120  
 ATAGGCCCAA GCGACTGTTT ATCAAAAACA CAGGTCTCTG CTAAACCGTA AGGANTGTAT 180  
 AGGGGCTGAC GCCTGCCCGG TGCTGGAAGG TTAAGAGGAG TGGTTAGCTT CTGCGAGTAC 240  
 25 GGAATCGAAG CCCAGTAAA CGGCGG 266

## (2) INFORMATION FOR SEQ ID NO: 4608:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4608:

TTCAGTACGT AAATACGCAC GTGAAAAAGG TGTTAnATTA AAGCAGTTTC TGGATCTGGT 60  
 40 AAAAATGGTC GTATTACAAA AGAAGATGTA GATGCATACT TAAATGGTGG TGCACCAACA 120  
 GCTTCAAATG AATCAGCTGC TTTACTGACA AGTGAAGAAG TTGCTGAAAC TCCTGCAGCA 180  
 CCTGCAnCAG TGAACATTAG AAGGCGACTT CCCAG 215

## (2) INFORMATION FOR SEQ ID NO: 4609:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GGGTTTCATAC ATGTCAATAG TAACCGTCTT AACTTGTTGT CGATTTTTTA AATCGAATCG 60  
 CTCGAAATAG GCACGCAAGA ATCTTGTAGT TCTATTTTCT AAAATATCTA TAACATCATG 120  
 GTATCATTAT CTATAAAAT GAAACTCATT GATCCAGTTA CATTTTTAAC GCTTTTAAAT 180  
 TCATCCATAG CGATGTGGTT CCTGCCAACC ATTAAAGGGG TTAATTCnGA ATnGATTAGC 240  
 C 241

## (2) INFORMATION FOR SEQ ID NO: 4610:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4610:

ATTCAATTTCT TGTCTAGCAA CGTTCTACTC TAGCGGAACG TAAGTTAGCT ACCATCCTCG 60  
 CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC 120  
 TTAATCATT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG 180  
 TTTCAnTTTCG CCAAGCCATT TTTCTTTGGT GnTTA 215

## (2) INFORMATION FOR SEQ ID NO: 4611:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4611:

GTGCCATCTT TCTTCATCAA TTCATTAATA ATTGCTGGGA CGCCACCAGC TTCATGCACA 60  
 TCATGCATTG AATACGATGA ACTAGGTGCT ATTTTGTGATA AATATGGCGT GCGTTTGGCA 120  
 ATAGCATTAA TCGCTCTAA GTCATAATCA ATACCAGCTT CATTGGCAAT GGCTAACGTA 180  
 TGCAGTACCG TGTTTGTGTA ACCACGGCAC ATCTTCGCCA ATTTCTTCTT TAAACAAGTT 240  
 TAAATTATCT TGTGATTGAG GTAAATCCAT CTTGTTAGCT ACTACGATTT GAGGTCTATC 300  
 TTCTAAACGT TGCTCGTACG GCGGCTAATT CTGGATTAAT GACTTTATAA TCTTCAATAG 360  
 GGTCTCTACC TTCAGAACCG CTCCATATCC ATCCTGTGGA 400

## (2) INFORMATION FOR SEQ ID NO: 4612:

(A) LENGTH: 258 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4612:

10 AATACTATTA AGAAGTCCTG AAAAATTCAC ATTAGCAGTT GGATTGTTCA ACTTTATTAA 60  
 TGATAAGTAT GCAAATAATT TCACAGTGTT TGCAGCAGGG GCAATTATGA TTGCAGTACC 120  
 TATAGCAATC GTATTCTTGT TCTTGCAACG CTATTTAGTA TCAGGTTTAA CAACAGGTGC 180  
 15 CGACCAAAGG GTTAGTTTGA ATTTAGGAGT GGGGCCAGAT TGGTTAAGGA CCnCTAATG 240  
 ACCGTTAAGG TThAAAGG 258

(2) INFORMATION FOR SEQ ID NO: 4613:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4613:

30 GACTTCGTTT CAGTGTA AAA TTTTCTAAT GTAACAGATA TGCTATTATT CATTGGAATG 60  
 ATTAGTGCTT CATCTTTTTT ACCCCAATAT TTTATAAGTG CAATTCGTAT GTGCACGTGC 120  
 TTTGCCACTT TTAATCAACG CTTAACCTCC TAAATTCTCA ATCCAAGTAT GTGCTGCACC 180  
 35 AGCTTTTTTC TACAGCTTTT ACAATATThn 210

(2) INFORMATION FOR SEQ ID NO: 4614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4614:

TAGCGTATTA ATCGGCGGAT CGGCTGAGCG TATCTGAGTC TGAATCGCTG TCTGAGTCTG 60  
 50 AGTCGTATCC GAGTCTGAGT CGCTGTCTGA nTCTGAATCA CTGTCTGAAT CCGnATCGCT 120  
 ATCTGAATCT GAATCGCTAT CCGAGTCTGA GTCGCTGTCT GAATCTGAAT CGCTGTCTGA 180  
 GTCCGAATCG CTATCTGAAT CTGAGTCGCT GTCTGAGTCT GAATCGCTAT CTGAA 235

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4615:

ATGTGCGTGG TTTATTTTAA TAGGTTAGTA ATATATTAGG TCATGTTATG TTTAAATTTA 60  
 TAATGAATAA ATAATTTAGA AATATGCTTC CGATTGTTTCG ATGCTTTAAT TCAGTTAGAA 120  
 GCATCATAGA ATGCATGATT ACTGTTGTAA AGATACGTAA TGTTTTGTAT TGACTGTATG 180  
 TCnTTGGATA GAGTTACAAA CTTATTTTG 209

## (2) INFORMATION FOR SEQ ID NO: 4616:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4616:

ATGCGCAAGA TATGGAGAAC ACCATCGCGA AGCGACTTTC TGGTCTGTAA CTGACGCTGA 60  
 TGTGCGAaAC nTGGGGATCA AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT 120  
 GAGTGCTAAG TGTTAGGGGG TTTCCGCCCC TTAGTGCTGC AGCTAACGCA TTAAGCACTC 180  
 CGCCTGGGGA GTACGACCGC AAGTTGGAAA CTCAAAGGAA TT 222

## (2) INFORMATION FOR SEQ ID NO: 4617:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4617:

CAGTTTGCAA CACCCCAATT CTTGCCAGTC AGCATGATTC TGTTCAATTC TGCGATTTCT 60  
 TTGTCGATAT TTTCAAATCT TGTTGGACTT GATCTAAATC AATTGGTGCT TCTTCTTCGA 120  
 ATGTATCAAC ATATCGCGGT ATGTTTAAGT TGTAATCGTT ATCGGnGATC TCTTGTAATG 180  
 TCGCGCTGTG GCTATATTTA TCAATCGTGG CTTTACGCTT ATATGGGGCT ATAATACGTT 240

## (2) INFORMATION FOR SEQ ID NO: 4618:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4618:

TCTAATTGAT AGTGAATATA ATTAGAGTTh GAGGCTGGGA CATAAATCCC TAAATTTCAh 60  
 CAGTAAGATA ATTTTCAATT AGAAAATATC TTACTGCTGT TCTCTATTIA TACAATACTT 120  
 CATTGGAATG GCTTCGCTTT CCTAGGGTGC CGTCTCAGCC TCGGTCTTCG ACTGGGCACT 180  
 GCTCCCTCAG GGGTCTCGCC ATTTAATACT ACGTAT 216

## (2) INFORMATION FOR SEQ ID NO: 4619:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4619:

ATGTATCGCG CCGAGCAACA CAAGATAAGC ATTGTAGATG TGGATGCCTT AACTGGGCAA 60  
 GCGATTnGTC GTCCTAAAC AGGTACATAT GCGCTATCTG ACCTAGTCGG TTTAGATATT 120  
 GCAGTGTCTG TAATTAAAGG CATGCAACAA GTACCTGAAG AACACCCnT ATTTTCATGA 180  
 TGGTCAAAT TTGTAAATAC GTTGTTTTGA CAATGGGCGC ACCTCGGACC GTAAAACG 238

## (2) INFORMATION FOR SEQ ID NO: 4620:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4620:

AACCATTGAA GCACCCCAATT ACGTTTTGGC TGACACGnAC GTATATCGCC TGCCCAAGCA 60  
 GATGCAGCCT TATTAACACC TGAACCACTT CGAACGCCAC TACCTTTAAG TGACTTCAAC 120  
 CATTTTTCCT GGATCTTTAG CTGTATGCAT TGCCCTGGAT GCGACCCTTG nCATCAATTG 180

TTGACCAGC

249

## (2) INFORMATION FOR SEQ ID NO: 4621:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4621:

TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCA AGAAAGAACG 60  
 TAAATTTAAT CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG 120  
 TGAGAAGACA ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA 180  
 AGGTGAATCG AAGAGAAATC ACAAAGTCCG TTTTGGTTTA CAGGTACGGC AGAACGATAC 240  
 ACAGTCTCGG GCGATTGTCG AGTCCAC 267

## (2) INFORMATION FOR SEQ ID NO: 4622:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 231 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4622:

CAAAAGGTAG TTAAATTAG GAGTGGGGAA ATTGATAAGA CCACTAATGA CGATAAAGAT 60  
 TAAAAGGAGG ACGTTATGAT GACGATTAAA GTTGGATCAT TGGGTGTGGT GGTATTCCAA 120  
 TGGCAAGCAC ATGCCAAGTT TACAAAAAGT TGAAATGTTG AAATGAnCGC ATTTTGTGAC 180  
 GTAGACATTT CGAAGCAGCG AGTGCGGCAG AAGCATACGG ACTGACAATG C 231

## (2) INFORMATION FOR SEQ ID NO: 4623:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 301 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4623:

CGAAACCGGC CCGACCCGGA CCnACCCGAG GAAAGGTACC CnAAAGnTGA AGCCCCGGGAA 60

CCCAACACCC ACCCGGACAC CAGAAGTGCC GGAGTGAGCC AGAAACTCCA ACACCGCCAA 180  
 CACCAGAGGT ACCAGCTGAA CCTGGTAAAC CAGTACCACC TGCCAAAGAA GAACCTAAAA 240  
 5 AGCCTTCTAA ACCAGTGGA CAAGGTAAAG TAGTAACACC TGTTATTGAA ATCAATGAAA 300  
 A 301

## (2) INFORMATION FOR SEQ ID NO: 4624:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4624:

20 CGAGGTGCTG CAGAAGGTGT CATTGCTCGT TATTTAATTG AAGAAAAGAA CTACTTAGAA 60  
 GCTGTGATTG GTTTGCCAGC GAATATTTTC TATGGGACAA GTATTCCAAC ATGTATTTTA 120  
 GTATTTAAAA AATGTCGCCA ACAAGACGAC AACGTACTAT TTATCGATGC ATCCAATGGT 180  
 25 TTTGAAAAAG GGGNAAATCA TAATCATtng GCGATGCCCA AG 222

## (2) INFORMATION FOR SEQ ID NO: 4625:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4625:

TGGAAAGTGA ATCAAAGAGG TAATATCCGT AGTCGAAATG TTGTCTCTCT TGAGTGGAATC 60  
 40 CTGAGTACGA CGGAGCACGT GAAATTCCGT CGGAATCTGG GAGGACCATC TCCTAAGGCT 120  
 AAATACTCTC TAGTGACCGA TAGTGAACCC AGTACCGTGA GGGAAAGGTG AAAAGCACCC 180  
 CCGGAAGGGG AAGTGAAATT AGGAACCCTG AAAACCCGTG TGCTTTACCA AAGTTAnGTT 240  
 45 CAAGAGGCCC CGTTTAAATT GGGGTnnAAT TGGCGGTGCC CTTTTTTGGT AGGAATTGAA 300  
 A 301

## (2) INFORMATION FOR SEQ ID NO: 4626:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4626:

5 GAATGAAGGA AGACCATATG AAAAATGGCC AACTTAAGCC AGGATACAAT TTACAAATAG 60  
 CGACAAATTC TCAATTTGTT TTATCCTATG ACCTATTTCA AAACCCAACA GATACTAGAA 120  
 10 CATTAAATCCC ATTTTTCANCA ATGATTCAAA ATACCTTCGG TTATTTACCA GAGTATATTG 180  
 TAGCTGATGC AGGTTATGGT AGTGAGCAAA ACTATATGGC nat 223

## (2) INFORMATION FOR SEQ ID NO: 4627:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 221 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4627:

25 TTGTTGGGGC CCCGCCnCGC nCATTGCCTG TAGAATTCT TTTGAAATT CTCTGTGTTG 60  
 GGGCCCCTGA CTAGAATTGA AAAAAGCTTA TTACAAGCGC ATTTTCGTTT AGTCAATTAC 120  
 TGCCAATATA ACTTCGTAGA TCATAGAACA TTGATTIATT TCCCAGCCTA TTCTTTTCAT 180  
 30 AAAAAAAGA CGGATTAATT ATCCGCTTTT TCCTTATATC T 221

## (2) INFORMATION FOR SEQ ID NO: 4628:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4628:

40 ATATATTCGT ATTTATAGTA AAATTAAATA AAGAGnATTA TATAACACGA GGTGTAGTAA 60  
 GTATGAAATT TGAGnAAATA TATAGATCAC ACTTTATTGG AAGCCTGAGT CAACACGTAC 120  
 45 GCAAATCGAT CAAATCATCG ATGAAGCGAA GCATACCAAT TTAAATCTG TATGTGTGAA 180  
 TCCACCACAT GTTAAATATG CAGCAGAG 208

## (2) INFORMATION FOR SEQ ID NO: 4629:

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 305 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4629:

5 ACAATAATGC ATCATAATGC GCAACAACAA TCAATACTGC GAAAACAGAA GCACAACAAG 60  
 TGATTAATAA TGAGCGTGCA CACCACAACA AGTTTCTGAC GCACTAACTA AAGTTCGTGC 120  
 ACACAACTAA GATTGATCAG CTAAAGCTTA CTTCAAATAA AAGAGATATA GCCATTAGTA 180  
 10 ACGTTAAAAT AACTTACAAG nTCTGTGACC AGTACCTCAC TGTGGTATGA CGCACAAGTA 240  
 TTGATACTnT ATCGAGAGCG TGAGnGAACT GAATACTGCG CTCACGGTAT TACATGCGTG 300  
 CACTG 305

## (2) INFORMATION FOR SEQ ID NO: 4630:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4630:

25 TCGACTACCA TCGACGCTAA GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGTGTGACT 60  
 CCTTGCTATA GTCACCAGAC ATATGAATGT AATTATACAT TCCAACTAG ATAGTAAGTA 120  
 30 AAAGTGATTT GCTTCGCCAA ACATTTATTT TGATTAAGTC TTCGATCGAT TAGTATTCGT 180  
 CAGCTCCACA TGTCACCATG CTTCCAnCTn GAA 213

## (2) INFORMATION FOR SEQ ID NO: 4631:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4631:

45 GAnGTGAAAT AGAACCTGAA ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA 60  
 TGGCGTGCCT TTTGTAGAAT GAACCGGCGA GTTACGATTT GATGCAAGGT TAAGCAGTAA 120  
 ATGTGGAGCC GTAGCAAAAA CnAAGTTCTG AATAGGGCGT TTAGTATTTG GTCGTAGCCG 180  
 50 GAAACCAGGT GATCTACCCT TGGTCAAGTT GAA 213

## (2) INFORMATION FOR SEQ ID NO: 4632:

(A) LENGTH: 205 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4632:

10 GCTTTTAAAT CAAATGATAG CGGAAGGGnA TTTTAAAATT ATTCGAACCA TTATTTACAG 60  
 CAGCAGATGG ATGGATTGGT GTCACAATTA TCTTTGGTGC CTTTGCATTA TTCTGGTTTG 120  
 TAGGTATTCA TGGTCCGTCA ATTGTAGAGC CAGCAATTGC AGCCATTACA TATGCGAATA 180  
 15 TCGAAGCGAA CTTCAAGTTG CTTCA 205

(2) INFORMATION FOR SEQ ID NO: 4633:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 204 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4633:

AGTTATATTG ACAGTAGTTG ATGGGGCCCC AACATAGAGA AATTGGAACA CCAATTTCTA 60  
 30 CAGACAATGC AAGTTGGGGT GGGCTCTAAC ATAAAGAAnt ACTTTTCTn TAGAAATTAG 120  
 TATTTCTTAT ACATGGGTTT TACTCAGTAT TTCCTATTCT TAAGTGCACA TTAGCAGCGG 180  
 CTAATGTGTT AAGAACTACT ACAT 204

35

(2) INFORMATION FOR SEQ ID NO: 4634:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 226 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4634:

GCCGATGGAT TAGAGTATAT GACGTGGTGG CATGTCATTA ATTTAGGTGA TGTAGGTAAG 60  
 AACGTTnGGG CAAGGTATGA GTGGTGGTAT TCGGTTACGT TAGCCCGTCT GATGTAGAAG 120  
 50 CTTTGTGTTGA AAATAATCAA CTAGATACGC TTTCGTTTAC AAAGATTAAA CACCAAGAAG 180  
 AAAAAGCATT CATTAAGCAA ATGCTGGAAG AnCCATGTGT CACACA 226

55

(2) INFORMATION FOR SEQ ID NO: 4635:

- (A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4635:

10 CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA ATATACTCTG GTAAATAACC 60  
 GAAGAGTTGT TGAATCATTG TTAAAAATGG GATTAATGTT CTAGTATCTG TTGGGTTTTG 120  
 AAATAGGTCA TAGGATAnAA CnGTACGGAG AATTTGTCGC TATTTGTAAA TTGTATCCTG 180  
 15 GCTTAAGTTG GCCATTTTTTC ATATGGTC 208

## (2) INFORMATION FOR SEQ ID NO: 4636:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 228 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4636:

TTTTTCTTTG TGTTTATTTT TATTTTGAAC GTTTTAGGAC ATAAAAAATA GTAGACCTTG 60  
 30 CGGTCTCAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA 120  
 CGTAAGTTGG CTACCATCGA CGCTAAGAAC CTTTCTTGAC TTGTGACAAT CGCTTGCTTC 180  
 TTTCCGCTTC TTCTGCTCGn GCTTACTCAT TGAGCnCTAC TAAACTCG 228

35

## (2) INFORMATION FOR SEQ ID NO: 4637:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4637:

CATGGTTCAA AAGTGAAAGA CGGTCTTGCT GTCACCTATA GATGGATCCG CGCTGCATTA 60  
 GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA TAGCCGnCT GAGAGGGTGA 120  
 50 TCGGCCACAC TGGAGCTGAG ACACGGTCCA GACTGCTACG GGAGGCAGCA GTAGGGnATC 180  
 TTCCGCAATT GCGGAAAGCT GTACGGGCAA CG 212

55

## (2) INFORMATION FOR SEQ ID NO: 4638:

(A) LENGTH: 256 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4638:

10 ATnTnATTAA ATAGAGAACA GCAGTAAGAT ATTTTCTAAT TGAAAATTAT CTTACTGCTG 60  
 TTTTITAGGG ATTTATGTCC CAGCCATTTT TGTATTCATA TTAAATTTT GATAATTTTT 120  
 CAGGAAGCAT TTAAATTTTA CTAATGAAGC CATATTTTTA GATTAACCAA AATTAATATT 180  
 15 TACATTTTCT AACCATTTTT ATGTAACATT TACAGTTCCA AAAATGGGGG TAATAATCCA 240  
 GGTTAGGATA AAGAGG 256

(2) INFORMATION FOR SEQ ID NO: 4639:

20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 209 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4639:

30 AnAGnAACCA CTACATAATA AATCATTAGT GGCTCTTTAT CATTCTGTG CCACTCCCCCT 60  
 GAGAAGTTTA AAATTTTATA TGTGCTTG TTATGTTAAG GGAATTAACA TGGTTGTCTT 120  
 GTTTATATTA TGTGATTCCA ACATTACTAG TCCTGGTAAA TCTAATCCG TAAATGCTA 180  
 35 AATCTAACCA TCTATTAAAT TTAAAACC 209

35

(2) INFORMATION FOR SEQ ID NO: 4640:

40

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 224 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4640:

nGnAAAGGTG AAAAGCACCC CGGAAGGGAG GTGAAATAGA ACCTGAAACC GTGTGCTTAC 60  
 50 AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA CCGGCGAGTT 120  
 ACGATTGAT GCAAGTTAAG CAGTAAATGT GGAGCCGTAG CAGAAGCATG GTCTGAATAG 180  
 55 GTGCGTTTAG TATTTGGTCG TAGCCCGCAG AACCAGGGTG ATCT 224

55

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4641:

CACTCACnCA GATTTTAAAG TCCTGTGCGT CTGCCAGTTC CGCCACCCCG GCACTATAAA 60  
 AATGGAGCAG AAGACGGGAT TCGAACCCGC GACCCCAACC TTGGCAAGGT TTTATTCTAC 120  
 CGCTGAACTA CTTCTGCATA TCGGGGTGAA GGGAGTCGAA CCCCCACGCC GTAAGCTANG 180  
 ATCCTAAGTC TAGTGCGTCT GCCAA 205

## (2) INFORMATION FOR SEQ ID NO: 4642:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4642:

AGCTGACATG ATCAGTCAGC TTACAACAAT GTGCCGGTTG GGGTGGCTGG ACACGGCACC 60  
 CTGAGGGAAG GGCACCCGTC ATCAAAAATT CTATTTATAG AATTTTACAG TAATGTGACA 120  
 GACGGGCAAA GCGAACCATT CAATACGAAG TATTGTATAA ATAGAGAACA GCAGTAAGAT 180  
 ATTTTCTAAT TGAAAATTAT CTTACTGCTG TnTTTTTAGG GATTTATGTn CCCAG 235

## (2) INFORMATION FOR SEQ ID NO: 4643:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4643:

AGnAAGGTGG GGATGACGTC AAATCATCAT GCCCCTTATG ATTTGGCTAC ACACGTGCTA 60  
 CAATGGACAA TACAAAGGCA GCGAAACCGC TAGTCAAGCA AATCCCATAA ATTGTTCTCA 120  
 GTTCGATTGT AGTCTGCGAC TCGACTACAT GAAGCTGGAA TCGCTATAAT CTAGATCAGC 180  
 ATGCTACGTG ATAGTTCCGG GTCTnTACAC ACGCCCGTCA CACCACGGAG GGTTTTACAC 240

## (2) INFORMATION FOR SEQ ID NO: 4644:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4644:

CAGCAGGCCA CCAAAATTGT GGTCCGAGAT GTTCATATAA AACTTTATAT AATTCATCAG 60  
 TTCCTAACAT TTACACCCTC CATTTTAGAG GGAGTGGGAC AGAAATGATA TTATCGTAAA 120  
 ATTTATTTTCG TCGTCCCACC CCAACTTGCA TGTCTGTAGA AATGGGGATC CAATTCnCTT 180  
 GTTGGGGGCC CGCGGGCAAG GTnACTAGAA TGAAAAAAGC CTGTTACAAG CGATTTTCGG 240  
 TTCAGTCCAC TACTGGCAAT ATAAC TTGTA GAGCTAGGAC ATTGG 285

## (2) INFORMATION FOR SEQ ID NO: 4645:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4645:

GCTATTACTC TGCTATCAAT GTACCTAAAG CTACCGATGA TTTCCGAGAC ATAGACCGTG 60  
 CGCTTGnTG GGGGTTCAAC TGGAACTTG GTCCATTCCA ATTATGGGAT GCAATGGGGn 120  
 TACGAACGTG TTAAACAGT ATGGAAGACG AACTTGGAGA CTTACCACAA TGGGTTAGTG 180  
 ATTTAGATGG TGGCTTTTGA TAAACA 206

## (2) INFORMATION FOR SEQ ID NO: 4646:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4646:

ACAGTTACCG ATACAACTGA AGATGATAAC GATGCAGATG GTGGCGACGT TGACGTCACA 60  
 CTTACGGATC ATGATGATTT CACACTTGAT AACGGATACT TCGAGATGAT ACATCAGACA 120

CnGACAGTGA TTCAGATTCA GACAGCGACT CAGATTcGnGA TA

222

## (2) INFORMATION FOR SEQ ID NO: 4647:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4647:

GTACTATTCG TGTGTGACAA TGTTCTTCCA GCATTGCTT AATGAATGCT TTTTCTTCGT 60  
 TTAATCTTTG TAAACGAAAG CGTATCTAGT TGATTATTTT CAACAAAAGC nTCTACATCA 120  
 GnCGGGATAA CGTAAGCAAT ACCACCACTC ATACCTTGAC CGAAGTTCTT ACCTACATCA 180  
 CCGAAATTAA TGACAGTCCA 200

## (2) INFORMATION FOR SEQ ID NO: 4648:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 201 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4648:

CCACCATTAA TTTAATACCT ATTTGGGGGC TTAGCTCAGC TGGGAGAGCG CCTGCTTTGC 60  
 ACGCAGGAnG TCAGCGGTTG GATCCCGCTA GTCTCCACCA TTATTTGTAC ATTGAAAAC 120  
 AGATAAGTAA GTAAAATATA GATTTTACCA AGCAAAACCG AGTGAATAnA GAGTTTTTAA 180  
 TAAGCTTGGA ATTCATTAAG A 201

## (2) INFORMATION FOR SEQ ID NO: 4649:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 218 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4649:

AGTAAATACA GATGGAATAA ATCTTTTAAG GCTTATAAAC GTCATCTGn CATTGTAGCA 60  
 ATTCATGCTT TCAAAAGACG ATATACTACG ACACTCCTAC GAACTTGTCC AAGGATTACG 120

AAAGTCTGTG AGTAAGGGTG TATGGAAAGT GGTnAAAT

218

## (2) INFORMATION FOR SEQ ID NO: 4650:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4650:

GTGGCGGTGC GACTGTCAGA AGCACGTAA ATTAATGAAA GATACAGTAG GTGCTGATGT 60  
 AGAAGTAAAA GCCATCAGGT GCGGTACGTA ATTTAGAAGA TTTCAATAAA ATGGTTGAAG 120  
 CAAGTGCAC ACCTATTGGT GCGAGCGCAG GTGTTCAAAT TATGCAAGGT TTAGAAGCAG 180  
 ATTCnGATTA CTAATATnTA TG 202

## (2) INFORMATION FOR SEQ ID NO: 4651:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4651:

AGCGGCGGAC GGGTGAGTAA CACGTGGATA ACCTACCTAT AAACTGGnA TAACTTCnGG 60  
 AAACCGGAGC TAATACCGGA TAATATTTTA AACCGCATGG TTCAAAAGTA AAAGACGGTC 120  
 TTGCTGTCAC TTATAGATGG ATCCGCGCTG CATTAGCTAG TTGTAAGGT AACGGCTTAC 180  
 CAAGGCAACG ATGCATAGCC GACCTGAGA 209

## (2) INFORMATION FOR SEQ ID NO: 4652:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4652:

TGAAGATGCA GGTACCCGC GACAGGACGG AAAGACCCCG TGGAGCTTTA CTGTAGCCTG 60  
 ATATTGAAAT TCGGCACAGC TTGTACAGGn TAGGTAGGAG CCTTTGAAAC GTGGAGCGCT 120

CCACTTATCG TGGTTGGAGA CA

202

## (2) INFORMATION FOR SEQ ID NO: 4653:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4653:

CCGTGCGACC CCTTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC GTTCCCCGGTA 60  
 TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTTAGT CAAACGCTCT 120  
 ATCCAATTGA GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG 180  
 AACCGGTACG TGATCACTCA ACnGn 205

## (2) INFORMATION FOR SEQ ID NO: 4654:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4654:

AGACGAAACG TTGTTGTTGC GAAGATAAAT CGCACAGCGA TTGAGCCTAT CTGCTGCACC 60  
 ATTAAGTGGT GAAGTAACAC CATTATCAGA AGTGCCTGAT CAAGTGTTCA GCGAAAAAAT 120  
 GATGGTGCAG GTATCGCTAT CAAACCTTCA CAAGGTGAAG TTCGTGCACC ATTCAACGGT 180  
 AAAGTACCAA TGATTTCCTA ACCAAACATG CCATTGGTCC TGTATCAGAT AGTGGTTAGn 240  
 CTATTAATCC ACACGGGTGA GAnG 264

## (2) INFORMATION FOR SEQ ID NO: 4655:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4655:

GACGATTACA TATCATCGCT AATAACTTAG CATTAAAACC GCTTGATGCG CCACCACAAG 60

AACACAACGA ACTGGGnACA TGCTTCGGTT AAATCCATCA ATTTCAACGC TTGTnACGCG 180  
 AAATCAGTTT GCTCTTGGCT GCAGTAAATC G 211

(2) INFORMATION FOR SEQ ID NO: 4656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4656:

TTTACATTTA TCGGTTTAGT CAGATTCAAA CGTTTTCCT TCGCCAAGCC ATCTTTCTTT 60  
 GTGTTTGCTT TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTTGCGG TCTCAATGCG 120  
 GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTCGACT 180  
 ACCATCGACG CTAAGGnGCT TAACTGnTGG GT 212

(2) INFORMATION FOR SEQ ID NO: 4657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4657:

TGGGTTTCGAA nTCCAATTAG GACCCACCAT TAACTTAATA CCTATTGGG GGCTTAGCTC 60  
 AGCTGGGnAG AGCGCCTGCT TTGCACGCAG AGGTCAGCGG TCGATCCCG CTATCTCCAC 120  
 CATTATTGT ACATTGAAAA CTAGATAAGT AAGTAAATA TAGATTTTAC CAAGCAAAAC 180  
 CGAGTGAATA AAGAGTTTTA 200

(2) INFORMATION FOR SEQ ID NO: 4658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4658:

TACAGTATAT CGGGAAGACA GGATTCGAAC CTGCGACCCC TTGGTCCCAA ACCAAGTGCT 60

CTCTTGATCC GTAGTCAAAC GCTCTATCCA ATTGAGCTAC GGGCGCATAT GTTTTTATTG 180  
 AAAAn 185

(2) INFORMATION FOR SEQ ID NO: 4659:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4659:

AAGTGTTAGG GGGTTTCCGC CCCTTAGTGC TGCCAGCTAA CGCATTAAAGC ACTCCGCCTG 60  
 GGGAGTACGA CCGCAAGTGT ATAAC TCAA GGAATTGACG GGGACCCnCA CAAGGTTGGA 120  
 GCATGTGGTT TAATTGAAAn CAACGCGCAG TAACCTTACC AAATCTTGAC ATCCTTTGAC 180  
 AACTCTAGAG ATAGAGCCTT CCCCTTCG 208

(2) INFORMATION FOR SEQ ID NO: 4660:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 365 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4660:

ACGTCGCGAG AACGCAATTA GCTGAAAAAG ATTACAACAT TAGAACAAGA TTAAAGTCA 60  
 CATTTAGTGA ACATCAAAGG CCGAATAACA TCATAAATTA CGATTAGATA TAACAAAAGA 120  
 GCTTGGGACA TAAGTCCTAA AGTCTTAGGC AAGTAAAAAA GTGATTCTA TTATTTATTT 180  
 GATAGAAATC ACTTTTGTAT ATGTATTnT ATGTACAGCT CGTTGAGChC TATTTTCCTT 240  
 ATATTAGTGC CATAATACAA ACCTAGCTCT TGTTTAACTT TATTATTCCG AACTGACATC 300  
 GGTGAACCCA ATAGCCTCAT AAGCAAACAG CTTACATCAT TTTCTTGAnT GGTTTTCGTT 360  
 CTGTC 365

(2) INFORMATION FOR SEQ ID NO: 4661:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 209 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4661:

AAAGTATTTC TTTATGTTGG GGGGCACCCC ACTTTGnCAT TGTCTGTAGA AATTGGGAAT 60  
 5 CCAATTCTCC TnATGTTGGG GCCCCGCAGT TCAACTACTG CCAATATAGT GTTGTAGTGT 120  
 CTAAGACATA AAAGTTCATC TCAGTCACAA TTACTTTATA GCCTATCCAT CATCTTTTCT 180  
 10 ACATGAAATT TTTCCAAGTG ATATATTTT 209

## (2) INFORMATION FOR SEQ ID NO: 4662:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4662:

TTATGGCACT TAAAACCAGC GATGACGATT GCAGTATCAC ATGGTATCTT CAACATAACA 60  
 AATACTTTGA TTCAATTACC ATTTGTAGCA GGTTTAGCAT GGATTGTTAC AAAGCTTGTC 120  
 25 CCAGGTAAAG ATATTGCTGA TGA CTATAAA CCTCAGCACT TAAACCAAGG TCTGTTATCA 180  
 CGCACCTGGT GTTTGCATAC CAGGAACTCC AAAAGGATTA CCAAATGTnG GGGCAGAnTG 240  
 30 GCCTAA 246

## (2) INFORMATION FOR SEQ ID NO: 4663:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4663:

AATGGTGTAT TATGAGTAGT AATAATTAGC AAAGAGGTAA ATTAAGTGAT GTCGCGTCAT 60  
 TTAAGGAAGC GATTCACAAT CGAGAATCAC AAAGTACAAC TGGTATCGGC GAAGGTATnG 120  
 45 CCATTCCACA TGCCAAAGTG GCCGCAGTTA AGTCACCAGC TATTGCGTTT GGTAAATCTA 180  
 AAGCAGGCGT AGATTATCAA AGnTTTTGGT ATGCAACCAG CACACT 226

## (2) INFORMATION FOR SEQ ID NO: 4664:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4664:

5 TTCCGTCTCG GCACCATTTT AGCGCCGTAG CTCAATTGGA TAGAGCGTTT GACTACGGAT 60  
 CAAGAGGTAT GGGTTCGACT CCTATCGGGC GCGCATTTTT AAATTAATTG AATAACGGGA 120  
 GTAGCTCAGC TTGGTAGAGC ACTTGGTTTG GGACAAGGGC GCAGGTTTCA ATCCTGTCTC 180  
 10 CCGATTACTT CTAAATCCAT TTATGGGGCT ACTCACTGGG nACGCCTCTT nCAC 234

## (2) INFORMATION FOR SEQ ID NO: 4665:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 196 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear
- 20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4665:

GTACATCTAA AATCATCCAT GAAGGTTTGT TACCTGAATT ACGGAATGAT TCAACAACCTT 60  
 25 CTAAACGTTT AATTnACCAG TAAGTCTTTG CCAAGTAGCT GATTCCAACCT CATCGCGTAC 120  
 AATTTAAGTC TTCGTCAAGA TCAATCCTCT TCAAGTAAAT CTTTAATAAC CTTCTGCACC 180  
 CATTTTGGCA CGAATT 196

## (2) INFORMATION FOR SEQ ID NO: 4666:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 226 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4666:

CCGCCGAACA ACTACTTTGT TTGTTGATTC TCTCCACCTG TTTCAGTAGT TCAGATTTCT 60  
 TAGATTGTGG TTTTTTAGTT GGTGCCATGC TTAAACCTTT TCATTGATTT CAATAACAGG 120  
 45 TGTTACTACT TACCTGTTCC ACGGTTTAGA AGGCTTTTAG GTTCTTCTTG GCAGTGGTAn 180  
 GGTTTACCAG TTCAGCGGTA CCGCGGTGTT GGnCGTGTG GATTTC 226

## (2) INFORMATION FOR SEQ ID NO: 4667:

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 187 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4667:

5 GTTCTGAATA GGGCGTTTAG TATTTGGTCG TAGCCGAnAA CCGGTGATCT ACCCTTGGTC 60  
 AGGTTGAAGT TCAGGTAACA CTGGAATGGG AGGACCGAAC CGACTTACGT TGAAAAGTGA 120  
 10 GCGGATGAAC TGAGGGTAGC GGAGAAATTC CAATCGAACC TGGAGATAGC TGGTTCTCTC 180  
 CGAAATA 187

## (2) INFORMATION FOR SEQ ID NO: 4668:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 182 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4668:

25 CTAAGTGGAG TTGTCACAAC ATCTTTAAAC GTTCCAGGTA AATAGTCTTT TGCCATTTCT 60  
 GAAAATGCTT TTGCCAACGT TTTATAAATA TCCCAGTCTG AACGCGATTC CCATAACGGA 120  
 TCAATGGCAG GATTGAAAGG ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATGn 180  
 30 TT 182

## (2) INFORMATION FOR SEQ ID NO: 4669:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 182 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4669:

40 AGTTACGTTA AAAGATGAAA ACGACAAAGT TTTAAAAACA GTTACAACAG ATGAnAATGG 60  
 TAAATATCAA TTCACTGATT TAAACAATGG AACTTATAAA GTTGAATTCG AGACACCATC 120  
 45 AGGTTATACA CCAACTTCAG TAACTTCTGG GAAATGATAC TGCAAAAAGA TTCTAATGGT 180  
 TT 182

## (2) INFORMATION FOR SEQ ID NO: 4670:

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 185 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4670:

5 GGGGCAAAGT CATThCATAG ATTAATGGTT CTCCGATACC TAGGAAACCA ACTGGCAATG 60  
 CACCTTTTAA AGTATTACGT AATGTTGTGT TGCCTTTACA TCTTACCCAA AGTGCTAATG 120  
 CGGCACCTAC TTGTCCAGCA CCAGCCATCG CTGCAATTGG CAATAAGTAA GTAGCACCTG 180  
 10 ATTGG 185

## (2) INFORMATION FOR SEQ ID NO: 4671:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4671:

CTGACGAACG AGAAAAGAGC GCAACGATTT AGTAGAGTAA ATGAGTTAAG CGAGACCGAA 60  
 25 GAAGAGGAAA GAAGCAAGCG ATTGTCACAA GTCAAGAAAG GTTCTTAGCG TTCGATGGTA 120  
 GCCAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAA AAAAATGGAT GCGATGACCG 180  
 30 CATTGAGACC GCAAGGnTnT 200

## (2) INFORMATION FOR SEQ ID NO: 4672:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4672:

CCCCGGGTAC AGTTATTCCC CAGAGTCAAC GCGGGGGTTG GACTCGATGT CGGTCAATCGC 60  
 ATCCTGGGCT GTAGTCGGTC CCAAGGGTTG GGCTGTTTCG CATTAAAGCG nACGnTGCTG 120  
 45 GGTTCAGACG CGTGAGCAGT CGTCCCTAT CCGTCGTGGG CGTAGGAAAT TTGAGAGGGC 180  
 TGTCCTTAGT ACGAGAGGCC GGGATGGCAT ACCTTGGTGT ACCATTGTCTG TGCCACGCAT 240  
 50 AGTGGGTAGT ATGTGTGGAC G 261

## (2) INFORMATION FOR SEQ ID NO: 4673:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4673:

ATAGGGCGTT TAGTATTTGG TCGTAnCCAG AAACCAGGTG ATCTACCCTT GGTCAGGTTG 60  
AAGTTCAGGT AACACTGGAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA 120  
ACTGAGGGTA GCGGAGAAAT TCCAATCAAA CCTGGAGATA GCTGGTTCTC TCCGAAATAG 180  
CGTT 184

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(2) INFORMATION FOR SEQ ID NO: 4674:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 203 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4674:

CCCAGTCAAA CTGCCCCCCT GACACTGTCT CCCACCACGA TAAGGTCGTG GGTTGAGAAA 60  
GCCAACACAG CTAGGGTAGT ATCCCACCAG CGTnCTCCAC GTAAGCTAGC GCTCACGTTT 120  
CAAAGGCTCC TACCTATCCT GTGACAAGnT GTGCCGAATT TCAATATCAG GCTACAGTGA 180  
AAGCTCCACG GGGTTCTTTC CGT 203

30

(2) INFORMATION FOR SEQ ID NO: 4675:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 229 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4675:

nnGTTTGTAA ATAATATGGT GGAGACTAGC GGGATCGAAC CGCTGACCTC CTGCGTGCAA 60  
AGCAGGCGCT CTCCCAGCTG AGCTAAGCCC CCATAATAAT TACAGTATAT CGGGAAGACA 120  
GGATTGGAAC CTGCGACCCC TTGGGTCCCA AACCAAGTGC TCTACCCAGC TGGAGCTTAC 180  
TTTCCCGGTA TTATTTAACG CGGCCCGATA GGGAGTCGGA ACCCATTA 229

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(2) INFORMATION FOR SEQ ID NO: 4676:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 178 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4676:

TCTAAAAATC GCGCACTTAA ACCGCTTATG ACAATCATT TACCTCAAT ATGCTTGTCA 60  
TCACTTGCCT TTATCGTCGT TCATTGGCTA TATAGTTAAT ATGAAAAGAC GCTCAAACAC 120  
TTACAAATTT AGTGTGCGnGA GCGTCTTATT TTTATACTTT AAAAGTCGTA TTGGTTGT 178

(2) INFORMATION FOR SEQ ID NO: 4677:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 286 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4677:

GCAAGTAAGC ATAATGTGGA GCCGTAGCGA AACAGTCTGA ATAGGGCGTT TAGTATTTGG 60  
TCGTAGACCG GAAACCAGGT GATCTACCCT TGGTCAGGTT GAAGTTCAGG TAACACTGAA 120  
TGAAGGACC GAACCGACTT ACGTTGAAAA ATGAGCGGAT GAACTGAAGG TAACCGGAGA 180  
AAATCCCAAT CGAACCCTGG GAGATAAGCT TGGGnTCTCC TCCCgAAAAT AAGCCTTTTA 240  
GGGGCTTAAG CCTCCAAAGT GGATGATTTA ATTTGGAAGG TAAAAA 286

(2) INFORMATION FOR SEQ ID NO: 4678:

35

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 229 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4678:

CACACGGCTT ATGGTAACAA AAAATTCCTT TGGAGCATT TGGAGCGGAA GATAGGTTTA 60  
CACCTATACC TCGTTCCGGA AGGAnTGTTT TAAAAGTGAA CTACTCCGC AATATTAAAT 120  
ATGGAGCGGA GATAGGATTT ACACCTATAC CTCATTCCAG AGGATGTATT CTAAGAGTGA 180  
AATACTCCCC ATATATTAA TATGGAGCGG AGATAGGATT GACCATACn 229

(2) INFORMATION FOR SEQ ID NO: 4679:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 173 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4679:

ATGACTGCTT TTTATTATAC TTTACATTTT TCGTTTCGTC AGATTCAAAC GTTTTCACCTT 60  
CGCCAAGCCA TCTTTCTTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG 120  
ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTG CCTGGCAACG TTC 173

(2) INFORMATION FOR SEQ ID NO: 4680:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 183 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4680:

AAAAGTAACA AGAGAAGGAC AAAAAGGTGA GAAGACAATA ACGACGCCAA CAAAATCCA 60  
TTAACTGGAG AAATTATTAG TAAAGGTGAA TCGAAAGAAG AAATCACAAA AGATCCCATT 120  
AATGnATTAA CAGAATACGG ACCAGAAACG ATAACACCAG GTCATCGAGA CGAGTTTGAT 180  
CCC 183

(2) INFORMATION FOR SEQ ID NO: 4681:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 203 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4681:

CGGTGCTTTC ACTTTCCTAC AGACTGGTTA CTATCGGTCA GAGAGAGATT TAGCnTTAGG 60  
AGATGGTCCT CCCAGATTCC GACGAATTTT ACGTGTTCCTG TCGTACTCAG GATCCACTCA 120  
AGAGAGACAA CATTTTCGAC TACAGGATTA nTACCTTCTT TGATTCATCT TTCCAGATGA 180  
TTCGTCTAAT GTCGTCCTTT GTA 203

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(2) INFORMATION FOR SEQ ID NO: 4682:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 187 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4682:

GGGTCACACC TGTTCCTCATG CCGAACACAG AAGTTAAGCT CCTTAGCGTG CGATGGTAGT 60  
 5 CGAACTTACG TTCCGCTAGA GTAGAACGTT GCCAGGCAAA AAGTGGGATG CGATGGAGCC 120  
 GCATTGGAGA CCGCAAGCCT CTGTTCTTTG ATGTCTAAAA CGTnCAAAAT AAAAGCGAAC 180  
 10 ACAAAGA 187

## (2) INFORMATION FOR SEQ ID NO: 4683:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4683:

GGCTACACTG GTCATGATGC TGCTAAACTA CGTGATTATn ATGAAACACA TCATGCTTTG 60  
 TCTGGATATG AAATGATTGA CGCAGCAAAG GTGCCATTGC AACAAATGAA GTCAATGCTG 120  
 25 CGATGGGTAT ATTTGTGCAA CGCCAACAAC TGGTTCCTCC GGTACCATCC CGGTGCAGTT 180  
 TTAAATT 187

## (2) INFORMATION FOR SEQ ID NO: 4684:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4684:

AGTGCCAAGG CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA TCCTACAGGA 60  
 AACCGTTATT AATCTTGTA GTGTTCTTTC GAACACTAGC GATTATnTCT TATGAATTCA 120  
 45 AGCTTATTTA AAACCTTTTA TTCACTCGGT TTGTGAAAT CTATATTT 168

## (2) INFORMATION FOR SEQ ID NO: 4685:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4685:

ACGGGAAGTA GCTCAGCTTG GTAGAGCACT TGGTTTGGGA CCAAGGGGTC GCAGGTTGGA 60  
 ATCCTGTCTT CCCGATTACT TCTTAAATTC CATTTTATGG GGGCTTAGCT CAGCTGGGAG 120  
 AGCGCCTGCT TThCACGCAG GAGGTCAGCG GTTCGATCCC GCTAGTCT 168

## (2) INFORMATION FOR SEQ ID NO: 4686:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4686:

ATGATTCAAG CTTATTTAAA ACTCTTTATT CACTCGGTTT TGCTTGGTAA AATCTATATT 60  
 TTACTTACTT ATCTAGTTTT CAATGTACAA TTTCTTTTGA GTCAAGCGCT CGCATACTGC 120  
 nTTATTTTCA AAAAATCAAA TGCTCATTTA CAAAAGTAAA CTCCGCTTTT AATT 174

## (2) INFORMATION FOR SEQ ID NO: 4687:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4687:

TGTTGTTGAA TATGAAGAAG ATACAAACCC AGGTGGTGGT CAGGTTACTA CTGAGTCTAA 60  
 CTTAGTTGAA TTTGACGAAG AGTCTACAAA AnGTATTGTA ACTGGCGCAG TGAGCGATCA 120  
 TACCACAGTT GAAGGTACGA AAGAATATAC AACTGAAGTA ATCTGA 166

## (2) INFORMATION FOR SEQ ID NO: 4688:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4688:

AGAACCTTAC CAAATCTTGA CATCCTTTGA CAACTCTAGA GATAGAGCCT TCCCCTTCGG 60

GCAACGAGCG CAACCCTTAA GCTATTGCCA TCATTAAGTT GGGCATCTAA TTGACTGCCG 180  
GTGACAAAC 189

(2) INFORMATION FOR SEQ ID NO: 4689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4689:

TAACCACTCC TCTTAACCTT CCAGCACCGG GCAGGCGTCA CCCCTATACA TCACCTTACG 60  
GTTTAGCAGA GACCTGTGTT TTTTGATAAC AGTCGCTTnG GGCTATTAC TGCGGCTCTT 120  
CTGGGCGTTA ACCCTAAGan ACCCTTCTCC CGAAGTACGG GGGCATTTTG CGAGTCCTAA 180  
CGAGGTCGTC GTCACCTAGA TTCTCATCTT GATACTGTGT GGTTCG 227

(2) INFORMATION FOR SEQ ID NO: 4690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4690:

AGATAATGCA CCATCAACTA ATGGATATTT ATGTCCAGTT GGGGGCCAGA AATCATAAAC 60  
GTCTTCAGTG TAAGCAACAG CATCTTCATT TnGCAGCCAA AATGCTTGA TTATGTGCAA 120  
TAACCATCGC AACTGCGCCA CACCTTGTGT TGGCTCGCCG CCTGAAGTGG GGTG 174

(2) INFORMATION FOR SEQ ID NO: 4691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4691:

TTTTTTTTTA AAAAAAGGGA AGGGAAAAan AAAAGGGAAA AAAATTTAAC CCAAGGGTTT 60  
TTAAAGGGGG CCCAATTTTT CCCAAAAAAA AAACCCTTGT GGTAAATTT TTTTAAAAAA 120

GTTAAATTTT TTTAAAAAGG GTTCCCTTTT AAATTTTGGG AAAAACCCCC TTTTTTTTTT 240  
 TTAAGGGAAT TTAATAAATT TAAGGCCCTC CCCTAAATTA AAATTAAAGG TGGGAAAAAA 300  
 AAAATTAATT AAAAACCCTA TTTTTTTTTT TTAATTTTAA ACCCAAAGG GGGTAATTG 360  
 GCC 363

(2) INFORMATION FOR SEQ ID NO: 4692:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4692:

TAGTGTCAAT TTTATTGATA TTGCAATTA AACTGAAATT TAATTTTTCG GATGTATTTT 60  
 nTTTACTTAA AGTAAATAG AACACGATTT TGATGTCTGG GAATAGTGGG AATGATAAAA 120  
 ACTACTAATG ATTGATTAAG TAGTGGTTCT TAACATTAGC CTCAGCTAAT TGTTACTTAA 180  
 AAATAGGAAT ACATGAGTAA AACTCAnTGG 210

(2) INFORMATION FOR SEQ ID NO: 4693:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4693:

ATAGTAGTAA AGTATTTTCT TCCAACATT TATTTTGATT AAGTCTTCAT CATTAGTATT 60  
 CTCAGCTCCA CATGCACCAT CTTCCACCTC AACCTATTAA CCTCATCATC TTTAGGATCT 120  
 TATAACCAAT TGGAAATCTC ATCTTGAGGn nGCTTCATCT TAGATGCTTT CACACTTATC 180  
 CCTCCACACA TAGCTACCCA GCTATCCGT 209

(2) INFORMATION FOR SEQ ID NO: 4694:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 222 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

GCACATTAAC CnAAGCACCA GGCCATATAG CAATTGTTGA TACAGTATTT AAATATTTAG 60  
 CATGTGACGG AATAGTTACA TATGTATTCA CTAAGGCCAT AATGACAAAT CCATTAAAAA 120  
 5 GTTGGATGCT TATTCGACCC TGCTAGATGA TCTGATGAAC GGAACGCATA TTAAATAAGT 180  
 ACGTGGTTAT GGATCAGTAA GATACTCTAC CAGTTACCAG nG 222

## (2) INFORMATION FOR SEQ ID NO: 4695:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4695:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60  
 TCTATTTCTT CTATTGTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT 120  
 TCTTCAACTA AGTCACGATA TAATGTTTTT GAATTTTCG 159

## (2) INFORMATION FOR SEQ ID NO: 4696:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4696:

AATATGGTAG TTTTAACTT ATCTATTAAG GTACAATTGA CCAAATCGAT AAAACAAATA 60  
 ATACGTATCG TCAGACAATT TATGTCAATC CAAGTGGAGA TAACGTTATT GCGCCGGTTT 120  
 40 TAACAGGTAA TTTAAAACCA AATACGGATA GTAnTGCATT A 161

## (2) INFORMATION FOR SEQ ID NO: 4697:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4697:

CCAAACTCAA TATGGCTTTA TTGGCACAGG GAACAGATAT GGAAGGTTTT ATTTATGGnT 60

ATATGGGATC AACACACAAA GCCGGACGCA GTGAATATTA CGCAAAATGA

170

(2) INFORMATION FOR SEQ ID NO: 4698:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 161 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4698:

CCACGGCTAA CTACTGCCAG CAGCCGCGTA ATACGTAGTG GCAAGCGTTA TCCGGAATTA 60  
 TTGGGCGTAA ACGCGCGTAG GnGTTTTTTA AGTCTGATGT GAAACCCACG GTCAACCGGA 120  
 GGGTCATTGG AAACCTGAAA CTTGAGTCAG AAGAGGAAGT G 161

(2) INFORMATION FOR SEQ ID NO: 4699:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 248 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4699:

TAAATCTTCA TCAATATGAT CTAACCAATA TTGATAAAAC CTTGATGTGT TTCGTGTCAA 60  
 TGACATACCA TATCGACTAG GTACCTTTTT AGAATGTTGA TTAATCACAA CAAATATCAT 120  
 GGGCAAGGTC ATCTTGCAAA ATGGATTGGA TTCAAGTGGG AGGGnCGATG ATGGACGTGC 180  
 TGCATGCACT GATGACCCCTT TTTGCCCAT TTTGGCAAATC CCACCATGAA ATGACTGACG 240  
 CGGACGCh 248

(2) INFORMATION FOR SEQ ID NO: 4700:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 175 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4700:

CCCGACGAAG CGAACGTTTG GCACTGTCTC AACGAGAGAC TCGGTGAAAT CATAGTACCT 60  
 GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT 120

## (2) INFORMATION FOR SEQ ID NO: 4701:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4701:

TACAGGGTAG TGAGATTTTCG AAACAATATG GAGAAGCAGG ACTTCCTGGA AAATACAATT 60  
AATGTTTATA CGAATGGTCA TGCTGGTCAA AGTTCTTGCA GGCATATGCA CCGAAAGCTT 120  
AATGATTCAT CATACTGGAG ATGCGAATGA CTATGTTGGG TAAAGGATTT ATCTGGT 177

## (2) INFORMATION FOR SEQ ID NO: 4702:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4702:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA 60  
GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTT CAACTGCCGA 120  
GAAAAGNCTC TAGATAGAAA ATAGGTGCCC GTACCG 156

## (2) INFORMATION FOR SEQ ID NO: 4703:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4703:

CTTGAAAAAG ATGGTTATTC TGTGAAGTA ATTGACTTAC GTACTGTTCA ACCAATCGAT 60  
GTTGACACAA TTGTAGCTTC AGTTGAAAAA ACTGGTCGTG CAGTnGTCAG CAAGACGCAC 120  
AACGTCAAGC TGGTGTGGT GCAGCAGTTG TAGCTGAATT AAGTGA 166

## (2) INFORMATION FOR SEQ ID NO: 4704:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4704:

GCGGTGTCTT AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGnCT CGAACCTACG 60  
ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGATTAA TATTATGCCT 120  
GGCAACGTTT TACTCTAGCG GAACGTAAGT TCG 153

(2) INFORMATION FOR SEQ ID NO: 4705:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 163 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4705:

AGGTAGAGCA CTGTTTGGAC GAGGGGCCCC TCTCGGGTTA CCGAATTCAA ACAAACTCCG 60  
AATGCCAATT AATTAACTT GGAAGTCAG ACACATGGGT GATAAGGTCC GTATTCGAAA 120  
nGGAAACAGC CCAGACCACC AGCTAAGGTC CCAAATATA TGT 163

30

(2) INFORMATION FOR SEQ ID NO: 4706:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 203 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4706:

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TAAGGTTGGG ATTGTTTGTG GGCTCGTTGC CACCCATTGT ACGGCACTCA TCAnTTCAAG 60  
CCACCAGCTA CAGTATATCT CCTTGACCAG CCATAATTG ATGGCTGCA GTCGCGATGG 120  
TTTGTAAATCC TGATGAGCAG TAGCGATTCA TGTTTGACCh GTACCCGTCA GATATCCGCA 180  
GCAATGCAAT GTTGTGCAAG TTT 203

(2) INFORMATION FOR SEQ ID NO: 4707:

50

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 153 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4707:

CGGGTGAGAA TCCGTCCACC GATTGACTAA GGTTCACAGA GGAGGCTCGT CCGCTCTGGG 60  
 5 TTAGTCGGGT CCTAAGCTGA GGCACAGnGT AGGCGATGGA ATAACAGGTT GATATTCCTG 120  
 TACCACCTAT AATCGTTTTA ATCGATGGGG GGC 153

## (2) INFORMATION FOR SEQ ID NO: 4708:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4708:

10 nCTATAATGA ATAAATAATT TAGAAATATG CTTCCGATTG TTCGATGCTT TAATTCAGTT 60  
 20 AGAAGCATCA TAGAATGCAT GATTACTGTT GTAAAGATAC GTAATGTTTT GTATTGACTG 120  
 TATGTCTTTG GATAGAGTTA CAAACTTATT 150

## (2) INFORMATION FOR SEQ ID NO: 4709:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4709:

35 AAAATTCGGG TTCTCAAATC ATCGGAACAT AACAAAACAA CCTAAGCAAC ATGTAGGCCG 60  
 TTGTCACTTA ACTTCTTGTT TTTCCGATGA CAGCTTCTAT TnAGAGAATG TCATGATTAT 120  
 40 TTTATATTCA CTTCAATGTT ATCAGTATTG GTGCCA 156

## (2) INFORMATION FOR SEQ ID NO: 4710:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4710:

55 GTTGATATTC CTGTACCACC TATAATCGTT TAATCGATGG GGGGGACGCA TAGGATAGGC 60

TCGTTAAGGC TGAGCTGTGA TGGGGAGAA

149

## (2) INFORMATION FOR SEQ ID NO: 4711:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 160 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4711:

TTGACTTCAA TACCATGGGC CAGGTACnCT TTAAATGTTG TTGTCTCAGT TAATATTAAT 60  
 TGGCTTTTCT TTGCATAAT TGACAATGGC TTCTGCCAAT GGGTGTTTCAG AATCTTTTTC 120  
 AGCAGTAGCA AGTAGTTGGT AGCGTTTGAT TGGTCACCAG 160

## (2) INFORMATION FOR SEQ ID NO: 4712:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 151 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4712:

ATAGTGAACC ACTACCGTGA GGACnAGGTG AAAAGCACCC CGGAACGACG TGAAATAGAA 60  
 CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCGTTAAT GGGTGATGGC GTGCCTTTTG 120  
 TAGAATGAAC CGGCGAGTTA CGATTTGATG C 151

## (2) INFORMATION FOR SEQ ID NO: 4713:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4713:

ACCAGTTGAT CTACCCTTGG TCAGGTTGAA GTTCAGGTAA CACTGAATGG AGGACCGAAC 60  
 CGACTTACGT TGGAAAAGTG AGCGGGATGA ACTGnGGGTA GCGGAGAAAT TCCAATCGAA 120  
 CCTGGGAGAT AGCTGGTTCT CTCCG 145

## (2) INFORMATION FOR SEQ ID NO: 4714:

- (A) LENGTH: 151 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4714:

10 TGTnACGCAG AGATCGCGGG TTCGATTCCC GTCGAGACCG CCATTTAATT TTATAATTAA 60  
 TAGCGATGTA CCTATAATAA TGGAGGAATA CCCAAGTCCG GCTGAAGGGA TCGGTCTTGA 120  
 AAACCGACAG GCCTTAACGG GCCGCGGGGG T 151

15 (2) INFORMATION FOR SEQ ID NO: 4715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4715:

25 TCGTATTGAA TGGCTTCGTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT 60  
 GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAACG TGTAATTITTA CTTTGnAATA 120  
 30 CTTTAAAAAA ATAAGACACT TTGCCAACTT G 151

(2) INFORMATION FOR SEQ ID NO: 4716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4716:

40 GCTGTCATCG GAAAAACAAG AAGTTAAGTG ACAAGGGTTT ACATGTTGCT TAGCTTCTTT 60  
 45 TATTATGCGT AATGATGTAA AAAGACGAAT ATTCATTGT TTGTAAAAGT GGCATTCTA 120  
 TGTCTTAAAA GTGACGAAAC TTCACnCTGT GC 152

(2) INFORMATION FOR SEQ ID NO: 4717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4717:

GGATACTAGT AAAACCATAT TTAGTAAATA CAGATGGAnT AAATCTTTTA AGGCTTATAA 60  
 5 ACGCTCATCT GACATTGTAG AATTCATGCT TTCAAAAGAC GATATACTAC GACACTCCTA 120  
 CGAACTTGTC CAAGGATTAC GAAA 144

## (2) INFORMATION FOR SEQ ID NO: 4718:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4718:

ATCATAAGGG GCATGATGAT TTACGTCATC CCCACCTTCC TCCGGTTTGT CACCGCAGTC 60  
 20 AACTTAGAGT GCCCAACTnA ATGATGGCAA CTAAGCTTAA GGGTTGCGCT CGTTGCGGGA 120  
 CTTAACCCAA CATCTCACGA CACGA 145

## (2) INFORMATION FOR SEQ ID NO: 4719:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4719:

AAATACCTTT CCACGATCTT CAGCTGGGCG CCTCTGCACT CGCAAACGCA CTTGATGCAT 60  
 35 CAACAACACC ACCAAATAGT CCCTGCAATA ACCTCACAGT ACAAACGTGTA ATGGTGTCGT 120  
 40 ACACnATGCC ATTTAAAAAT AGCATACCGG CAAAGC 156

## (2) INFORMATION FOR SEQ ID NO: 4720:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4720:

TTAAATCGAG TCTCTTTTAC AGGTCCATAT TTTGTTACGT ATCGACCGGT GGCTAACTAC 60

TAACTCGGAT CAAATTCGTC TCGATGACCT GG

152

(2) INFORMATION FOR SEQ ID NO: 4721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4721:

CACTAGTTCA AGTTCAAGTG GCGACGATTG GTATTTTACA AGAATTTTAT CAACAAGGAT 60  
 TTAATTAGCT TAAACGCnGC AATCCCTGTG TTAGTAGGGC GGATAACATT GGTACCACGG 120  
 TTACAGCTAT CTTAGCTAGT TTAGCC 146

(2) INFORMATION FOR SEQ ID NO: 4722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4722:

CCACACCAAT -ATTTGCGCT AAGTAAATCG CATTAAACGT TTGTCTTCCG CCATTGAGC 60  
 CACACTGCTC CAGCTCATAG CGCTATATCG CAGGGAATAA TCATTCCGCC ACCACAACCC 120  
 TAACATTACC CAGCCATACA GCCATACCAG GGCCAC 156

(2) INFORMATION FOR SEQ ID NO: 4723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4723:

ACGGTCTTGC TGTCATTAT AGATGGATCC GCGCTGCATT AGCTAGTTGG TAAGGTAACn 60  
 GCTTACCAAG GCAACGATGG CATGAGCCGA CCTGGAGAGG GTGGATCGGG CCACACTGGG 120  
 AACTGAGACA CGGTCCAGAC TCCTACGGGG AGGCAGCAGT A 161

(2) INFORMATION FOR SEQ ID NO: 4724:

- (A) LENGTH: 165 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4724:

CAGAAAGCTC ACGGGGCTTT CGTCTGTGCG GGGTAACCTG CATCTTCACA GGTACTATGA 60  
 TTTCACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGnCTTTCGT GCGGGTCGGA 120  
 ACTTACCCGA CAAGTAATTT CGCTACCTTA GGACCGTTAT AGTTA 165

(2) INFORMATION FOR SEQ ID NO: 4725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4725:

GGACGTTATA AGTGCTGAAA CATCTAAGCA TGAAGCCCCC CTCAAGATGA nATTTCCCAA 60  
 CTTTCGGTTAT AAGATCCCTC AAAGATGATT AGGTTAATAG GTTCGAGGTG GAAGCATGGT 120  
 GACATGTGGA GCTGGACGAA TACTAATCG 149

(2) INFORMATION FOR SEQ ID NO: 4726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4726:

TTGAATTTTT GAAAAAAAAA TGCCGAAATA AAAGATGCCA AGATATCCGC CGGGTAAAAA 60  
 ATTAAGTTTC CGAAAAACCA GGTGTTGGTA CCCATTGCAT CTGGGGTGGC AAAAGCATT 120  
 GCAGATAAAA TTGTCATCAG TGATTACGAT GGTGGTACAG GGCTTCACCC AAACGAGTAT 180  
 CAGCATGCCG GTGTTCTG GAGATGGTTA GCAGAACACA TCAACATAAA CTAATGCTAA 240  
 GAnCGGTAAA GTAGACAnCG GTAGTATACT GAAAT 275

(2) INFORMATION FOR SEQ ID NO: 4727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4727:

ATCAATGAAC AACACATACA GATGGTACTG CGACGCCTAG AGTAACAAA TAAGTTTTGT 60  
AACTCTATCC AAAGACATAC AGTCAATACA AAACATTACG TATCTTTACA ACAGTAATCA 120  
TGCATTCTAT GATGCTTCTA ACTGAATna 149

(2) INFORMATION FOR SEQ ID NO: 4728:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 158 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4728:

GCACGTTATT CCATTATCTT AATGGTTATC TTATCCTCAA CTAAATTGGA GGAATCACTA 60  
TGACAATTAA TAAAGAACCG TTCTTGCGCG AGCACAATGG GCGCTCACTG GCAGACTTTT 120  
GTGATGCTGA CTTAAAGTAA ACTATTAGAT ATTGnGTG 158

(2) INFORMATION FOR SEQ ID NO: 4729:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 138 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4729:

TCATTGACAT CGCTGGAATA GGTGTAAATC CTGCGATTCTG ATCTGGACCA TATTTTTTTA 60  
TTGTATACAG TAATTGTGCT GCGATTATCT CTGTAACGTC TTTCCAATTT GAnCGCACGT 120  
GCCCTCCCAT ACCTCGGG 138

(2) INFORMATION FOR SEQ ID NO: 4730:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 187 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

TAAAGACTAT ACCATTCTAT CCAATAATAA TTGGATTGGG ATTTGTCTGA ATTCGTAACC 60  
 GAGAGGCCCC TCGTCCAAAC AGTGCTCTAN CTCCAATAAT CATCACTTGA GGCTAGCCCT 120  
 AAAGTATTTC GGAGAGAACC AGCTATTTC AGTTCGATTG GAATTTCTCC GCTACCCTCA 180  
 GTTCATC 187

(2) INFORMATION FOR SEQ ID NO: 4731:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4731:

CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT TCGCCATTAA AGCGGTACGA 60  
 AGCTGGGTTC AGAACGTCGT GAGACAGTTC GGTTCCTAT CCGTCGTGGG CGTAGGAAAT 120  
 TTAGAGGAG CTGTCCT 137

(2) INFORMATION FOR SEQ ID NO: 4732:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4732:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60  
 TCTATTCTT CTATTGTAA ATCGCTATCT CCATCTCTT TTATCTCTGG TATTATTTTT 120  
 TCTTCAACTA AGTCACG 137

(2) INFORMATION FOR SEQ ID NO: 4733:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4733:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60

TCTTCAACTA AGTCACG

137

## (2) INFORMATION FOR SEQ ID NO: 4734:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 153 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4734:

AAAACATAAA TACAAAAATA TAGCTATTAC TATAAAAAAC AGCAGTAAGC ATATTTCCAA 60  
 ATTGCAAATT ATCCTACTGC TGTTCCTTTT GGGCAGTGGG nACAGCAAAT GATATTTTCG 120  
 ACAAAATTTA TTTGTCGTC CCACCCCAAC TTG 153

## (2) INFORMATION FOR SEQ ID NO: 4735:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 142 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4735:

TAGAAATTAC GGACCCAATT TCTCTATGTT GGGGCCCATC CCCAACTTGC ACATnATTGC 60  
 AAGCTGACTT TTCGTCACCT GCTTTGTTGG GGCCCCGCCA ATAAGCGTTG TAGTGCCTAG 120  
 TACTTTGATT GATGTCCAAG TT 142

## (2) INFORMATION FOR SEQ ID NO: 4736:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4736:

ATGTTATTCA AAGTAAATTG CTTTGCTGA TTTTGACAGC TGATAAATCG CTTCAAGAAT 60  
 TTTTGTAACCT ACCATTGCTT GTTCCGGTTT CACAACTGGT TCAGTATCAT TTACAACnGC 120  
 ATCAATCCAA GCTTTTG 137

## (2) INFORMATION FOR SEQ ID NO: 4737:

(A) LENGTH: 144 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4737:

10 GGTCTTTTAG TATTTGGTCG TACACCGCAA ACCAGGTGCA TCTACCCTTG GTCAGGTTGA 60  
 AGTTCAGGTA ACACTGAAAT GGAGGACCGA ACCGACTTAC GTTGAAAAT GAGCGGATGA 120  
 ACTGAGGGTA GCGGAGAAAT TCCA 144

15

(2) INFORMATION FOR SEQ ID NO: 4738:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 157 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4738:

25

GGGTAGCTAT GTGTGGACGG GATAAGTGCT GAAACATCTA AGCATGAACC CCCCTCAAGA 60  
 TGAGATTTCC CACTTCGGTT ATAAGATCCT CAAAGATGAT GAGGTTAATA GGTGAGGTG 120  
 GAACATGGTG ACATGTAATC TGCTTTTCTA ATCATAC 157

30

(2) INFORMATION FOR SEQ ID NO: 4739:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4739:

40

GCTTTATGTC TAAACGTCA AAATAAAAAG CAAACACAAA GAAAAATGGC TTGGCGAAGT 60  
 GAAAACGGTT GAATCTGACG AAACGAGAAA AGAACGCAAC GAGTTTAGTA GAGCTAATG 120  
 AGTAAGTGAG AGCCGAAGAG AGGGA 145

45

(2) INFORMATION FOR SEQ ID NO: 4740:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4740:

TAGTAGCACC ACCCTTAGAC CTTCTTGATT TGACATCGTT GTTCTTCCTT CCTTCGGTCT 60  
 5 CGTTACTCAT TTAGCTCTAC TAAACTCGTT GCGTCTTTTC TCGTTTCGTC AGATCAAACG 120  
 TTTCACCTTCG CCAAGCCATT TTTCTTGTGT TTATTTTATT TGACGTTTAG ACATAAAAAA 180  
 GAGACCCACG TTCAACTTGC CnGCACGTTT TACTCTGCCG AnTAGTGGCT ACCA 234

## (2) INFORMATION FOR SEQ ID NO: 4741:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4741:

GCAAGTCTTT TTAAAGGTAA CACTATCATT TATGCAATAC GCGCATTAC CAGAGTTGCA 60  
 TGGTCAAAAT ATATTGTTGT CATTGAAGA TGGACGTGTA CAAAAATGCG TGTTACGTGA 120  
 25 TCATGATACT GTCAn 135

## (2) INFORMATION FOR SEQ ID NO: 4742:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4742:

ACCCTGGTAC AGTTGAATTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA 60  
 40 AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGA GAnAGCTGGT 120  
 TCTCTCCGAA ATAGCTTTAG GGCTA 145

## (2) INFORMATION FOR SEQ ID NO: 4743:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4743:

TGATTATCAT GGGTGC GGGT ATTAACCATT GGTTTAACTC AGATACGATT TATnGTGCAA 120  
TCTTAAACTT AGTTATGGTA TGTGGCGTCA A 151

(2) INFORMATION FOR SEQ ID NO: 4744:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 132 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4744:

TAAAGCTAAA AACACAGCTC ATAATATCAA AAAAGGTGCA GAAGAAATGG TTGAAGCGGC 60  
AGGCGATAAA ATCAnAGATG GTGCATCTTG GTTAGGCGAT AAAATCGGCG ATGTGTGGGA 120  
TTATGTACAA CA 132

(2) INFORMATION FOR SEQ ID NO: 4745:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 132 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4745:

CGTGCGCTCT AACCAGCTGA GCTATAGGCC CATTAAATTTG AATGAACAAA CATTCAAAAC 60  
TGAATACAAT ATGTCACGTT ATTCCGCATC TTCTGAAGAA GATGTTCCGn ATATATCCTT 120  
AGAAAGGAGG TG 132

(2) INFORMATION FOR SEQ ID NO: 4746:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 138 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4746:

GTGATCCGAC TCAGATAGCG ATCCGACTCA GATAGCGACT CAGATTCAGA CAGCGATTCA 60  
GATTCAGACA GCGATTTCAGA TTCAGATAGC GATTCAGATT CCGACAGTGA CTCAGATTCC 120  
GACAnTGACT CGGATTCA 138

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 bas pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4747:

CATTATTGTA AACTGAACTT TTCGTCACCT GCTGGTGnTT GGGGACCCCA CCAACTTGGC 60  
 ACATTATTGG TAAGCTGACT TTTCGTCACCT TACTGTGTG GGGCCCCGCC AACTTGCATT 120  
 GTCTGTAGAA ATTGGGAATC CAATTTCTCT ATGTTGGGGC CCACACCCCA ACTCGACATT 180  
 GCCTG 185

## (2) INFORMATION FOR SEQ ID NO: 4748:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4748:

ACCGAATCCC TTCAGACCGG TACTTGGGTA TTCCTCCAAA ATTATATGGA CCTTGACAGT 60  
 ACTCGAACCT GACGTACCGA AACGGTTATG AAGACCGTTA nCTCTAACCA ACTGAGCTAA 120  
 AGGATCCTAA ATATAATTTT ACAACTAATA AATAGTGGAC GGTGGAGGGA TCG 173

## (2) INFORMATION FOR SEQ ID NO: 4749:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4749:

ACACAAGGAT AAGGCATTGT TGGATGTGGG ATGCTTTAAC TGGGCAAGCG ATTGGTCGTC 60  
 CTAAAACAGG TACATATGCC GGCTATCTGA CCTAGTCGGT TTAGATATTG CAGTGTCTGT 120  
 AATTAAAGGG CATGCAACCA AGTAnCTGAG GAAACAACTT ATTTTCATGG TGTCAAAAAT 180  
 TGnTAAATAC GGTGTTTGAC AATTGCGCAC CT 212

## (2) INFORMATION FOR SEQ ID NO: 4750:

- (A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4750:

10 AATCTCAGGT TTTACCAAGC AAAACCGATG AATAAAGAGT TTAAATAAG CTTGAATTCA 60  
 TAAGAAATAA TCGCTAGTGT TCGAAAGACn GCAGCAAGAT TAATAACGCG TTAAATCTT 120  
 TTTATAAAAG AAAACGTTTA 140

15

(2) INFORMATION FOR SEQ ID NO: 4751:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 184 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4751:

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ATTCGTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT CATCATCTTT 60  
 GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGTTTCAT GCTAGATGCT 120  
 30 TCAGACTATC CCGTCCACAC ATGTAACCAG nATGCGTGGA CGCATGGAAC AGGGATGTCA 180  
 TCCG 184

30

(2) INFORMATION FOR SEQ ID NO: 4752:

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 133 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4752:

45 GGGATCTTCC GCAATGGGCG AACTGTACG GAGCAACGCC GCGTGAGTGA TGAAGGTCTT 60  
 CGATCGTAAA ACTCTGTTAT TAGGGAAGAA CATATGTGTA AGTAACTGTG CACATCTTnA 120  
 CGGTACCTAA TCA 133

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(2) INFORMATION FOR SEQ ID NO: 4753:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 162 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4753:

5 GTATGCTGTG TGGCTTGTCA TGTTCGGGTT TGGTGGCGGA CCTGATTATT CCTGCGnTAT 60  
 ACGCTATGGC TGGAGCAGTG TGGCCAAATG GCGGAAGACA AACGTTTAAT GCGATCTACT 120  
 TGGCGCAAAA TATTGGTGTG GCTGTCGGTG CTGCAATGGG CG 162

## (2) INFORMATION FOR SEQ ID NO: 4754:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 134 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4754:

20 AATTCGATTG CCTTAGTAGC GGCGACGAAA ACGGGAANGA GCCCAAACCA ACAAGCTTGC 60  
 TTTGGGGGTT TGTAGGACAC TCTATACGGG GTTAACAAAG GACGACATTA GACGAATCAT 120  
 CTTGGGAAAG ATGA 134

## (2) INFORMATION FOR SEQ ID NO: 4755:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 139 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4755:

35 AGAGTGCGTA ATAGCTCACT AGTCGAGTGA CACTGCGCCG AAAATGTACC GGGGCTAAAC 60  
 ATATTACCGC AAGCTGTGGA TTGTCCTTTG GACATGGCTA GGAGAGCGTT CTAAGGGCGT 120  
 40 TGAAGCATGn ATCGTAAGG 139

## (2) INFORMATION FOR SEQ ID NO: 4756:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 163 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4756:

CGTGAAATGC GCAGAGATAT GGAGGAACAC CAGTGGCCGA AAGCCACTTT CTGGTCTGTA 120

ACTGGACGCT GGATGTGCCA AACCTGGGGG ATCAAACAGG TTA 163

(2) INFORMATION FOR SEQ ID NO: 4757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4757:

CATGAACTA GATAAGTAGT AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG 60

TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ATCACAGAT 120

TAATACCGCG TTTAATCTTT TATAAAGGAC CGTAACTTCA 160

(2) INFORMATION FOR SEQ ID NO: 4758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4758:

TACATGGGTT TATTGTTGAA GATGACGAAA TTGTAGAAAT TTAATATTCT AAAAAGGTTG 60

GGGACATAAA TCCCCCTAAA AAAACCAGCA GTAAGATAAT TTTCAATTAG AAAATATCTT 120

ACTGCTGTTT TCTATTTATA CCAATTACT TTCGTAATTG TTAAAATTTT AAAAGGA 177

(2) INFORMATION FOR SEQ ID NO: 4759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4759:

CGGTGTGTAC AAGACCCGGG AACGTATTCA CCGTAGCATG CTGATCTACG ATTACTAGCG 60

ATTCCAGCTT CATGTAGTCG AGTTACAGAC TACAATCCGA ACTGAGAACA ACHTTATGGG 120

ATTGCT 127

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4760:

GGGCCCCCTCG TCGGGTTACC GAATTCAGAC AAACCTCCGnA ATGCCAATTA ATTTAACTTG 60  
 GGAGTCAGAA CATGGGTGAT AAGTCCGTGT TCGAAAGGAA ACAGCCCAGA CCACCAGCTA 120  
 AGTCCCAAAT ATATGTTAAT GAAAG 145

## (2) INFORMATION FOR SEQ ID NO: 4761:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4761:

TAAACAAGGC GCGTTGGGCC TATTCCTGCG GGCTCTTCTG GCGGTTAACC CTAAAGAGCA 60  
 CCCCTTCTCC CGAAGTTACG GGGTCATTTT GCCGAGTTCC TTAACGAGAT TGCTCGCTCA 120  
 CCTTAGAATT CCATCTGACT ACGGTCGTTG CGTACGGCAC TATTCTTCA AGCTTCCGCA 180  
 TTAACACACC AAAACAGCTC CCACCACCAC TAnATCGAnC AACACTAG 228

## (2) INFORMATION FOR SEQ ID NO: 4762:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4762:

TnGCCAAATC TTAGTAGTCG CTTGGTTCGG TTGTGGTGGC ACAGCTGTGA AATCATCACT 60  
 ACGTTGCTCA TCACTCACTG TCTCTCCGCT TCCTTGGCTT GCAACAGCTT GAATTGTATC 120  
 AGCAGGGTTG 130

## (2) INFORMATION FOR SEQ ID NO: 4763:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4763:

CAACTCGTAG TCAGGGTCGA AAGACGGGAC TTAGTGATCC GGTGGTTCCG TCATGGGTAG 60  
GGCCATCGTC TCAACGGTAT AAAAGCTACC CCGGGGATAA CAGGCTTATC TnCCCCAAGA 120  
GTTACATCG ACGGGGAGGT TTGGCACCTC G 151

(2) INFORMATION FOR SEQ ID NO: 4764:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 128 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4764:

ACCCCAACTT GCATTGnCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCCGC 60  
CGGCAAGGTT GACTAGAATT GACCAAAAGC TTGTTACAAG CGCATTTTCG TTCAGTCAAC 120  
TACTGCCA 128

(2) INFORMATION FOR SEQ ID NO: 4765:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 135 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4765:

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AATACAGCCC CAGAGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT CGATGTGAAC 60  
TCTTGGGGGA GATAAGCCTG TTATCCCCGG GGTAGCTTTT ATCCGTTGAG CGGATGGCCC 120  
TTCCATGTG GnaAC 135

45

(2) INFORMATION FOR SEQ ID NO: 4766:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 126 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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GATTCTCACC CGTCTTTTCG TACTCACACC GGCATTCTCA CTTCTAAGCG CTCCACATGT 60  
 CCTTACGATC ATGCTTCAAC GCCCTTAGAA CnCTCTCCTA CCATTGTCCA AAGGACAATC 120  
 CACAGC 126

## (2) INFORMATION FOR SEQ ID NO: 4767:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4767:

TTAATAGTTT TATAAGAGAG GTGTTTGATC TTGAGCTAAC CACnTCATTC GAGTACTGTC 60  
 ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT GGGGTATATG CATATAAGAT 120  
 GATTTTAAAC 130

## (2) INFORMATION FOR SEQ ID NO: 4768:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4768:

GTTAACCCTA AAGAGCACCC CTTATACCGA AGTTACGGGG TCATTTTGCC GAGTTCCTTA 60  
 AnGCGCGTTC GATCGCTCAC CTTAGGAATT CTCATCTTGA CTACCTGTGT CGGTTTGCGG 120  
 TAGGGCACCT ATTTTCCTAT CT 142

## (2) INFORMATION FOR SEQ ID NO: 4769:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4769:

CCTTGGGACC GACTACAGCC CCAGGATGCG ATGAGCCGAC ATCGAGGTGC CAAACCTCCC 60  
 CGTCGATGTG AACTCTTGnG TGGAGATAAG CCTGTTATCC CCGGGGTGAG CTTTGTATCC 120

## (2) INFORMATION FOR SEQ ID NO: 4770:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4770:

CTAAAAGTTG TATTTTAAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA 60  
 ACCGTTAAAC AATGCATAGT TTGCTTAACT TCCAATATTG ACTCATCATT ACAATTGACA 120  
 TAGAGCTATT AAGCGTnGCC ATGAG 145

## (2) INFORMATION FOR SEQ ID NO: 4771:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4771:

TCGAGTGACA CTGTCGCCGA AAATGTACCG GGGCTAAACA TATTACCGAA GCTGTGGATT 60  
 GTGCCTTTGG AAATGGTGAG GnGAGCGTTC TAAGGGCGTT GGAAGCATGA TCGTAAGGAC 120  
 ATGTGGGA 128

## (2) INFORMATION FOR SEQ ID NO: 4772:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4772:

GGGCAGATGT TCCTGCAGTC ATAGTGCCGT CAACTTTAAA TACTGTACGT AATTTGGCTA 60  
 ATGCCTCCAT CGTGGnTGTC AGGGCGTATA AATTCATCTT GGGTCAAAGA TATTTGGTGT 120  
 GTACTT 126

## (2) INFORMATION FOR SEQ ID NO: 4773:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4773:

GTCTTTTCTC GTTTCGTTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT 60  
 10 GTTTACTTTT TATTTTGACG TTTTAGGATA AAAAAAGAn ACCTTGCGGT CTCAATGCGG 120  
 CTCATC 126

(2) INFORMATION FOR SEQ ID NO: 4774:

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 124 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4774:

25 ATTTCAATAT CAGGCTACAG TAAAGCTCCA CGGGGTCTTT CCGTCCTGTC GCGGGTAACC 60  
 TGCATCTTnA CAGGTACTAT GATTTCACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 120  
 TACG 124

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(2) INFORMATION FOR SEQ ID NO: 4775:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 124 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4775:

40 ACCAAGTGAG CCGGAAACAC CAACGCCACC AACACCAGAA GTACCAAGTG AGCCGGAAAC 60  
 ACCAACACCA CCGACACCAG AAGTGCCGAG TGAnCCAGAA ACTCCAACAC CGCCAACACC 120  
 45 AGAG 124

(2) INFORMATION FOR SEQ ID NO: 4776:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 135 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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CCCCGTAGTC TCCACCATTT ATTTTTTACA CGATGAACAT TGAAAACt<sub>n</sub>A ATACAATATG 60  
 CAACGTTAAT TCCAAAAAAC GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT 120  
 5 AATCAAACAT CATAA 135

## (2) INFORMATION FOR SEQ ID NO: 4777:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4777:

AGTGCAGAAG AGGAAAGTGG AATAnCCCCA ACATAGCGGT GAAATGCGCA GAGATATGGA 60  
 20 GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAAC TG GACGCTGGAT GTGCGAAACG 120  
 TTGGGGGTTC AAACAGGATT TAGA 144

## (2) INFORMATION FOR SEQ ID NO: 4778:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4778:

AATTTTTGAT GACGGGTCCC TTCCTAGGGT GCCGTCTCAG CCACCCCAAC CGGCACATTG 60  
 TTGTAAGCTG ACTATATGTC nTTCATGTGT TGGGGCCCCCT GTCTTCGACT GGCAC TGCTC 120  
 CCT 123

## (2) INFORMATION FOR SEQ ID NO: 4779:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4779:

GCGCATTAAC TATCGCGATA TTAATCGCTA TTCTATATCG TCACTTTAGA GGATATCCTG 60  
 AACAAATATAG CTCAGGTATT ACGTTTTTCAT CTAAATATTT ATTAAGATTT GCAATCATCC 120

## (2) INFORMATION FOR SEQ ID NO: 4780:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4780:

GGTAATATGT TTAGCCCCGG TACATTTTCG GCGCAnTGTC CTCGACTAGT GAGCTATTAC 60  
 GCACTCTTTA AATGATGGCT GCTTCTAAGC CAACATCCTA GTTGTCTGGG CAACGTCACA 120  
 TCCTTTT 127

## (2) INFORMATION FOR SEQ ID NO: 4781:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4781:

ACACnGGGTG AGAATTTGTC GCTATTGTA AATTGTATCC TGGCTTAAGT TGGCCAAAGT 60  
 GTCTTATTTT TTAAAGTAT TAAAAGTAA AATTACATGT TAATACGTAG TATTAAATGG 120  
 CGAGACTCC 129

## (2) INFORMATION FOR SEQ ID NO: 4782:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4782:

CTCATTCCCG TTGCATTTTA TCTTCTGCAA CAACAACATT TCGTCTTTAT CGTCTTCCAT 60  
 AGTAGTAGGA TTTTCTACTA CTTGACCATT CATAATCTGT TGCATTTTCAT GTTTGnTTTG 120  
 GTCAGATTTA GGACCA 136

## (2) INFORMATION FOR SEQ ID NO: 4783:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4783:

CATCAACATC GGCGCATTAA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC 60  
AGTGGTTAAA GCTGCGAAAG GTCACACAGT AAAAGTGATT ATTGnGACGG TATTGTTGG 119

(2) INFORMATION FOR SEQ ID NO: 4784:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4784:

ATCACTAATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC ATACGTGTTT TAACCTGCGT 60  
nATCCCATTC CATCCATAA TTGTGAATGG ACCAAGTTTC CAGTTGAACC CCCAGACAAG 120  
CGCACGG 127

(2) INFORMATION FOR SEQ ID NO: 4785:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4785:

ACACCGGCAT GCTGAATACT CGTTTTGGGT GAAGCCCCTG nACCACCATC GTAACCACTG 60  
ATGACAATTT TATCTGCAAA TGCTTTTGCC ACCCCAGATG CAATGGTACC AACACCTGT 119

(2) INFORMATION FOR SEQ ID NO: 4786:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4786:

CTTCTAAAC CCGnACCAC TTTATCGTGG TGGGGAGACA GTGTTcAGGC GGGCCAGTTT 60

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AATCATT CAT AGAGTGT

137

(2) INFORMATION FOR SEQ ID NO: 4787:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 119 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4787:

GTTTTTAACA CTGTTACCGT TTTCATCTTT TAATGTTACC GTTACGCCAG AnATACCTTT 60

TTCATCTTGG TCTTGGATAC CATTTTTATT TGTATCTTCC CAGACATAGT CACCTAAGT 119

(2) INFORMATION FOR SEQ ID NO: 4788:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 141 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4788:

CATGCTTCCA CCTCGAACCT ATTAACCTnC ATCATCTTTG AGGGATCTTA TAACCGCAGT 60

TGGGAAATCT CATCTTGTAG GGGGGCTTCA TGCTTCAGAT GCTTTGCAGC ACTTAGCCCCG 120

GCCACACATA GCTACCCAGC T 141

(2) INFORMATION FOR SEQ ID NO: 4789:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 139 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4789:

CTGGGTT CAG AACGTCTAAG CAGTTCGGTC CCTATCCGTC GTGGGCGTAA GAAATTTGAG 60

AGGAGCTGTC CTTAGTACGA GAAGACCGGG ATGGACTACC TCTnGTGTAC CAATTGTCGT 120

GCCAACGCAT AGCTGGGTA 139

(2) INFORMATION FOR SEQ ID NO: 4790:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 129 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4790:

CATTATTTAG TATTTATGAG CTAATCAAAC AnCATAATTT TTATGGAGAG TTTGATCCTG 60  
10 GCTCAGGATG AGCGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGACGAGATG 120  
CTTGCTTCG 129

(2) INFORMATION FOR SEQ ID NO: 4791:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 120 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4791:

GGGTGCTCTT TAGGGTTAAC GCCCAGAAGA GCCGCAGTGC AATAGGCCCA AGCGACTGTT 60  
25 TATCAAAAAnC ACAGGTCTCT GCTAAACCGT AAGGTGATGT ATAGGGGCTG ACGGCTTCCC 120

(2) INFORMATION FOR SEQ ID NO: 4792:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4792:

CAAATTCCTT CGCTACTTGA ATGACAACAC TTTGTTTTAC GCCTGAAATG GCTTCTTGCC 60  
40 AAGCAGGTGT ATATTTTGAT TCTGCATCGT CGTATCCTTT TGATCTAATT ATGATCAAAC 120  
CGn 123

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(2) INFORMATION FOR SEQ ID NO: 4793:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 130 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4793:

AGTTTTGAAT GTTTGTTTCAT TCAAATTAAT GGGCCTATAG CTCAGCTGGT TAGAGCGCAC 120  
 nCCTGATAAC 130

(2) INFORMATION FOR SEQ ID NO: 4794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4794:

CACAGCCACA AGTGATTAAA GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT 60  
 TAACTCATTT TTCAATAGAT CAGGAAGACT ACCAAGCTTA TGTnGAAGGA CATCT 115

(2) INFORMATION FOR SEQ ID NO: 4795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4795:

NTTAAAAAAA ATTCCAATT TTTTTTGGGG GGTGGAAT TTAAAAATTT GGTTTTTTAA 60  
 CCAAGGCC TTTTCCCAA AATTAAAT CCCTTAAAAA TTAAAAATTT GGGAATTTTT 120  
 TTTTnGGCCC AAAATTTTTT CCCTTTTTTT AAAGGCCCA ATTTTAAAT TAACCCTTAA 180  
 AACCCCAAA CCTTTTTTCC TTTTTTAAAA TTTTTTAAAA TGGA 224

(2) INFORMATION FOR SEQ ID NO: 4796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4796:

TCGCGTACCG CTTTAATGGG CGAACAGCAA GACCTTGGGC ACCGACTACA GCCCCAGAT 60  
 GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCCTCGAT GTGAACTCTT GGGGGCAGAT 120

(2) INFORMATION FOR SEQ ID NO: 4797:

(A) LENGTH: 125 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4797:

10 AATTCGATTCTCTTAGTAGC GGCGAGCGAA ACGTGAAGAG CCCCAnACCA ACAAGCTTGG 60  
 CTGTTGTGGT TGTAGGACAC TCTATAACGG GAGTTACAAA GGACCGACAT TAGACGAATC 120  
 ATCTG 125

15 (2) INFORMATION FOR SEQ ID NO: 4798:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4798:

25 CAAAATAATG ACTCCTACGG GnCTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT 60  
 AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACC 113

30 (2) INFORMATION FOR SEQ ID NO: 4799:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4799:

40 CCGGTGGGAG GTAACCTTTT AGGAGCTAGC CGTCGnAGGT GGGACAAATG ATTGGGGTGA 60  
 AGTCGTAACA AGGTAGCCGT ATCGGAAGGT GCGGCTGGAT CACCTCCTTT CTAAGG 116

45 (2) INFORMATION FOR SEQ ID NO: 4800:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 50 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4800:

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TCAGTGGGAT GATTCTGTGAA ATTGAAACGC AAGATTTCGA TATCGAnCAC CT

112

## (2) INFORMATION FOR SEQ ID NO: 4801:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4801:

ATAGGATAGG CGACGTGCGA TTGGATTGCA CGTCTAAGCA nTAAGGCTGA GTATTAGGAA 60  
 ATCCGGTACT CGTTAAGGCT GACTGTGATG GGGAGAAACA TTGTGTCTTC 110

## (2) INFORMATION FOR SEQ ID NO: 4802:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4802:

GAACCAAGTT GTTATTGAAA AntCGTTCGT AAAGTTACGG TACGCCACCC GTGAGTGCTT 60  
 TTACTTCTAT ATGAGCACCT ACTGTATCTT TCATTAATTT AACGTCTTCT GCAGTCGCAC 120  
 CGCCACCTGC AAAACCTGTT GAATTTTACG AGTCCGCACC GCGCTTTGTA ATCATnCTTA 180  
 CATTCTCTGT CACAACGCCA TACCTTCGGG ACTGACTCAC AGCTCAGCGG AACACAA 237

## (2) INFORMATION FOR SEQ ID NO: 4803:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4803:

CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA CCAATTGAGC TAAGCCGGGC 60  
 AATATGTAAG AATAAATGGT GGAGAATTGA CGGGTTCGAA CCGCCGAnCC TCTG 114

## (2) INFORMATION FOR SEQ ID NO: 4804:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4804:

GGATCAAACA GGATTAGATA CCCTGGnTAG TCCACGCCGT TAAACGCATG AGTGCTAAGT 60

10 GTTAGGGGTT TCCGCCCTT AGTGCTGCAG CTAACGCATT AAGCACTCCG CCT 113

(2) INFORMATION FOR SEQ ID NO: 4805:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4805:

TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTCGC GCATCAGCGT CnGTTACAGA 60

25 CCAGGAAAGT CGCCTTCGCC ACTGGTGTTC CTCCATATCT CTGCGCAT 108

(2) INFORMATION FOR SEQ ID NO: 4806:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 115 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4806:

TTTCAGCACT TATCCCGTCC ACACATAGTC TACCCAGGCT ATGCCGTTGG CACGACAACT 60

40 GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGAnAGCTC CTCTC 115

(2) INFORMATION FOR SEQ ID NO: 4807:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 167 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4807:

CAGCCACATA ACATAACTAA GTTTAAGATT GAACGATAAA TCGTATCTGA GTTAAACCAA 60

55 TGGTTAATAC CCGCACCCAT GATAATCATT GAACGCCTTC AGTATCGTAG GTTTGGAATT 120

## (2) INFORMATION FOR SEQ ID NO: 4808:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4808:

TGCTTACATC ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGCAGCTAA ATTACCTTGC 60  
ATCATTGCTA GCTTTTCTTG TATTAAGTGA TATTACTAA TTGGTTTGCC GAATTGCT 118

## (2) INFORMATION FOR SEQ ID NO: 4809:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4809:

TTGAGGTAGC CTAAAGCTAT TTCGGAGAGA CCAGCTATCT CCAGGTTCGA TTGGAATTTTC 60  
TCCnATACCT CAGTTCATCC GCTCACTTTC AACGTAAGTC GGTTCGGTCC TCATCAGTGG 120  
TACCTGACTT CAACTGACCA GGGTAGACAC 150

## (2) INFORMATION FOR SEQ ID NO: 4810:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:

AAGAAGGCCGA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCA 60  
AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA 107

## (2) INFORMATION FOR SEQ ID NO: 4811:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4811:

AGAGTGnATT AGGTTATGAA GGTGGGCAAA ATAGGGTAAC CAGTCATTTCG AGGAAGACAC 60  
 5 AGAAGAAGAC AAACCTAAAT ATGAACCAAG GTGGCATATC GTAGATATCG ATTTCCA 117

## (2) INFORMATION FOR SEQ ID NO: 4812:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4812:

CTTTTATCCG TTGAACGATG GCCCTTCCAT GCGGAACCAC CCGATnACTA AATCCGTCTT 60  
 20 TCGACCCTGC TCGACTTGTA AGTCTCGCAA TCAAGTCCCT TATGCCTTTA CACTCTATGA 120  
 ATG 123

## (2) INFORMATION FOR SEQ ID NO: 4813:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4813:

TAACCCGAGA GGGTCCCCTn GTCCAAACAG TGCTCTACCT CCAATATCAT CACTTGAGGC 60  
 35 TAGCCCTAAA GCTATTTTCGG AGAGAACCAG CTATCTCCAG GTTCGA 106

## (2) INFORMATION FOR SEQ ID NO: 4814:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4814:

CTATTGCTTT AGATGCATAT GAATCATTGA nTGACGCGAT GCCGATGATT TCTGAACACG 60  
 50 GAATCGCGAA CGTTGGCCAA CTGCCAACGA TTGGCGTGGG AATCATCCAG TG 112

## (2) INFORMATION FOR SEQ ID NO: 4815:

(A) LENGTH: 125 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4815:

10 ACGTGGAGAG CATGTCCGTT CAAGCAGAGG GCGGGCGGTT GAACCCGTCA TTCTGCACCA 60  
 TTTATTCTTA CATATTGCCG GcTAGCTCA ATTGGTAGAG CAACTGACCT TGTAAATCAGT 120  
 AGGTT 125

15 (2) INFORMATION FOR SEQ ID NO: 4816:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4816:

25 GTGCTGGCGC AGTTGCGATG GTTATTGCAC ATAATCCAAG CATGGCATT AATGAAGATG 60  
 CTGTTGCTTA CACTGAAGAC GTTTATGnTT TCTGGCGTCC AACT 104

30 (2) INFORMATION FOR SEQ ID NO: 4817:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 117 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4817:

40 GTCGGGTAAG TTCGGGCCCC CACGAAAGGC GTAACGATTT GGGCACTGTC TCAACGnGAG 60  
 ACTCGGTGAA ATCATAGTAC CTGTGAAGAT GCAGGTTACC CGCGGCAGGG CGGAAAG 117

45 (2) INFORMATION FOR SEQ ID NO: 4818:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4818:

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TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGACGCTCT TTTCTCGnTT CGTCAGATTG 120

A 121

(2) INFORMATION FOR SEQ ID NO: 4819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4819:

TCAGTTCGGT ATTGTGAGTC TGCAACTCGA CTGACATGAA GCTGGAATCG CTAGTAATCG 60

TAGATCAGCA TGCTACGGTG AATACGTTCC CGGGTCTTGT ACACAACGCC CGTnAAGA 118

(2) INFORMATION FOR SEQ ID NO: 4820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4820:

CAAAACAGTGC TCTACCTACA ATAATCATCA CTTGAGGCTA GCCCTAAAGC TATTTCCGGAG 60

AGAACCAGCT ATCTnCAGGT TCGATTGGAA TTTCTCCGCT ACCC 104

(2) INFORMATION FOR SEQ ID NO: 4821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4821:

TCGTAGTGGT TTCCAACCAA GTTTTATAA GTCAAACGCT CACATACGGC TTCGTTTTCA 60

TTATTTTAAA TGCTCATTTA CATAGTnAAC TCGCTTTAAA ATAATTTAAC TCATGTCGCT 120

AACGTTTTCT TTTATAAAAG TTTAACGGTT TTATCTGTGG TGTCT 165

(2) INFORMATION FOR SEQ ID NO: 4822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4822:

GAGTTTGATC CGGGCTCAGG ATGAACGCTG GCGGCGTGCC TAATACATGG CAATCGAGCG 60

10 AACGGACGAG AAGCTTGCTT CnCTGAGGTA GCGGCGGACG GGTGAGTAAC ACG 113

(2) INFORMATION FOR SEQ ID NO: 4823:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4823:

CCGGCAACGT TCTACTCTAG CGGAACGTAA GTTGGCTACC ATCGACGCTA AGAACCTTTC 60

25 TTGTGAnTTGT GACAATCGCT TGCTTCTTTC CTCTTCTTCG GCTCTC 106

(2) INFORMATION FOR SEQ ID NO: 4824:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4824:

TAAACGGCGG CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCCTTGTC GGGTAAGTTC 60

40 CGACCCGCAC GAAAGGCGTA ACGATTTGGG CACTGTCTCA ACTAGAGn 108

(2) INFORMATION FOR SEQ ID NO: 4825:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4825:

TCTAGTGACC GATAGTGAAC CAGTACCGTG AGGATAAGGT GAAAAGCACC CCGGAAGTAG 60

55 nTGTAATAG AACCTGAAAC CGTGTGCTTA CAAGTAGTCA GAGCCCGGTA ATGGGT 116

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4826:

ATAATATTGT AAATTAATCC ATTGATGCCA CAAGTGCCGG ACCAGAAATG ATGGTATTTA 60  
 ATAATGTGCC ATCTTTATCT TTACGCCAAT CATAATTGGT AAAAATTCCC CCTTCTAATA 120  
 ATCCTTGAT TGC GTGCAT AAGTCTTTG CTCCTTGCAC 160

## (2) INFORMATION FOR SEQ ID NO: 4827:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4827:

CGCATTGAGA CCGCAAGCTC TTTTTTTTAT GTCTAAAACG TCAAAATAAA AAGTAAACAC 60  
 AAAGAAAATG GTTGCCnAG TGAAAACGTT TGAATCTGAC GAAACGAGAA AGAGC 115

## (2) INFORMATION FOR SEQ ID NO: 4828:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4828:

CCAAAATAGC CTTCATAATC CAAAACAGG CTCCTTTGAC TATAGATTTT CGTTTCTGGT 60  
 TCAGAAAGCT TTTGATTAACTTTAAAGTAT nCCCAATTAT AAT 103

## (2) INFORMATION FOR SEQ ID NO: 4829:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GGACCGAACT GTCTCAGGAC GTTCTnAACC CATCTCGCGT ACCGCTTTAA TGGGCGAACA 60  
 GCCAACCCTT GGGACCGACT ACAGCCCCAT GATGCGATGA GCCGACATCG A 111

(2) INFORMATION FOR SEQ ID NO: 4830:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4830:

GTTGTTGGGG CCCC GCCGGC AAGGTTGACT AGAATTGAGA AAAGCTTGTT ACAACGCTAT 60  
 TTTCGTTTCTAG TCAACnACTG CCAATATAAC TTTGTAGAGC ATTGA 105

(2) INFORMATION FOR SEQ ID NO: 4831:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4831:

ACATTGAGTC TTCGAGTCGT TGCATTTTAC ACTGCCGnGA AAAGCCTCTA GATAGAAAAT 60  
 AGGTGCCCCGT ACCGCAAACC GACACAGGTA GTCAAGATGA GA 102

(2) INFORMATION FOR SEQ ID NO: 4832:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4832:

TTnTAGAATG AACC GGCGAG TTACGATTTG ATGCAAGGTT AAGCAGTAAA TGTGGAGCCG 60  
 TAGCGATAAG GAGGTCTGAA TAGGGCGTTT AGTATTTGGT CGTAGCC 107

(2) INFORMATION FOR SEQ ID NO: 4833:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 144 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4833:

5 TGCAACTAAT GAAAAGTAGA GTTCCGGGGA GTTAAAACCA GTGACTGTTG ACCTTGTTGT 60  
 CTCCATTGGA ATGTACTACC TGATGCAAGA TAATTATCAT CACTTTGTTG ACGTGCTTnA 120  
 TTTTCAGCAT CAATTTGATC AATC 144

## (2) INFORMATION FOR SEQ ID NO: 4834:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4834:

20 GGCTCAGATG nACGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGCACCAGAA 60  
 GCTTGCTTCT CTGGATGTTA GCGGCGGACG GGTGTAGTAA CACGTGGG 108

## (2) INFORMATION FOR SEQ ID NO: 4835:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4835:

35 GACAATGGTA GGNAGCGTT CTAAGGGCGT TGAAGCATGA TCGTAAGGAC ATGTGGAGCG 60  
 CTTAGAAGTG AGAATGCCGG TGTGAGTAGC GAAAGACGCA GT 102

## (2) INFORMATION FOR SEQ ID NO: 4836:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 109 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4836:

50 TTGCAGACTA CAATCCGGAA CTGGAGTAAC AACTTTATGG GATTThCTT GACCTCGCGG 60  
 TTTGCTGGC CCTTTGGTAT TGTCCATTGT AGCACGTGTG TAGCCCAA 109

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 103 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4837:

CTCCACGTAA GCTAGCGCTC ACGTTTCAAA GGCTCCTACC TATCCTGGTA CAAGCTGTGC 60  
 CGGAATTTC AATTGCAGC TACAGTAAAG CTCCACGGGG GTC 103

(2) INFORMATION FOR SEQ ID NO: 4838:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4838:

TCAAACACTC nCATACTGCT TTATTTTCAT AAACAATATC ACTTTAACCA AAAAATATTT 60  
 GAATGTTAAA TAAACATTCA AAACGAATA CAATATGTCA CGTTATTCCA CATCTTCTGG 120  
 A 121

(2) INFORMATION FOR SEQ ID NO: 4839:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4839:

AAACCATGAA TTAAGAATCC AGAAACAGGA GATGTAGTTA GACCACCGGT CGATTAGCGT 60  
 ACCAAAATAT GGACCTGTAA AAGGAGACTC GATTGTAGAA AAAG 104

(2) INFORMATION FOR SEQ ID NO: 4840:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

CCGTGGAGTT TATGTAGCCT GATATTGAAT TCGGCACAGT TGTACAGGTA GGTAGGAGCC 60  
 TTGAAACGTG AGCGCTATTA GTGnAGGCGT GGTGGGTACT ACCCTAGCTG TGTGGCTTT 120  
 CTAACCC 127

## (2) INFORMATION FOR SEQ ID NO: 4841:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 125 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4841:

CATCCCACCC CGGGCAAGGT TGACTAGAAT TGGAAAAAAA CTTGGTTACA ACGTTATTTT 60  
 CATTCACTCA ACTACTGCCA ATATAATATT GnaAACTATA GGACATTTAT TAGTGTTTCA 120  
 GTTCT 125

## (2) INFORMATION FOR SEQ ID NO: 4842:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4842:

TGGTACGGCA TCTCACCCGT CTTTCGCTAC TCACACGGC ATTCTCACTT CTAnGCGCTC 60  
 CACATGATCC TTACGATCAT GACTTCAACG CCCTTAGAAC GCTCGTCC 108

## (2) INFORMATION FOR SEQ ID NO: 4843:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4843:

TAATGAAGGT CTTCGGATCG TAAAACTCTG TTATTAAGnA GGAACATGTG TGTAAGTAGC 60  
 TGTGCACATC TTGACGGTAC CTAATCAGAA AGCCACGGCT AACTACGT 108

## (2) INFORMATION FOR SEQ ID NO: 4844:

(A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: lin ar

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4844:

10 CCGTCTCAAT GCGGCTCATC GCATCCATTT TTTGACCTGG GCAACGTTCT ACTCTAGCGG 60  
AACCTAAGTT GGGCTACCAT CGACGnCTAA GAACCTTTCT TGAATTGTGT ACAATCG 117

(2) INFORMATION FOR SEQ ID NO: 4845:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4845:

25 GACTGTTTAT CAAAACACA GGTCTCTGCT AAACCGTAAG TGATGTATAG GGGGCTGACG 60  
CCTGnCCGGG TTCTGGTAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAA 108

(2) INFORMATION FOR SEQ ID NO: 4846:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4846:

40 CAATATTTGA AGCGATTGGC TTGTCTCATG ATGTGATTGA TCGTTATTTT ACTGGGACAC 60  
AGTCTAAGTT ATCTGGTATT TCGATTGATC AAATThTGCC TGAAAAAGAC GCACAAGT 118

(2) INFORMATION FOR SEQ ID NO: 4847:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 104 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4847:

55 GATCCCCGGA CGGAGTGCTT AATGCGTTAC TGACAGCACT AAGGGGCGGA AACCCCCCTAA 60

## (2) INFORMATION FOR SEQ ID NO: 4848:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4848:

CTGGCGATTA TGCTCTGTAA CGTGCTTTCC AATTTGGAAC GCACGTGnCC CTGCCCATAC 60  
 CTACGGGACT TGACTTATAT TGTTTGGCTT TGTACGTCAT TTCAACAATA GACGCCCATG 120  
 CCAGCAACGC GATTACC 137

## (2) INFORMATION FOR SEQ ID NO: 4849:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4849:

GTTTAGGCTC ATCTTAAGAT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTA CTTACCG 60  
 TTTTGGCAGA CGGCACTTGG TGGTACTTTA GAAGTCAAAG ACAnGGGGGG GGGGGG 116

## (2) INFORMATION FOR SEQ ID NO: 4850:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4850:

TCCTTTCGTG ACGGGCTCGG TAACTTACCC GACAAGGTAA TTTCGCTACC TTAGGnACCG 60  
 TTATAGTTAC GGTCCGCCGT TTA CTTGGGGC TTCGATTCTGT ATCTTCGCAG CTATATCTCA 120  
 CTCCT 125

## (2) INFORMATION FOR SEQ ID NO: 4851:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4851:

5 AAGTTGTATT TAAAAAATAG TTCTTTAAAT TATATACCCA CCACATTG TGGGAGAACC 60  
 TAAAAAAAG CACTTTCCCC AAAAAATGGGA AAGTGC 96

## (2) INFORMATION FOR SEQ ID NO: 4852:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4852:

20 ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGnAT 60  
 GAACCGGCGA-GTTCACGATT-TAGATGCAAG-GTTGAAGCAG- 100

## (2) INFORMATION FOR SEQ ID NO: 4853:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4853:

30 CCGACAGCGT AGnCGATGGA TAACAGGTTG ATATTCCTGG TACCACCTAT AATCGTTTTTA 60  
 35 ATCGATGGGG GACCCATAGG ATAGCGAACC TGCGATTGGA T 101

## (2) INFORMATION FOR SEQ ID NO: 4854:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4854:

45 GGACATCTCC TAAGGCTAAA TACTCTCTAG TGACCGTAGT GAACCAGACC GTGAGGAAAG 60  
 50 GTGAAAnACC CCGGAGGGGA GTGAATAGAC CTGAAACCGT GT 102

## (2) INFORMATION FOR SEQ ID NO: 4855:

- (A) LENGTH: 104 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4855:

10 ATAACCGCAA TTGGCGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA 60  
CTTATCCCGT CCACACATAn CTACCCAGCT ATGCCGTTGG CACG 104

(2) INFORMATION FOR SEQ ID NO: 4856:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 138 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4856:

CTACTGTCTT CATTCTTTCA GTTCTTTTTT ACGGGTCTGT TTTCTAATTT GAGCACATCT 60  
25 TCGATTCTTT ATCAAATGAC TACCAATTAA ATCTATTCTT CTnTGGTAAA TCGCTAACTC 120  
CATCTCCTTA ACCCGGTA 138

(2) INFORMATION FOR SEQ ID NO: 4857:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 100 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4857:

40 TCAAACGnTT GTCATCTATT AAAGAAGTAG GTCTAGATAT ATCACGTACG TAATGTGTAA 60  
TGGATGGCGC TATTGCTTTA GGTATCCAT TAGGTGCTAC 100

(2) INFORMATION FOR SEQ ID NO: 4858:

45

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4858:

55

CCTGTGTGTT TGATAAACAG TCGGTTGGGC CTATTCAGTG CGGCTT

106

## (2) INFORMATION FOR SEQ ID NO: 4859:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 152 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4859:

GTAACGCGCC GGTTCATTCT ACAAAGGGC ACGCCAATCA CCCATTAACG GGCTCCTGAA 60  
 CTACTTGTTA AGCAACACGG TTTCCAGGGT TCTATTTCCTA CTTCCCCCTT CCGGGGTnGC 120  
 TTTTCAACC TTTTCCCCC TCCACGGTTA CT 152

## (2) INFORMATION FOR SEQ ID NO: 4860:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 100 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4860:

GCCCGTACCG CAAACCGACA CAGGTAGTCA AGATGAnGAA TTCTAAGGTG AGCGAGCGAA 60  
 CTCTCGTTAA GGAACGCGC AACTGACCC CGTCACTTCG 100

## (2) INFORMATION FOR SEQ ID NO: 4861:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4861:

CAGGTAACAC TGAATGGAGG ACCGAACCGA CTTACGTTAA AAAGTAAGCG GATGAACTAA 60  
 AGGTAGCnGA GAAATTCCAA TCGAACCTGG AGATAGCTGG TTCT 104

## (2) INFORMATION FOR SEQ ID NO: 4862:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 87 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4862:

TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA 60  
 CCTCCTGCGT GCAAAGCAGG CGCTCTG 87

## (2) INFORMATION FOR SEQ ID NO: 4863:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4863:

ACCGTTTGAT TTCTTATCTA ATTCAAGCTT ATTTAAACT CTTTATTCAC TCGGTTTTGG 60  
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAnTTTTCA ATGTA 105

## (2) INFORMATION FOR SEQ ID NO: 4864:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4864:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60  
 TGCCTTGCTG GATGATGCTA TGATATTGCA CATATCGAAT CAACAGTGGT GCATGAACCT 120  
 GCAnTGGCT 129

## (2) INFORMATION FOR SEQ ID NO: 4865:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4865:

AAACCGCAAG GTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC 60  
 TCGACTACnT GAAGCTGGAA ATCGCTATAA ATCGTAGATC 100

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 115 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4866:

GTGATAAGAT TAGCAGAAAA TGGATGGTGT TAAGAGAGTT AATTGGTTTG GGGGTATGCT 60  
TATTTTAAAT GGCATTGTGT ACGAGAGCAT TAGAGTTTGT ACTTGTGAGG TTATT 115

(2) INFORMATION FOR SEQ ID NO: 4867:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 90 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4867:

ACACCACTCC TCATTAACCT TCCAGCACCG CAGCAGGCGT CACCCCTATA CATCACCTTA 60  
CGGTTTAGCA GAGACCTGTG TTTTGTATAA 90

(2) INFORMATION FOR SEQ ID NO: 4868:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4868:

CACGAACGAT TGTCTTGCCT GCGGGGATTA TCTGACACGG TACCGGTCAA ACAGTGAATC 60  
GCTACTGCTC ATCAGGGATT ACAAACC 87

(2) INFORMATION FOR SEQ ID NO: 4869:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 165 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4869:

CGCTCACCTT AGAATCTATT TACACTGGTG TTGGTAGGCA CTTTTTTCAA GCTTCCGATT 120  
 AACACATGAA AAGCTTCCAA AGTACTAGGA CGTTCAATAC ATGTA 165

(2) INFORMATION FOR SEQ ID NO: 4870:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 111 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4870:

AATATCATTT ATAACATTAA GTAATAACTT TTTTATCTT GTCCATTTTA TTTTnAACC 60  
 AAAATTGAT TAAAAAACTG CCTGGCAACG TTCTACTCTA GCGGAACTAA G 111

(2) INFORMATION FOR SEQ ID NO: 4871:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 84 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4871:

TAGCAGAGAC CTGTGTTTTT TGATAAACAG TCGCTTGGGC CTATTCCTG CGGCTCTTCT 60  
 GGGCGTTAAC CCTAAAGAGC ACCC 84

(2) INFORMATION FOR SEQ ID NO: 4872:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4872:

ACAGTAAAGC TCCACGGGTC TTTCCGTCCT GTCGCGGGTA ACTGCATCTT CACAGGTACT 60  
 ATGATTTCAC CGATCTCTCh ATGAACAGTG CCAAATCGTA C 101

(2) INFORMATION FOR SEQ ID NO: 4873:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 87 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4873:

5 GACAGGCGTA GGCGATGGAT AACAGGTTGT ATTCTGTAC CACCTATGAT CGTTTTAATC 60  
GATGGGGGGA AGCATAGGAT AGGCGAA 87

## (2) INFORMATION FOR SEQ ID NO: 4874:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 81 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4874:

20 GGGAGAGCGC CTGCTTTGCA CGCAGGAGGT CAGCGGTCG ATCCCGCTAG TCTCCACCAT 60  
TATTTGTACA TTGAAACTA G 81

## (2) INFORMATION FOR SEQ ID NO: 4875:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 81 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4875:

TATGTTTCGA AATATCTTTA TCACTCTAAA ATGATATACA AGAAATCCAA GAAAAATAAG 60  
35 CGAACTGAAT AAATAAAGAT T 81

## (2) INFORMATION FOR SEQ ID NO: 4876:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 87 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4876:

AACGCGTTAA ATCTTTTAT AAAAGACGTA ACTTCATGTT AACGTTGCTT ATAAAAATGG 60  
50 TGGAACATAG ATTAAGTTAT TAAGGGC 87

## (2) INFORMATION FOR SEQ ID NO: 4877:

55

- (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4877:

10 ACRACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG TTCACATCGA 60  
 CGGGGAGGTT TGnCTCAAT GTGGCTCATC GGATCTTGGG G 101

(2) INFORMATION FOR SEQ ID NO: 4878:

15

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 79 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4878:

25 ATTATTAGG TGTACAAATG ACCACCGCAT CAACAAGTTT AAACAGCTCG CTAGGTGTCT 60  
 CAACTGCATG AGGTATATT 79

(2) INFORMATION FOR SEQ ID NO: 4879:

30

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 83 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4879:

40 ACATCGTTTC AATGGGTCGC TAACGCTGCT AGGACATTAT AACAGACGTG TACAAAAAGA 60  
 AAATTGGTAT GGTAATTGTG GCA 83

(2) INFORMATION FOR SEQ ID NO: 4880:

45

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 84 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4880:

55 CTTTCATCCTG ATCCAGATCA AACTCTCCAT AAAAATTATG ATGTTTGATT AGCTCATAAA 60

## (2) INFORMATION FOR SEQ ID NO: 4881:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4881:

TTGTGCAGTT GCATCGCCAT TGATCAATAA CACGTTGAGC TGCAGTTATT TCAGTTTCTG 60  
 CTTACAGCTT CTTTCGATTA 80

## (2) INFORMATION FOR SEQ ID NO: 4882:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4882:

TCTGATGTGA AAGCCCACGG CTCAACCGTG GAGGGTCATT GGAAACTGGA AAACCTTGAGT 60  
 GCAGAAGAGG AAAGTGGGTT CCATGT 86

## (2) INFORMATION FOR SEQ ID NO: 4883:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4883:

TGATCGCATA TCTACGCAAC ATCGGCATAA GTnTGATGAC AAACAAGCTT CCATGACAAA 60  
 AGTAATGGAC GAATATCGCA TTTGGGGAAA GTCCTCTAAA AATGCCTTTT GAAGGAACGT 120  
 CGGTTAA 127

## (2) INFORMATION FOR SEQ ID NO: 4884:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4884:

AGTAGGAATC GAACCCACAC CAAAGTTTTG GAGACCTCTA TTCTACCTTG AACTATGCCC 60  
CTATTAAAAA TAATAAAT 78

(2) INFORMATION FOR SEQ ID NO: 4885:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 84 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4885:

CTCACTATTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT 60  
GTGGATTGTC CTTTGGAAT GGGT 84

(2) INFORMATION FOR SEQ ID NO: 4886:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4886:

GGTATCTGTT CACTCTTCG GTGGTGCAGT TGCGACCAAC AATGGGTTGG AGATTGGATT 60  
TCATCCTTCT CAATTAATCG TTGCCGTACT TTTCAANTGG TACCCCATCC AAAAGGG 117

(2) INFORMATION FOR SEQ ID NO: 4887:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 80 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4887:

CGGATCTGGG AGGAAATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCACT 60  
ACCGTGAGGA AAGGTGAAAA 80

(2) INFORMATION FOR SEQ ID NO: 4888:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4888:

AATATGCAAG CACATGGTGA ATATGACGAG GTTGCAACTT CAACGGCGAA GATGATGGAA 60

10

GGCCTTACGT TTGCGTG 77

(2) INFORMATION FOR SEQ ID NO: 4889:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4889:

TCTTCTGGGC GTTAACCTA AAGAGCACCC CTTCTCCCGA GTTACGGGGT CTTTGGCGA 60

25

GTTCCTTAAC GAGAGT 76

(2) INFORMATION FOR SEQ ID NO: 4890:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4890:

GTGGGGGCCC CAACATAGGA GCTGATTTTC TGTCAGCTTA CCATATGTG GCAAGTTGGC 60

GGGGGCCCCC AAACCAAGGA GCTGGCTTTC TGTCACITTA CCATTAATGT GGCAAGT 117

40

(2) INFORMATION FOR SEQ ID NO: 4891:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4891:

TTAATCCnCC TGCATATGAT GACTTTGTTG AACCGTCATT GCATACTTTC AACATGAATA 60

CGCTGAACAC CTTCACTTAC TGCATATCTT AGTTCCTCGG TCTGTCTTA 109

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4892:

CTCTTAACCT TGCAGCACCG GGCAGGCGTC AGCCCGTATA CATCACCTTA CGGTTTGCAG 60  
 AGACCGTGTG TTTTGTAGAA ACAGGTGC 88

## (2) INFORMATION FOR SEQ ID NO: 4893:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4893:

TAGCGAATGA GATAAACGCG GCGGACTGTA AATCCGCTCC TTCGGGTTCC GCAGTTCGAA 60  
 TCTGCCCCCC TCCATTTATT ATTTTAAAAA AAAGCATAGT TC 102

## (2) INFORMATION FOR SEQ ID NO: 4894:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4894:

CGAGCGATTC CGACTCAGAC AATGACTCGG AATTCAGATA ACGAATCTGA CTCAGACAGT 60  
 GACTCAGATT CCGACAGT 78

## (2) INFORMATION FOR SEQ ID NO: 4895:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4895:

TTAGTATTTCG CACTCACATG TCACATGCTT CACTCGACCT ATTACCTCAC ACTTGGGGAC 120  
TTATACCGAG TnGGAATCTC A 141

5 (2) INFORMATION FOR SEQ ID NO: 4896:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 80 base pairs  
    (B) TYPE: nucleic acid  
10      (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4896:

GTTTCGGATT T AATTTGATT C ATTTGTTGCG TAATTTT CAG A GCCATTTTA TGAAAAGAGT 60  
GATTTAATTC ATAAATTTCT 80

20 (2) INFORMATION FOR SEQ ID NO: 4897:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 73 base pairs  
    (B) TYPE: nucleic acid  
25      (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4897:

30 GGTATGGCTG GCGCTTTACG TGCCACATTA GATTATGTCA CTGAGCGTAA GAAGTTCGGC 60  
AAACCAATTA GTA 73

(2) INFORMATION FOR SEQ ID NO: 4898:

- 35 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 71 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
40      (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4898:

45 GTGCCGAGGA CCGGAATCGA ACCGGTACGG TGATCACTCA CCGCAGGATT TTAAGTCCTG 60  
TGCGTCTGCC A 71

(2) INFORMATION FOR SEQ ID NO: 4899:

- 50 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 116 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4899:

5 AGCCGCTGGA TTCCACGGTG TAAGCAGTAA GGCTGAGTAT TAGGCAAATC CGGTACTCGT 60  
 TAAGGCTGGA GCTGTnCATG GGGAGAAGAC ATGTGTGCTT ACGTAGTGCg TGGTTT 116

## (2) INFORMATION FOR SEQ ID NO: 4900:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 113 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4900:

15 TTCCGGCCCC TGGCGGTnTC CTAGGAGTTC CACGGAACCC CAGGATTTTG TAGGACCCCC 60  
 20 CGGGCAGAGT CCCCTTCGAC TAAGAAAATC TCACATTCTT CAGGGACTTT TAC 113

## (2) INFORMATION FOR SEQ ID NO: 4901:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 78 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4901:

30 ACTTAATGGA TTGATTAAGT AGTGGGTTCT TAACATTAGG CCTCAGCTAA TGTGGTACTT 60  
 35 AAAAATAGGG AATACATG 78

## (2) INFORMATION FOR SEQ ID NO: 4902:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 84 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4902:

45 ATGGGACATG GTGTGCCTCC TTGCTATAGT CACCAGACAT ATGAATGTAA TTTATACATT 60  
 50 CAAAACTAGA TAGTAAGTAA AAGT 84

## (2) INFORMATION FOR SEQ ID NO: 4903:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4903:

10 TTGTCGGGTA AGTCCGACC CGCAGGAAG GCGTAACGAT TTTGGCACTG TCTCAACGAG 60  
AGACTCGGTG 70

(2) INFORMATION FOR SEQ ID NO: 4904:

15

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 151 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4904:

25 TAAGTTGGCT ACCATCGACG CTAAGAACCT TTCTTGACTT GTGACAATCG CTGCTTCTT 60  
TCCTCTTCTT GGCTCTGCTT CTATTTGCCT CTAATGTGGC TTTTGTGTGT AATAAGTTAT 120  
GCGCTTCGGT GTTATnGTGA AAAAGCGGTC A 151

30 (2) INFORMATION FOR SEQ ID NO: 4905:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 75 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4905:

40 TGAATTGTAG GCGCTGGTGG GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC 60  
TTATCGTGGT GGGGA 75

45 (2) INFORMATION FOR SEQ ID NO: 4906:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 112 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4906:

55

ACTCAGACAG TGA CT CAGAT CAGATAGT G<sub>n</sub> CTCGGATTCA GCGATTATTC AG

112

## (2) INFORMATION FOR SEQ ID NO: 4907:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4907:

GTAAAAACAC CCCAGCCAGG TCACTTTACG CCTACGCATC GCTTGACAC GTGCTACTAA  
AGGTTTACCA

60

70

## (2) INFORMATION FOR SEQ ID NO: 4908:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 121 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4908:

AGAAGATACA AATAAAG<sub>n</sub>TA AACCCAAATT ATTCAATTTTC GGTGGGACAC AATAGTGTG  
ACTTTGAAGA AGATACACTT TCCACCAAG TTAAGTGGGT CCATAATTGA AGGGTCCAAC  
C

60

120

121

## (2) INFORMATION FOR SEQ ID NO: 4909:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4909:

GGGAACAAAG TGGACAGGTG GTGCATGGTT GTCGTCAACT CGTGTCGTGA GATGTTGGGG  
TTAAGTCCCG

60

70

## (2) INFORMATION FOR SEQ ID NO: 4910:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 100 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4910:

5 GGACACCCCG AGAACTGAAA CATTTAGTAC CCGGAGAAGA GAAGAAATTC GTTCCCTTAG 60  
TAGCGGGACG AACGGGAGAG CCCAAACCAC AGCTTGTGnG 100

(2) INFORMATION FOR SEQ ID NO: 4911:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 155 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4911:

20 nTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGCTA TAGTCACCAG ACAAATAAC 60  
TTACTTATTC ATGATACACG CTTAATTAAT AAGGTGCAAT AGTTAATTTT ACACTTTGAT 120  
GTAAACTTTG GCACATCAGC TTTTAGTGTG TTTGCG 155

(2) INFORMATION FOR SEQ ID NO: 4912:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4912:

35 CCCGTCACAC CACGAGATTT GTAACACCCG AAAGCCGGTG GAGTGAACCT TTAGGAGCT 60  
AGCCGTCGA 69

(2) INFORMATION FOR SEQ ID NO: 4913:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4913:

50 TATGCTCTCC CAGCTGAGCT AATTCTCCGA TTAAACTG CCTGGCAACG TTCTACTCTA 60  
GCGGAACGT 69

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 bas pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4914:

CAAATGCTTC TGTCAATTCG ATCAAATCAA TGTCTTCAAC AGATAGATTG CTGAGTGACA 60  
ATACTTCAT 69

(2) INFORMATION FOR SEQ ID NO: 4915:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4915:

TATTTCCGGAG AGAACCAGCT ATTTCCAGGC TCGATTGGAA TTTCTCCGGT ACCCTCAGTT 60  
CATCCGCTCA 70

(2) INFORMATION FOR SEQ ID NO: 4916:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 67 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4916:

TCACCCATTA ACGGGCTCTA ACTACTTGTA AGCACACGGT TTCAGGTTCT ATTCACTCC 60  
CCTTCCG 67

(2) INFORMATION FOR SEQ ID NO: 4917:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 161 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4917:

TCCACCGTTG ACTAAGGTTT CAGAGAGGCT CGTCCCTCTG GGTAGTCGGG CCTAAGCTGA 120  
GGCGCACGTA GGCGATGATA CAGGTTATAT CCTnACACCT A 161

5 (2) INFORMATION FOR SEQ ID NO: 4918:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 68 base pairs  
    (B) TYPE: nucleic acid  
10     (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4918:

GCACGTAGTT AGCCGTTGGC TTTCTGATTA GGTACCGGCA AGATGTGCAC AGTTACTTAC 60  
ACATATGT 68

20 (2) INFORMATION FOR SEQ ID NO: 4919:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 78 base pairs  
25     (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4919:

GAAAGCAAAT GTCTTCGTTG CAATTCGATC AAATCAATGT CTTCAACAGA TAGATTGCTG 60  
AGTGACAATA CTTCAGGG 78

35 (2) INFORMATION FOR SEQ ID NO: 4920:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 68 base pairs  
    (B) TYPE: nucleic acid  
40     (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4920:

AATTTGCTA CCTTAGGGAC CGTTATAGTT ACGGCCGACG TTTACTGGGG CTTGATTTCG 60  
TACTTCGC 68

50 (2) INFORMATION FOR SEQ ID NO: 4921:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 67 base pairs  
    (B) TYPE: nucleic acid  
55     (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4921:

5 AATCATAGTA CCTGTAAAGA TGCAGGTTAC CCGCAACAAG ACGGAAAGAC CCCGTGGAGC 60  
TTTACTG 67

(2) INFORMATION FOR SEQ ID NO: 4922:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4922:

GGGAGCTGTA ATAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT 60  
20 GTCATG 66

(2) INFORMATION FOR SEQ ID NO: 4923:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4923:

GTGGAGGCGC TGGTGGGATA CTACCCTAGC TGTGTTGGCT TTCTAACCCG CAACCACTTA 60  
35 TCGTGGGTGG GAG 73

(2) INFORMATION FOR SEQ ID NO: 4924:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 89 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4924:

GAGGTCAGCG GTTCGATCCC GCTAGTCTCA CCATTTATTT TTTACACGAT GACATGAAAC 60  
50 TGATGACATA TGCACCGTAA TTCCAAAAA 89

(2) INFORMATION FOR SEQ ID NO: 4925:

- (A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4925:

10 AATGGCATCG GAGTTGTCTG AATTCGGTAA CCCGAGAGGC CCCTCGTCCA AACAGGCTCT 60  
ACCTCCAA 68

(2) INFORMATION FOR SEQ ID NO: 4926:

15

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4926:

25 ACGAAAGGCG TAACGATTTG GGCAGTGATC TCGACGAGAG ACTCGTGAAA ATCATAGATA 60  
CCTGTGAAGA TGC 73

(2) INFORMATION FOR SEQ ID NO: 4927:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4927:

40 ATTTCTATTA ATTATTGCA TAGAAATCAG CTTTTTGAT ATGTATTTTA TAATGTACAG 60  
CTCGTTGAG 69

(2) INFORMATION FOR SEQ ID NO: 4928:

45

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4928:

55 AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACATCTC CTCTCAAATT TCCTACGCCC 60

## (2) INFORMATION FOR SEQ ID NO: 4929:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4929:

GGCGGGGCCC CAACACAGAG GCTGGCGGAA AGTGCAGCTT ACAATAGTGT GCAAGTTGGG 60  
GTGGGTCCCG ACACAGAGAA ATT 83

## (2) INFORMATION FOR SEQ ID NO: 4930:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4930:

CTTGGTAGAG CACTTGGTTT GGGACCAAGG GGTCGCAGTT CGAATCCTGT CTTCCCGATT 60  
ACTCTA 66

## (2) INFORMATION FOR SEQ ID NO: 4931:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4931:

AAGAAGCTTG TTATGCTGCA ACACCAGCAA TTCAAGTAGC TAAAGATTAT TTAGCAACTA 60  
GACCG 65

## (2) INFORMATION FOR SEQ ID NO: 4932:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TGCAGAAGAG GAAAGTGGAA TTCCATGTGT AGGGTGAAAT GCGCATAGAT ATGGCAGGAA 60  
CACCAGTGGG CGA 73

(2) INFORMATION FOR SEQ ID NO: 4933:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4933:

TCGCTATCCG AGTCTGGGTC GCTATCTGAG TCTGAGTCGC TATCTGAGTC TGAAATCGCT 60  
GTCTG 65

(2) INFORMATION FOR SEQ ID NO: 4934:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 120 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4934:

GAGCATGTGG GTTTAATTCG AAGCAACGCA GAGAACCCTG ACCAAATCTT GGACATCCT 60  
TGACAACTCT GAGAGATTAG AGCCTTGCCC CTTGCGGGGT AACAAATGTA CAGGTTGGTG 120

(2) INFORMATION FOR SEQ ID NO: 4935:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4935:

GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA GGCCGAGCAG GTACGGCGAT 60  
GGATAACGGT TG 72

(2) INFORMATION FOR SEQ ID NO: 4936:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4936:

5 CACATCAGCG TCAGTTACAT ACCAGAAAGT CGCCTTCGCC ACTGGTGTTC CTCCATATCT 60  
CTGC 64

## (2) INFORMATION FOR SEQ ID NO: 4937:

- 10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4937:

15 ATCACCTGGT GTAAACCAAT TAGTACGTGT ATATATCGTT CAAAACCGTA AAATTCATGT 60  
20 TGGT 64

## (2) INFORMATION FOR SEQ ID NO: 4938:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4938:

30 CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAACATC TAAGCATGAA GCCCCCTCAA 60  
35 GAT 63

## (2) INFORMATION FOR SEQ ID NO: 4939:

- 40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4939:

45 TAGAAATCAG CTTTTTTGCA TATGTATTTT ATAATGTACA GTCGTTGAG CTGCTATTTT 60  
50 CCT 63

## (2) INFORMATION FOR SEQ ID NO: 4940:

- (A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4940:

10

GGTAGTCGAA CTTACGTTCC GCTAGAGTAG AACTTGCCAG CAAATGACAA ATCGGAGAAT 60

TAGCTCAG 68

## (2) INFORMATION FOR SEQ ID NO: 4941:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4941:

25

CTGAAACATC TTAGTACCCG GAGAAGAGAA AGAAAATTCG ATTCCTTAG TAGCGGCGAG 60

CG 62

## (2) INFORMATION FOR SEQ ID NO: 4942:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4942:

40

TTACAACAAT GCAATTGGCG GGGCCCAACA TAGAACTGGC AATAGTTACT TTCAATAATG 60

TGCAAGTTGG GGTAGGGCCC AACACAGAA 89

## (2) INFORMATION FOR SEQ ID NO: 4943:

45

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4943:

AATGGACAAT ATGTCAACGT TAATTCCAAA AAACGGTAAC TATAATTTAC AAACATTATT 60

55

## (2) INFORMATION FOR SEQ ID NO: 4944:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4944:

CCCGTGAAAG ATGATGAGGT TAATAGGTTT GAGGTGGAAG CATGGTGACA TGTGGAGCGT 60  
 GACGAATACG TAATTGA 77

## (2) INFORMATION FOR SEQ ID NO: 4945:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4945:

GAATAGGTCG ATGTATTTGG CGACCGAAAC CAGGAATCTA CCCTTGGTCA GGTGAAGTT 60  
 CAGGTAACAC TGAAT 75

## (2) INFORMATION FOR SEQ ID NO: 4946:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4946:

ATCAGAAGGC ACACCCGAGA ATGAAACATC TAGTACCCGG AGAAGAGAAA GAAATTCGAT 60  
 TCCCTATAGC GGCGnCGAAA CGGAAGAGCC AACCACAGCT GCTTTGGTTT GACCCATCGG 120  
 TACAGCGCTG AACT 135

## (2) INFORMATION FOR SEQ ID NO: 4947:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4947:

GATTGGGCT CTTCATTTC GCTCGCCGCT ACTAAGGGAA TCGAATTTC TTTCTCTTC 60  
 5 T 61

## (2) INFORMATION FOR SEQ ID NO: 4948:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4948:

GCTTTTGAGG AATTTAATAT CAATATATAT TCTGTGTATG AAAATATTTT TCATAAAAAT 60  
 20 TGTTTGAATC 70

## (2) INFORMATION FOR SEQ ID NO: 4949:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4949:

CTTCGACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACCAAGT ACTAAACGCC 60  
 35 CTATTC 66

## (2) INFORMATION FOR SEQ ID NO: 4950:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4950:

GGGTGTTACA AAATATCGTG GTGTGACGGG GCGGTGTGTA CAAGACCCCG GGTACGTTTT 60  
 50 TCACCGTAGG CATGCTGG 78

## (2) INFORMATION FOR SEQ ID NO: 4951:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4951:

CCGCGATAAT AAAAATAAT GGCGGAGGAA GAGGGATTCTG AACCCCGTG GCCCGTTAAG 60

G 61

(2) INFORMATION FOR SEQ ID NO: 4952:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4952:

ACTTATCTAG TTTTCAATGT ACAATGTCTT TTTAGTCAGC GCTCGCATAA GCAATATCAC 60

TGTAACCA 68

(2) INFORMATION FOR SEQ ID NO: 4953:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4953:

ACTGACGCTG ATGTGCGAAA GCGTGGGGAT CAAACAGGAT TAGATACCCT GGTAGTCCA 59

(2) INFORMATION FOR SEQ ID NO: 4954:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4954:

CGTGAGCGCT AGCTGTACGT GGAGGCGCTG GTGGGATACT ACCCTAGCTG TGTTGGCTTT 60

(2) INFORMATION FOR SEQ ID NO: 4955:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4955:

AAGGCGTAAC GATTGGGCA CTGTCTCAAC GAGAGACTCG GTGAAATCAT AGTACCTGT 59

10

(2) INFORMATION FOR SEQ ID NO: 4956:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4956:

20

AATAGGTGCC CGTACCGCAA ACCGACACAG GTAGTCAAGA TGAGAATTCT AAGGTGAGC 59

(2) INFORMATION FOR SEQ ID NO: 4957:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4957:

ACACGTTTAG TTCACGCGGG TTTGCTTGG TAAATCTAT ATTTACTTA CTTATCTAGT 60

35

TTCAATGTA CAATTTT 77

(2) INFORMATION FOR SEQ ID NO: 4958:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4958:

TGTCGTCAGC TCGTGTCTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCTTAA 59

50

(2) INFORMATION FOR SEQ ID NO: 4959:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4959:

GACTTGAACC CCCAACCTAC TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG

59

(2) INFORMATION FOR SEQ ID NO: 4960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4960:

TATTAAGTGG TGACTTAGCG AGATGGACAA CGATGGCGAT ATATTTATTA TTGACCGCA

59

(2) INFORMATION FOR SEQ ID NO: 4961:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4961:

ATGATTATCA TATTGCCTTA AATATCGCCA CAATTTTAGC GGGTGGTGAT TTACCAAGA

59

(2) INFORMATION FOR SEQ ID NO: 4962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4962:

CGCCGAAAAT TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACA

59

(2) INFORMATION FOR SEQ ID NO: 4963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TTAAGCTTAG TTGCCATCAT TAAGTTGGGC ACTCTAATGT TGACTGCCGG TGACAAACCG 60

(2) INFORMATION FOR SEQ ID NO: 4964:

- 5 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 59 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4964:

15 TAGTTTTGGT ACGGTAACAA ATTTATTTGA AGAAACAATC TCAAATAAAG AATTGTTTG 59

(2) INFORMATION FOR SEQ ID NO: 4965:

- 20 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 59 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4965:

AGTTCGGTCC CTATCGTCG TGGGGCGTAG GAAATTTTAG AGGAGCTGTC CTTAGTACG 59

30 (2) INFORMATION FOR SEQ ID NO: 4966:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 59 base pairs  
    (B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4966:

40 TACAAAGGGC AGCGAAACCG TGAGTCAAAG CAAATCCCAT AAAGTTGTTC TCAGTTCGG 59

(2) INFORMATION FOR SEQ ID NO: 4967:

- 45 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 65 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4967:

CCATTGCAGC ACCGACAGCC ACACCATTTA TTTTTCGCT ATGTATATCG CATTAAACGT 60

## (2) INFORMATION FOR SEQ ID NO: 4968:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4968:

GCCTCCGTTA CTTTtagagg CGACGCCAG TCAAAGTCC CGCTGACACT GTCTCCACCC 60

## (2) INFORMATION FOR SEQ ID NO: 4969:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4969:

CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC GCCGTTTACT GGGGCTTCG 59

## (2) INFORMATION FOR SEQ ID NO: 4970:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4970:

CATCTGTCAC AGGTACTATG GATTTACCG GAGTCTCTCG TTGAGACAGT GCCCAAATCG 60

TTACG 65

## (2) INFORMATION FOR SEQ ID NO: 4971:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4971:

CTAGAGTTGG CATACCAGTC CGTCGCTAAG GAACCTTTCT TGACTTGATG ACAATCGACT 60

## (2) INFORMATION FOR SEQ ID NO: 4972:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4972:

AGACCCCGTG GAGCTTTACT GTAGCCTGCA TATTCGAATT CGGCACAGCT TGTACAGGAT 60  
AGGTAGG 67

## (2) INFORMATION FOR SEQ ID NO: 4973:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4973:

TGTGTACTTA AAAATATGAA TACATGAGTA AAATCATGC ATAAGAAATA CTAATTTTC 58

## (2) INFORMATION FOR SEQ ID NO: 4974:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4974:

ACCTCCAATA ATCATCACTT GAGGCTAGCC CTAAAGCTAT TTCGGAGAGA ACCAGCTA 58

## (2) INFORMATION FOR SEQ ID NO: 4975:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4975:

GACGCCACAT CCTTTTCCAC TTGGCGTGTG TTTTGGGACC TTGGCTGGTG GTCTGGGCTG 60

(2) INFORMATION FOR SEQ ID NO: 4976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4976:

TCACTAAGTC CGTCTTTTGA CCTGACTCG ACTTG TAGGT CTCGCAGTCA AGCTCCCTT

59

(2) INFORMATION FOR SEQ ID NO: 4977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4977:

TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG TTTTAAAT

58

(2) INFORMATION FOR SEQ ID NO: 4978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4978:

GTGAGGTACG TCCAGAATGG GGATTGGCTA AAAATGCATC ATTTATAATT GGACGACG

58

(2) INFORMATION FOR SEQ ID NO: 4979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4979:

TCGCTATCTG AATCCGAGGT CGCTATCCGA ATCTGGAGTC GCTATCTGGA GTCTGGAATC

60

(2) INFORMATION FOR SEQ ID NO: 4980:

- (A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4980:

10 AAGAAGGTAA TAATCCTGTA GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGAGTAC 58

(2) INFORMATION FOR SEQ ID NO: 4981:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 75 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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~~(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4981:~~

GTGGTGTGTT AGGGCACTCT ATACGGGTTA CAAGTACGA CATTAGACGG ATCATCTGGA 60

AAGATGAATC AAAGT 75

25

(2) INFORMATION FOR SEQ ID NO: 4982:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4982:

GTTTTTCATT TTCATTTATA TTTATATTAG TGTTAATCCA ATCATAGATT TATCTATA 58

(2) INFORMATION FOR SEQ ID NO: 4983:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4983:

50 TGACAGCTAA CTATTGGCCA GCTTCTATGT TGGGGCCCCG CCAACTTGCA TTGTCTGTAG 60

A 61

(2) INFORMATION FOR SEQ ID NO: 4984:

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- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4984:

10 GGTGTTTTTA AGTCTGATGT GAAAACCCAC GGCTCAACCG GTAGAGGTCA TTGGAAACTG 60  
GAAA 64

(2) INFORMATION FOR SEQ ID NO: 4985:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 59 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4985:

25 CAGCATACAA TAATGTGCAA GTTGGTCGGG GCCCCAACAT AGAGAATTTC AAAAGAAAT 59

(2) INFORMATION FOR SEQ ID NO: 4986:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 57 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4986:

TGATGAAGGT CTTCGGATCG TAAACTCTG TTATTAGGGA AGAACATATG TGTAAGT 57

(2) INFORMATION FOR SEQ ID NO: 4987:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 57 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4987:

50 AAAGAATTTC CGCAAACGC TATCGATACT GAAGGGCGTT CAATGATTAT CATGGGT 57

(2) INFORMATION FOR SEQ ID NO: 4988:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 57 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4988:

TTGTCACAAG TCAAGAAAGG TCTTTAGCGA CGATGGTAGC CAACTTACGT TCCGCTA

57

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(2) INFORMATION FOR SEQ ID NO: 4989:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4989:

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TAGGACCGTT ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAG

57

(2) INFORMATION FOR SEQ ID NO: 4990:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4990:

AAAGTCAACG TTAATTCCAA AAAACGTAAC TATAAGTTAC TAACATTATT TAGTATTTAT

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(2) INFORMATION FOR SEQ ID NO: 4991:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4991:

TCCACGGGGT CTTTCCATCC TGTCTCGGGT AACCTGCATC TTCACAGGTA CTATGATTTT

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ACCGA

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(2) INFORMATION FOR SEQ ID NO: 4992:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4992:

GTGCGGCTGG ATCACCTCTT TCTAAGGAT ATATTCGGAA CATCTTCTTC AGAAGAT

57

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(2) INFORMATION FOR SEQ ID NO: 4993:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4993:

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CCAATGCGGC TCATCGCATC CATTTCCTGC CTGGCAACGT TCTACTCTAG CGGAACG

57

(2) INFORMATION FOR SEQ ID NO: 4994:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4994:

CTGGTTTCGG GTCTACGACA AATACTAAAC GCCTATTCAG ACTCGCTTTC GCTACGG

57

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(2) INFORMATION FOR SEQ ID NO: 4995:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4995:

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CAAACCTCTCG TGGTGTGACG GGCAGGTGTGG TACAAGCCCC GGAACGTAT TCACCGTAGC

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ATGCCGGTCT ACG

73

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(2) INFORMATION FOR SEQ ID NO: 4996:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4996:

5 ACTAATTTCT ATAGGAAAAG TATTCCTTAT CGTCGTCCCA CCCCAACTCG CACATTATTG 60  
TAAGC 65

## (2) INFORMATION FOR SEQ ID NO: 4997:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4997:

20 ATTGGATTCC CAATTTCTAC AGACAATGCA GTTGGGGTGG GACGTCGAAA TAAATTTT 58

## (2) INFORMATION FOR SEQ ID NO: 4998:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4998:

30 AACTTCAACA GGTTTTGCAG GTGGCGGTGC GACTGCAGGA AGACGTTAAA TTAATG 56

## (2) INFORMATION FOR SEQ ID NO: 4999:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4999:

45 GGGCAGGCGT CAGCCCTATA CATCACCTTA CGGTTTAGCA GAGACCTGTG TTTTGT 56

## (2) INFORMATION FOR SEQ ID NO: 5000:

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5000:

TTAGGACCCG ACTAACCAG AGCGGACGAG CCTTCCTCTG GAAACCTTAG TCAATC

56

(2) INFORMATION FOR SEQ ID NO: 5001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5001:

GACGGGATTC TCACCCGTCT TTCGCTACTC ACACCGGCAT TCTCACTTCT AAGCGC

56

(2) INFORMATION FOR SEQ ID NO: 5002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5002:

CCTGTCCGCC TCAGCTTAGG ACCCGACTAA CCCAGAGCGG ACGAGCCTTC CTCTGG

56

(2) INFORMATION FOR SEQ ID NO: 5003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5003:

TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCA

56

(2) INFORMATION FOR SEQ ID NO: 5004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5004:

(2) INFORMATION FOR SEQ ID NO: 5005:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5005:

GACATAGATT AAGTTATTAA GGGCGCACGG TGGATGCCTT GGCACTAGAA GCCGATG 57

(2) INFORMATION FOR SEQ ID NO: 5006:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5006:

GGAACCACTA CATAATAAAT CATTAGTGGC TCTTTATCAT TCTGTCCCAC TCCCCTG 57

(2) INFORMATION FOR SEQ ID NO: 5007:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 69 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5007:

CGCTACGTTT TTCCTCAACA TTTAAGAAAA TAAAGAATGC TACAATTACG ATTGCAATCA 60

AACCAAAGA 69

(2) INFORMATION FOR SEQ ID NO: 5008:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5008:

AAAAGCTTGT TACAAGCGCT ATTTTCGTTT AGTCAACTAC TGCCAATATA ACTTCGT 57

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5009:

ACATCTTAGT ACCCGGAGAA GAGAAAGAAA ATTCGATTCC CTTAGTAGCG GCGAGC

56

(2) INFORMATION FOR SEQ ID NO: 5010:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 65 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5010:

GTTTGGACGA GGGGCCCTCT CGGTTACGA TTCAGACAAA CTCCGATGCA ATTAATTTAC

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TTGGG

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(2) INFORMATION FOR SEQ ID NO: 5011:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5011:

TTTACTTGTA TTGGAATAAT TTCATCTTTG AACCGACCAT CACGTTGTGC GTCATA

56

(2) INFORMATION FOR SEQ ID NO: 5012:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5012:

CCTTATACAT CACCTTTACG GTTTTAGCAG AAACCTGTGT TTTTGTATAA ACAGTCGCTT

60

(2) INFORMATION FOR SEQ ID NO: 5013:

- (A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5013:

10 GGGCCCAACA CAGAAGCTGG CGAAAAGTCA GCATACAAAA TTGTGCAAGT TGGCGGGTCC 60

ACA 63

(2) INFORMATION FOR SEQ ID NO: 5014:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5014:

25 TAGGGTAGTA TCCACCAAGT GGCCTCCACG TAAGCTAGCG CTTCACGTTT CAAAGGCT 58

(2) INFORMATION FOR SEQ ID NO: 5015:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5015:

CAACTCCGAT GCAATTAATT TAACTTGGGA nCAGACATGG GTGATAAGGT CGTGTTTCGAA 60

40 GGGAACAGCC AGACACAGCT AAGTCCAGAT ATATGTAAGT GGAAA 105

(2) INFORMATION FOR SEQ ID NO: 5016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5016:

CAAACGATTT ATTTATATGC TTATTTCTTT ATTTATTATT ATTACAATTA CATTTT 56

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(2) INFORMATION FOR SEQ ID NO: 5017:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5017:

10 TCTGTAGAAA TTGGGGAATC CAATTTCTCT TGGTTTGGGT CCCATCCCCA ACTTGCACAT 60  
TATTG 65

(2) INFORMATION FOR SEQ ID NO: 5018:

15

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 56 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5018:

25 GGGGATGGGC CCCAACAAAG AGAAATTGGA TTCCCAATTT CTACAGACAA TGCAAC 56

(2) INFORMATION FOR SEQ ID NO: 5019:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5019:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTC 55

(2) INFORMATION FOR SEQ ID NO: 5020:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 58 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5020:

50 TACGGCGTTT AGTATTTGGT CGTAGCCGGA AACCAGGTGA TCTACCCTTG GTCAGGTT 58

(2) INFORMATION FOR SEQ ID NO: 5021:

55

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: lin ar

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5021:

TTGTGCGGGT CCCCGTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCCA

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(2) INFORMATION FOR SEQ ID NO: 5022:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5022:

20

AGAGTTCACA TCGACGGGGA GGTITGGCAC CTCGATGTCG GCTCATCGCA TCCTG

55

(2) INFORMATION FOR SEQ ID NO: 5023:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5023:

CCTTAGCTGG TGGTCTGGGC TGTTTCCCTT TCGAACACGG ACCTTATCAC CCATGGTC

58

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(2) INFORMATION FOR SEQ ID NO: 5024:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5024:

TAAAGGCTAA ACTACCAATG TTTCAATGG ATTTCCAAAA TGAATCATCT GGGAT

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(2) INFORMATION FOR SEQ ID NO: 5025:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5025:

TCAAACCGGA GGGGTCATTG GAAACTGGAA AACTTGAGTG CAGAAGAGGA AAGTGAATT 60  
CCA 63

(2) INFORMATION FOR SEQ ID NO: 5026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5026:

GCTTGCGTAC CTAAAGAGCA CCCCTTCTCC GAATTACGGG GTCATTTTGC CGAGTTCCTT 60  
AACG 64

(2) INFORMATION FOR SEQ ID NO: 5027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5027:

AATACATAGC ATATCATAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGA 56

(2) INFORMATION FOR SEQ ID NO: 5028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5028:

GGGCCCCCTCT CGGGTTACCA ATTCAGACAA ACTCCGAATG CCAATTAATT TAACT 55

(2) INFORMATION FOR SEQ ID NO: 5029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5029:

CGTAACTATA ACGGTCCTAA GGTAGCCGAA ATTCCTTGTC GGGTAAGTTC CGAC

54

(2) INFORMATION FOR SEQ ID NO: 5030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5030:

ATCCCCGGGG CCCCAACACA GAGAATTTTCG AAAAGAAATT CTACAGGCAA TGCAAGT

57

(2) INFORMATION FOR SEQ ID NO: 5031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5031:

TGCTTGGTAA AATCTATATT TTACTTACTT ATCTAGTTTT CAATGTACAA TTTC

54

(2) INFORMATION FOR SEQ ID NO: 5032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5032:

TCCCTATCCG TCGTGGGCGT AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGA

54

(2) INFORMATION FOR SEQ ID NO: 5033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5033:

(2) INFORMATION FOR SEQ ID NO: 5034:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5034:

TATCTGAATC TGAGTCGCTG TCTGAATCTG AATCGCTATC CGAGTCTGAG TCGC 54

(2) INFORMATION FOR SEQ ID NO: 5035:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5035:

CACCAGCAAT TCAATTAGCT AAAGATTATT TAGCAACTAG ACCGGAATGA AAAA 54

(2) INFORMATION FOR SEQ ID NO: 5036:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5036:

CTACCATCGA CGCTAAGAGC TTAACCTCTG TGTTCGGCAT GGAACAGGT GTGA 54

(2) INFORMATION FOR SEQ ID NO: 5037:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5037:

CGGCGAGTTA CGATTGTATG CAAGGTAAAG CAGTAAATGT GGAGCCGTAG CGGAAG 56

(2) INFORMATION FOR SEQ ID NO: 5038:

- (A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5038:

GACCGGGATG GACATACCTC TGGTGTACCA GTTTGTCGTG CCAACGCATA AGCT

54

(2) INFORMATION FOR SEQ ID NO: 5039:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5039:

TTTCACCGAG TCTCTCGTTG AGCAGTGCCC AAATCGTTAC GCCTTTCGTG CGGG

54

(2) INFORMATION FOR SEQ ID NO: 5040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5040:

TTATAACACG TATGCTTGGG GAGTGTAATA AGCTTGATCA GAGATTCCnA TGGGAACCAG

60

CATGAGTTAT GTCATTTATC ATATGTGATC ATAGCATATC AAAGG

105

(2) INFORMATION FOR SEQ ID NO: 5041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5041:

GGCACCTATT TTCTATCTAG AGGCTTTTCT CGGCAGTGTG GAAATCAACG ACTC

54

(2) INFORMATION FOR SEQ ID NO: 5042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5042:

ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCG

54

10

(2) INFORMATION FOR SEQ ID NO: 5043:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5043:

20

CGTTCAGTCA ACTACTGCCA ATATAACATC GTAGAGCATA GAACATTGAT TTA

53

(2) INFORMATION FOR SEQ ID NO: 5044:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5044:

ACTAGAGAGT ATTTAGACTT AGGAGTGGTC CTCCCAGATT CCGACGGATT TCACGTGCT

59

35

(2) INFORMATION FOR SEQ ID NO: 5045:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5045:

TTTCGTCGTC CCACCCCAAC TTGCACGCTA TTGTGAGCTG ACTTTTCGCC AGCTTCTGTG

60

TT

62

50

(2) INFORMATION FOR SEQ ID NO: 5046:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5046:

CGTCATCCCC ACCTTCCTCC GGTTCGTCAC CGGCAGTCAA CTTAGAGTGC CCA

53

(2) INFORMATION FOR SEQ ID NO: 5047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5047:

TATTTATTAA ACCTAATAAA GATGAATTAG AAGTGATGTT TAATACAACA GTG

53

(2) INFORMATION FOR SEQ ID NO: 5048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5048:

CCTCGGCACC ATTTTCAATA AAAACATATG CGCCCGTAGC TCAATTGGAT AGA

53

(2) INFORMATION FOR SEQ ID NO: 5049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5049:

AAATGGCCAA CTTAAGCCAG GATACAATTT ACAAATAGCG ACAAATTCTC AATGTGTTT

59

(2) INFORMATION FOR SEQ ID NO: 5050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CGAAAGACAC nCACAAGATT AATAACGCGT TTGAGTCTTT TTATAAGAC GTACTTCATG 60  
TTACGTTGAC TTTAAGATGG TGGAACATAG TTAGTTTTAG GGCCACGGGG G 111

5 (2) INFORMATION FOR SEQ ID NO: 5051:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 53 base pairs  
    (B) TYPE: nucleic acid  
10     (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5051:

ACGTTGACAT ATTGTCATTC AGTTTTCAAT GTTCATTAAT GTTCAATCTC TTT 53

(2) INFORMATION FOR SEQ ID NO: 5052:

- 20 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 53 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
25     (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5052:

30 CTGAATTCGG TAACCCGAGA GGGCCCCTCG TCCAAACAGT GCTCTACCTC CAA 53

(2) INFORMATION FOR SEQ ID NO: 5053:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 53 base pairs  
35     (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5053:

TACATAGCAT ATCAGAAGGC ACACCCGGAG AACTGAAACA TCTTAGTACC CGG 53

(2) INFORMATION FOR SEQ ID NO: 5054:

- 45 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 54 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
50     (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5054:

(2) INFORMATION FOR SEQ ID NO: 5055:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5055:

TAGGGCTAGC CTCAAGTGAT GATTATTGGA GGTAGAGCAC TGTTTGGACG AGG 53

(2) INFORMATION FOR SEQ ID NO: 5056:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5056:

ACTGCTTTGA AATGTTGTTG TCTCAGTTAA TATTCAATTG CTTTTCTTTT GCATAATTGA 60

CAA 63

(2) INFORMATION FOR SEQ ID NO: 5057:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5057:

CTATGTTGGG GCCCCGCCAA CTTGCATTGT CTGTAGAATT CCTTTTCGAA ATTC 54

(2) INFORMATION FOR SEQ ID NO: 5058:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5058:

CTGAATCCGA GTCGCTATCC GAGTCTGAGT CGCTATCTGA GTCTGAATCG CTG 53

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5059:

TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG TGATGTCAA

(2) INFORMATION FOR SEQ ID NO: 5060:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5060:

AAATAACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT AAAAAACAGC AGT

(2) INFORMATION FOR SEQ ID NO: 5061:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5061:

TTAAAGAGTG CGTAATAGCT CACTAATCGA GTGACAATGG CGCCGAAAAT GTACC

(2) INFORMATION FOR SEQ ID NO: 5062:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5062:

TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTCGC ACATCAGCGT CA

(2) INFORMATION FOR SEQ ID NO: 5063:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5063:

TCGCCAAGCC ATTTTCTTT GTGTTTCTTT TTATTTGAC GTTTTAGACA TA

52

10

(2) INFORMATION FOR SEQ ID NO: 5064:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5064:

20

CTCAAGCTCC CTTGTGCCTT TACACTCTAT GTGTGCTTTC CGACCGTTCT GGGGGGAAC

60

TTGGAGCGCC TCCGTT

76

25

(2) INFORMATION FOR SEQ ID NO: 5065:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5065:

35

CCACCGCTTG TCGGGTCCC CGTCAATTCC TTTGAGTCGC AACCTTGCGG TCGT

54

(2) INFORMATION FOR SEQ ID NO: 5066:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5066:

TCCCCGGGCT AAACATATTA CCGAAGCTGT GGATTGTCCT TTGGACAATG GTAGG

55

50

(2) INFORMATION FOR SEQ ID NO: 5067:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5067:

GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AA

52

(2) INFORMATION FOR SEQ ID NO: 5068:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5068:

CGGACACCAG AAGTACCAAG CGAGCCGGAA ACACCAACAC CACCGACACC AGACGTACAA

60

GCGAGCCGGAA ACAACAACAA CG

82

(2) INFORMATION FOR SEQ ID NO: 5069:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5069:

TCCATAACGT GCTGTATCTG TAGCAATAAC TAATACTTTT TCATTGGTC TA

52

(2) INFORMATION FOR SEQ ID NO: 5070:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5070:

CGACTCGAAG ACTCAATGTC TTCTCCCAT CACAGCTCAG CCTTAACGAG TA

52

(2) INFORMATION FOR SEQ ID NO: 5071:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5071:

GCGATGGATA ACAGGTTGAT ATTCCTGTAC CACCTATAAT CGTTTTAATC GA

52

(2) INFORMATION FOR SEQ ID NO: 5072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5072:

CACTTCACCA CAGCCGCCAT GGCATGGGCA GTAGGAATCG AACCCACACC AAA

53

(2) INFORMATION FOR SEQ ID NO: 5073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5073:

GTCCAGACTC CTACGGGAGG CAGCAGTAGG GAATCTTCCG CAATGGGCGA AA

52

(2) INFORMATION FOR SEQ ID NO: 5074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5074:

TGTTGGCTTA GAATCAGCCA TCATTTAAAG AGTGCCTAAT AGCTCACTAG TCGC

54

(2) INFORMATION FOR SEQ ID NO: 5075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5075:

AAACTTCCCT TTGG

74

## (2) INFORMATION FOR SEQ ID NO: 5076:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5076:

TGAGCTAATC AGACATCATA ATTTTATGG AGAGTTTGAT CCTGGCTCAA GAT

53

## (2) INFORMATION FOR SEQ ID NO: 5077:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5077:

GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTC CGCTAGAGTA GA

52

## (2) INFORMATION FOR SEQ ID NO: 5078:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5078:

GGGTAAGTTC CGACCCGCAC GAAAGGCGTA ACGATTGCGG CACTGTCTCA AC

52

## (2) INFORMATION FOR SEQ ID NO: 5079:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5079:

ATTAATCCAT TGTGCCACAA GTGCCGACC AGAAATGATG GTATTTAATA AT

52

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5080:

AATAGCGACG AATCACACCT TCTGCGGCAC CACGGAATAA TACACCATGT GG

(2) INFORMATION FOR SEQ ID NO: 5081:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5081:

CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAAGCGCTC CACATGTCCT TA

(2) INFORMATION FOR SEQ ID NO: 5082:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5082:

CAGACAGCGA CTCAGATCAG ATAGCGATCG GACTCAGACA ACGACTCAGA TTCAGA

(2) INFORMATION FOR SEQ ID NO: 5083:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5083:

AGGGTATGAT CCATCCCGGG TCCTCTCGGT ACTAAGGGAC AGCTCCTCTC AAATTCCTA

CG

(2) INFORMATION FOR SEQ ID NO: 5084:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5084:

10 GTGTACCAGT TGTCGTGCCA ACGGCATAGC TGGGTAGCTA TGTGTGGACG AG 52

(2) INFORMATION FOR SEQ ID NO: 5085:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5085:

TTGCTTACGC TTGCTATAGC CAATATATAG ATGTTGGAGG GGCAGATTC GAATGCGAAC 60

CCGAGGAGCG GATTAAACA 78

25

(2) INFORMATION FOR SEQ ID NO: 5086:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5086:

ACTGACGCTG ATGTGCGAAG CGTGGGGATC ACACAGGATT AGATACCCTG GT 52

(2) INFORMATION FOR SEQ ID NO: 5087:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5087:

50 AAGTTGTTCT CAGTTCGGAT TGTAAGCTGC AACTCGACTA CATGAAGCTG G 51

(2) INFORMATION FOR SEQ ID NO: 5088:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 51 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5088:

AATACTTTAA AAAAATAAGA CACTTTGGCC AACTTAAGCC AGGATACAAT T 51

10 (2) INFORMATION FOR SEQ ID NO: 5089:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5089:

20 AGAACGTAAA TTTAATCCTG ATTTAGCACC AGGGACAGAA AAAGTAACAA G 51

(2) INFORMATION FOR SEQ ID NO: 5090:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5090:

CCGCTACCCT CAGTTCATCC GCTCACTTTT CAACGTAAGT CGGTTCCGGTC C 51

35 (2) INFORMATION FOR SEQ ID NO: 5091:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5091:

CATGGGTGAT AAGGTCCGTG TTCGAAAGGG AAACAGCCCA GACCACCAGC T 51

(2) INFORMATION FOR SEQ ID NO: 5092:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5092:

TTGTGCGGAT CCCCGTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCA

55

(2) INFORMATION FOR SEQ ID NO: 5093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5093:

CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG A

51

(2) INFORMATION FOR SEQ ID NO: 5094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5094:

ACGAATACTA ATCGATCGAA GACTTAATCA AAATAAATGT TTTGCGACAA A

51

(2) INFORMATION FOR SEQ ID NO: 5095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5095:

AATCGTTGTT ACCTTCATTA TACCACTTAC TTGTGGAGTG ATCTTCTTCA AAGTAACACT

60

ATTGTGCCAC CGATTGA

77

(2) INFORMATION FOR SEQ ID NO: 5096:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TTCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CG

52

(2) INFORMATION FOR SEQ ID NO: 5097:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5097:

GGGTCTGTTT TCTAATTGA GCACAATCTT CGTTCTCAAT AGAATGATTT A

51

(2) INFORMATION FOR SEQ ID NO: 5098:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5098:

CTGTAGAAAT TGGGAATCCA ATTTCTCTAT GTTGGGGCCC ACACCCCAAC T

51

(2) INFORMATION FOR SEQ ID NO: 5099:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5099:

CTGTGGATTG TCCTTTGGCA TGAGATAGGA GAGCGTTCTA AGGGCGTTGA A

51

(2) INFORMATION FOR SEQ ID NO: 5100:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5100:

GGTTCAGAAC GTCGTGAGAC AGTTCGGTCC CTATCCGTCG TGGGCGTAGG A

51

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5101:

TGACTGATAC GATCAATGCG CTTGTAACAA GCTTTTTTCA ATTCTAGTCA GGGGCCCCAA 60  
CACA 64

(2) INFORMATION FOR SEQ ID NO: 5102:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5102:

TATTTGCATT TATATTGACG TTTTAAACAT AAAAAAAGAA ACCTTGCGGT CTCAATGG 58

(2) INFORMATION FOR SEQ ID NO: 5103:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5103:

ATTACCATTT TGGTATACCA CATCGTTATT CAACACATTA TCTTTTACTT 50

(2) INFORMATION FOR SEQ ID NO: 5104:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5104:

GGACACTGCT CCCTCAGGAG TCTCGCCATT AATACTACGT ATTAACATGT AAT 53

(2) INFORMATION FOR SEQ ID NO: 5105:

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5105:

10

ATTTCTTCTT TTTCTACAAT CGAGTCTCCT TTTACAGGTC CATATTTTGT

50

(2) INFORMATION FOR SEQ ID NO: 5106:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5106:

TGGTCAAGCG GTTAAGACAC CGCCCTTTCA CGGCGGTAAC ACGGGTTCGA

50

25

(2) INFORMATION FOR SEQ ID NO: 5107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5107:

35

TTTTTAGCAG TAATTGCCAC ATCTGTGTGA CGATAATGAT ATGCGACAGT

50

(2) INFORMATION FOR SEQ ID NO: 5108:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5108:

CAAGCCATTT TTCTTTGTGT TTACTTTTAA TTTTGACGTT TTAGACATAA

50

50

(2) INFORMATION FOR SEQ ID NO: 5109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5109:

AGCCGATGAA GGACGTTACT AACGACGATA TGCTTTGGGG AGCTGTAAGT

50

(2) INFORMATION FOR SEQ ID NO: 5110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5110:

ATCCATAACG TTTGGTATCT GTAGCAATAA CTAATACTTT TTCATTCGGT CTA

53

(2) INFORMATION FOR SEQ ID NO: 5111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5111:

CCCTTAGTAC TGCAGCTAAC GCATTAAGCA CTCCGCTGA GGAGTACGAC CTC

53

(2) INFORMATION FOR SEQ ID NO: 5112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5112:

GGAGTCAAAG TCCGTTGCCT TACCGCTTGG CTATAGCCCA ATATATAGAT

50

(2) INFORMATION FOR SEQ ID NO: 5113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

AGATTTCCTT TTCGAAATTC TTTATGTTGG GGCCCCGCCA ACTTGCATTG

50

(2) INFORMATION FOR SEQ ID NO: 5114:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5114:

GCTGTGATGG GGAGAAGACA TTGTGTCTTC GAGTCGTTGA TTCACACTG

50

(2) INFORMATION FOR SEQ ID NO: 5115:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5115:

CTTGATTAAC TCATTATCAA GTTATGCACG TGTAATGAA TTCGGCTTTA TCGAA

55

(2) INFORMATION FOR SEQ ID NO: 5116:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5116:

GTACTIONAAAA AATGAATACA TGAGTAAAGC TCATGGCATA AGAAATACTA

50

(2) INFORMATION FOR SEQ ID NO: 5117:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5117:

CAGAATCAGA TAGCGACTCA GAATCAGATA GTGAGTCAGA TTCAGCAGTn

50

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5118:

CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACnAA

(2) INFORMATION FOR SEQ ID NO: 5119:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 60 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5119:

AATCGTCGAA ACTTAATCAA AATAAATGTT TTGCGACAAA TCACTTTTAC TTACTATCTA

(2) INFORMATION FOR SEQ ID NO: 5120:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5120:

CCGAAGTTTA CGGGGTCATT TTGCCGAGTT CCTTAACGAG AGTTCGCTCG

(2) INFORMATION FOR SEQ ID NO: 5121:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 61 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5121:

ATAATCCTGT AGTCGAAAT GTTGTCTCTC TTGAGTGGAT CCTTAGTACG CCGGGGCACG

T

(2) INFORMATION FOR SEQ ID NO: 5122:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5122:

10 TAGCGACTCA GATTGAGACA GCGATTCAGA CAGCGACTCA GACTCAGATA 50

(2) INFORMATION FOR SEQ ID NO: 5123:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5123:

TATTTGTAAA TTGTATCCTG GCTTAAGTTG GCCATTTTTC ATATGGTCTT 50

(2) INFORMATION FOR SEQ ID NO: 5124:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5124:

35 CACGAGCTGA CGACAACCAT GCACCACCTG TCACTTTGTC CCCCAGAGAAG GTCTCTATCT 60

(2) INFORMATION FOR SEQ ID NO: 5125:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5125:

AGAACACATT GCAGTCTTCG AGTCGTTGAT TTCACACTGC CGTAGTAAAA GCCTCTAGAT 60

50

AGAA 64

(2) INFORMATION FOR SEQ ID NO: 5126:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 57 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5126:

GGACGACATT AGACGAATCA TCTGGAAAAG ATGAGTCAAA GAAGGTAATA GTCCTGT

57

10

(2) INFORMATION FOR SEQ ID NO: 5127:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5127:

20

GTCCTTAGTA CGAGATGACC GGGATGGACA TACCTCTGGT GTACCAGTTG

50

(2) INFORMATION FOR SEQ ID NO: 5128:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5128:

GCCGATTTTA GCAGTTGTTG CTTGTTCAA TTTTATGGGG CCATTTATGG

50

35

(2) INFORMATION FOR SEQ ID NO: 5129:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5129:

45

TCCACACATA GCTACCCAGT CTATGCCGTT TGCACTACAA CTGGTACACC A

51

(2) INFORMATION FOR SEQ ID NO: 5130:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5130:

CTCAGTTGGT TGAGCATCTG ACTTTTAATC AAAGGGTCAA GGGTCGAATC CTCTTTT

57

(2) INFORMATION FOR SEQ ID NO: 5131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5131:

TGATATTCAC TTCAATGTTA TCAATATTAG TGCCATCTAT GACATCTGCC A

51

(2) INFORMATION FOR SEQ ID NO: 5132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5132:

TCCTGTAGTC GAACGTGTTG TCTCTCTTGA GTGGATCCTG AGTACGACGG A

51

(2) INFORMATION FOR SEQ ID NO: 5133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5133:

ACTCAGACAT TGGATTGAGA TTCAGACAGC GACTCAGATT CAGATAGCGA CTCAGATTC

59

(2) INFORMATION FOR SEQ ID NO: 5134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5134:

## (2) INFORMATION FOR SEQ ID NO: 5135:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5135:

CAATACnAAG GGCAGCGAAA CCGTGATTCA AGCAAATCCC ATAAAGTTGG

50

## (2) INFORMATION FOR SEQ ID NO: 5136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5136:

GAAGCTGGCG AAAAGTCAGC TTACAAAATG TGCCAGTTGG CGGGGGCCCA AC

52

## (2) INFORMATION FOR SEQ ID NO: 5137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5137:

TGTAAAGGAA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGAnT

50

## (2) INFORMATION FOR SEQ ID NO: 5138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5138:

CTGTACAAGC TGTGCCGATA TTTCAATATC AnGnTACAGT AnAGCTCCAC

50

## (2) INFORMATION FOR SEQ ID NO: 5139:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5139:

10 GGTTCTGAATC CTGTCTTCCC GATATACTGT AATTATTATG GGGGCTTTGC TC

52

(2) INFORMATION FOR SEQ ID NO: 5140:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5140:

GCTACTGAAC CTATAAAATG TATGATGGCG GTCTCGAGGG AATCGAACCC AGATCT

56

25

(2) INFORMATION FOR SEQ ID NO: 5141:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5141:

35

AGGAGGCTCG TCCGCTCTAG GTTAGTCGGG TCCTAAGCTG AGGCCGACAG TA

52

(2) INFORMATION FOR SEQ ID NO: 5142:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5142:

CACGCTTTTCG ACATCAGCGT CAGTTACAGA CCAGAAAGTC GCCTTCGCAC TGGTGT

56

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(2) INFORMATION FOR SEQ ID NO: 5143:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5143:

CTCCTAAAAC AATTTACATC CAAACCTTCA TCACTCACGC GGC GTTGCTC CGTCAGCTTT 60  
CGCCATTGCG AAGAT 75

(2) INFORMATION FOR SEQ ID NO: 5144:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5144:

GAGGAGTGGT TAGCTTCTGC GGAGTACGAA TCGAGCCCCG TAAACGGCGG CCGGT 55

(2) INFORMATION FOR SEQ ID NO: 5145:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5145:

GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG 53

(2) INFORMATION FOR SEQ ID NO: 5146:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:

AGCTGTGGAT TGTCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T 51

(2) INFORMATION FOR SEQ ID NO: 5147:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5147:

CTCTTTGATC CGTAGTCAAA CGCTCTATCC AATTGAGCTA CGGGCGCATA

50

(2) INFORMATION FOR SEQ ID NO: 5148:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5148:

GAACTAATTC TCCAAAATAA TGACTCCTAC AGGAACTCGA ACCCGTATAA CCGCCGTAAA

60

(2) INFORMATION FOR SEQ ID NO: 5149:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5149:

AAAGCACACC CGGAAAACCTG AAACATCTTA AGTACCCGGA GAAAGAGAAA

50

(2) INFORMATION FOR SEQ ID NO: 5150:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 56 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5150:

GTAAGTTCGC ACTACCATCG ACGCTAAGGG AGCTTAACTT CTGTGGTTCG GCATGG

56

(2) INFORMATION FOR SEQ ID NO: 5151:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 56 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5151:

(2) INFORMATION FOR SEQ ID NO: 5152:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5152:

CTATTCTCTG TGTCGGGCTC ACCCCAATT GCACACTATT GTAAGCTGAC TTTCCTCCA 59

(2) INFORMATION FOR SEQ ID NO: 5153:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 65 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5153:

TAACCACATC ATTCGGATAC TGTTCATGGA AGTAATTTCT CTATTCTTCG GACCAGGAAA 60  
 ATACA 65

(2) INFORMATION FOR SEQ ID NO: 5154:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 91 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5154:

CCATATGTGT CAGTCACTGT GCACATCTTG ACGGTACCTA ATCAGACAGC CACGGCTAAC 60  
 TCCGTGCCAG CCGCCGCGGT ACTACGTGGT G 91

(2) INFORMATION FOR SEQ ID NO: 5155:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5155:

(2) INFORMATION FOR SEQ ID NO: 5156:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5156:

GACTCTGGGA GGACCATCTC CTAAGGCTAA ACTACTCTCT CGTGACCGAT AGTGAACC

(2) INFORMATION FOR SEQ ID NO: 5157:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5157:

TTGTAAGTCC GGTATAGGAG TGTCCTACAA CCCCAACAAG CAAGCTTGTT G

(2) INFORMATION FOR SEQ ID NO: 5158:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5158:

TAGTnACCGn TAGTGAACCA TTACCGTGAG GGAAAGGTGA AAAGCACCCC

(2) INFORMATION FOR SEQ ID NO: 5159:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5159:

TTCGCTCGCC GCTACTCAAG GGAATCGCAT TTCCTTTCTC TTCCTCCGGG T

(2) INFORMATION FOR SEQ ID NO: 5160:

(A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5160:

AACTGGAGAA ACAACTTTAT GGGGTTTGCT TGAACCTCGC GGTTCGCTG CCCTTTGTAT  
T

(2) INFORMATION FOR SEQ ID NO: 5161:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5161:

AGACCTCTGC CTTACCACTT GGCTATGCGC CAATAACTGG GCTACCTGGA T

(2) INFORMATION FOR SEQ ID NO: 5162:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5162:

CCGCTCACTT TTCAACGTAA GTCGGATCGG TCCTCCATTC AGTGTCACCT GAACT

(2) INFORMATION FOR SEQ ID NO: 5163:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 81 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5163:

CTTGATCTGT ATTTAAATG ATATTTTCTA TCTTTTCTTT ATTATTAACG TCTATGACGT  
CGTAGTATAA GATTCCGTGT A

(2) INFORMATION FOR SEQ ID NO: 5164:

- (A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5164:

10 GTTCGAATCC CGTCTTCTGC TCCATTATTT TGCCGGGGTG GCGGCAACTC TCACACGCAC 60  
AG 62

(2) INFORMATION FOR SEQ ID NO: 5165:

15

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5165:

25 CAGGGGTCTT TCGTCCTGTG TGGGTAAGTG CATCTTCACA GGTACTATGA TTTCA 55

(2) INFORMATION FOR SEQ ID NO: 5166:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5166:

AAGCTGAGGC CGACAGCGTA GGCGATGGAT GACAGGTGA TATTGCCGGT ACCACCCGAT 60

40

AA 62

(2) INFORMATION FOR SEQ ID NO: 5167:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5167:

CTTGCGTCTC CAGTTCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA CG 52

(2) INFORMATION FOR SEQ ID NO: 5168:

55

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5168:

TCGTCCGCTA TCTCCACCAT TATTTGTACA TTGAACTAG ATAAGTAGTA AATATA

56

(2) INFORMATION FOR SEQ ID NO: 5169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5169:

CTTGGACGTC GGTGGGTAGT CGAACTTAC GTTCCGCTAG AGTAGAACGT TGCCA

55

(2) INFORMATION FOR SEQ ID NO: 5170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5170:

CTACTGCTGC ATATGCGGGT GAAGGGAGTC GAACCCCCAC GCCGTAAGCA TA

52

(2) INFORMATION FOR SEQ ID NO: 5171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5171:

GGGCTTnGGA CATTAGTTC TnAGGCAATG TAAAAAGCT GATTCTATT

50

(2) INFORMATION FOR SEQ ID NO: 5172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5172:

AAATTACATG TTAATACGTA ATTAATGGCG AGACTCCTGA GGAACCATTG CCATTGGAAG 60

(2) INFORMATION FOR SEQ ID NO: 5173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5173:

GTTTTATTTT TTAAAGTAT GTAAAAGTAA AATTACATGn TAATACGTAn 50

(2) INFORMATION FOR SEQ ID NO: 5174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5174:

CAACTCTCGT TAAGGAAGTC GGCAAATAC CCGTAACTT CGGAGTAGGT CTCCTTA 57

(2) INFORMATION FOR SEQ ID NO: 5175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5175:

GGAAACTGGA ATAAATAAAC ATTCAATTGA GCGCATCAGT ATTAGGATTC ACTCTAAAAA 60

(2) INFORMATION FOR SEQ ID NO: 5176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GTAACGGACG CGCTCAAAGG TTCCCTCACA ATGGTTGGAA ATCATTGATA

50

(2) INFORMATION FOR SEQ ID NO: 5177:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5177:

AGTTACGTTT TTTTATAAAG AGGTTTGAGA CGCGTTATTA ATCTTGTGAG

50

(2) INFORMATION FOR SEQ ID NO: 5178:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5178:

GTGTGGATCC TGAGTACGAC GGAGCACGTG ACAATTCCGT CGGCAATCTG GGG

53

(2) INFORMATION FOR SEQ ID NO: 5179:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 83 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5179:

CGGTAACCTT ATACCTTTTA ACATATTTTG CATTTGATTG CGTTTACCTT TTTTACCTTT

60

ACCGCCACCA GTGAACTGTT TCA

83

(2) INFORMATION FOR SEQ ID NO: 5180:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5180:

TTTAAA

66

## (2) INFORMATION FOR SEQ ID NO: 5181:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 67 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5181:

GTTCGGTAAC TCGAGCGGGT CTCATAACCC GTAGGTCGGG TGGTTCAAAT CCGTCCTCCC  
GCAATAT

## (2) INFORMATION FOR SEQ ID NO: 5182:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5182:

TAGCGGTGAA ATGCGCAGAG ATATGGAGGA ACACCACTAG CGAAGGCAAC TTTCT

## (2) INFORMATION FOR SEQ ID NO: 5183:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5183:

GAATTCCATG TGTAGCGGTG AAATGCGCAG AGATATGnAC GAACACCAAT

## (2) INFORMATION FOR SEQ ID NO: 5184:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5184:

CC

62

## (2) INFORMATION FOR SEQ ID NO: 5185:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5185:

GAGACCTTGT CGGTCCATAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGT

## (2) INFORMATION FOR SEQ ID NO: 5186:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5186:

CCATCATTAAGTTGGGCACT CTAAGTTGAC TGCCGnGnC ACCnAAGAAG

## (2) INFORMATION FOR SEQ ID NO: 5187:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5187:

TTAATACGTT GCAATCCAAT CGCAGCTTC GCCTATCCTA CTGCCnTCCC

## (2) INFORMATION FOR SEQ ID NO: 5188:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5188:

AGTCGCTATC CGAATCTGAG TCGCTATCTG AGTCTnAGTC GCTAnnCCAG

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 bas pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5189:

ATAGATGCCC TTACCGCAAA CCGACACATG TAGTCAATAT GATAATTCTA AGGT

(2) INFORMATION FOR SEQ ID NO: 5190:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5190:

CTTTAATGGG CGAACAGnAC CCTTGGACCG ACTACAGCCC AGATCGATGA

(2) INFORMATION FOR SEQ ID NO: 5191:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5191:

ACATAGCACC CAGCGAGCCG TTGGACGACA ACTGGTACAC CAGAGGATGC CATCCGGCCT

(2) INFORMATION FOR SEQ ID NO: 5192:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 320 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5192:

Met Lys Met Ile Asn Lys Leu Ile Val Pro Val Thr Ala Ser Ala Leu  
 1 5 10 15

## EP 0 786 519 A2

	20	25	30
5	Leu Ile Ser Ser Lys Ala Gly Asp Val Thr Val Ala Asp Thr Met Lys 35 40 45		
	Lys Ile Gly Lys Asp Gln Ile Ala Asn Ala Ser Phe Thr Glu Met Leu 50 55 60		
10	Asn Lys Ile Leu Ala Asp Lys Tyr Lys Asn Lys Val Asn Asp Lys Lys 65 70 75 80		
	Ile Asp Glu Gln Ile Glu Lys Met Gln Lys Gln Tyr Gly Gly Lys Asp 85 90 95		
15	Lys Phe Glu Lys Ala Leu Gln Gln Gln Gly Leu Thr Ala Asp Lys Tyr 100 105 110		
	Lys Glu Asn Leu Arg Thr Ala Ala Tyr His Lys Glu Leu Leu Ser Asp 115 120 125		
20	Lys Ile Lys Ile Ser Asp Ser Glu Ile Lys Glu Asp Ser Lys Lys Ala 130 135 140		
	Ser His Ile Leu Ile Lys Val Lys Ser Lys Lys Ser Asp Xaa Glu Gly 145 150 155 160		
25	Leu Asp Asp Lys Glu Ala Lys Gln Lys Ala Glu Glu Ile Gln Lys Glu 165 170 175		
	Val Ser Lys Asp Pro Ser Lys Phe Gly Glu Ile Ala Lys Lys Glu Ser 180 185 190		
30	Met Asp Thr Gly Ser Ala Lys Lys Asp Gly Glu Leu Gly Tyr Val Leu 195 200 205		
	Lys Gly Gln Thr Asp Lys Asp Phe Glu Lys Ala Leu Phe Lys Leu Lys 210 215 220		
35	Asp Gly Glu Val Ser Glu Val Val Lys Ser Ser Phe Gly Tyr His Ile 225 230 235 240		
	Ile Lys Ala Asp Lys Pro Thr Asp Phe Asn Ser Glu Lys Gln Ser Leu 245 250 255		
40	Lys Glu Lys Leu Val Asp Gln Lys Val Gln Lys Asn Pro Lys Leu Leu 260 265 270		
45	Thr Asp Ala Tyr Lys Asp Leu Leu Lys Glu Tyr Asp Val Asp Phe Lys 275 280 285		
	Asp Arg Asp Ile Lys Ser Val Val Glu Asp Lys Ile Leu Asn Pro Glu 290 295 300		
50	Lys Leu Lys Gln Gly Gly Ala Gln Gly Gly Gln Ser Gly Met Ser Gln 305 310 315 320		

55

(2) INFORMATION FOR SEQ ID NO:5193:

(A) LENGTH: 330 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5193:

```

Met Asn Lys Val Ile Lys Met Leu Val Val Thr Leu Ala Phe Leu Leu
1          5          10          15
Val Leu Ala Gly Cys Ser Gly Asn Ser Asn Lys Gln Ser Ser Asp Asn
20          25          30
Lys Asp Lys Glu Thr Thr Ser Ile Lys His Ala Met Gly Thr Thr Glu
35          40          45
Ile Lys Gly Lys Pro Lys Arg Val Val Thr Leu Tyr Gln Gly Ala Thr
50          55          60
Asp Val Ala Val Ser Leu Gly Val Lys Pro Val Gly Ala Val Glu Ser
65          70          75          80
Trp Thr Gln Lys Pro Lys Phe Glu Tyr Ile Lys Asn Asp Leu Lys Asp
85          90          95
Thr Lys Ile Val Gly Gln Glu Pro Ala Pro Asn Leu Glu Glu Ile Ser
100         105         110
Lys Leu Lys Pro Asp Leu Ile Val Ala Ser Lys Val Arg Asn Glu Lys
115         120         125
Val Tyr Asp Gln Leu Ser Lys Ile Ala Pro Thr Val Ser Thr Asp Thr
130         135         140
Val Phe Lys Phe Lys Asp Thr Thr Lys Leu Met Gly Lys Ala Leu Gly
145         150         155         160
Lys Glu Lys Glu Ala Glu Asp Leu Leu Lys Lys Tyr Asp Asp Lys Val
165         170         175
Ala Ala Phe Gln Lys Asp Ala Lys Ala Lys Tyr Lys Asp Ala Trp Pro
180         185         190
Leu Lys Ala Ser Val Val Asn Phe Arg Ala Asp His Thr Arg Ile Tyr
195         200         205
Ala Gly Gly Tyr Ala Gly Glu Ile Leu Asn Asp Leu Gly Phe Lys Arg
210         215         220
Asn Lys Asp Leu Gln Lys Gln Val Asp Asn Gly Lys Asp Ile Ile Gln
225         230         235         240
Leu Thr Ser Lys Glu Ser Ile Pro Leu Met Asn Ala Asp His Ile Phe
245         250         255

```

Val Val Lys Ser Asp Pro Asn Ala Lys Asp Ala Ala Leu Val Lys Lys  
 260 265 270  
 Thr Glu Ser Glu Trp Thr S r Ser Lys Glu Trp Lys Asn Leu Asp Ala  
 275 280 285  
 Val Lys Asn Asn Gln Val Ser Asp Asp Leu Asp Glu Ile Thr Trp Asn  
 290 295 300  
 Leu Ala Gly Gly Tyr Lys Ser Ser Leu Lys Leu Ile Asp Asp Leu Tyr  
 305 310 315 320  
 Glu Lys Leu Asn Ile Glu Lys Gln Ser Lys  
 325 330

## (2) INFORMATION FOR SEQ ID NO:5194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5194:

Met Thr Arg Lys Phe Arg Thr Leu Ile Leu Ile Leu Ile Ala Thr Ile  
 1 5 10 15  
 Ala Leu Ser Gly Cys Ala Asn Asp Asp Gly Ile Tyr Ser Asp Lys Gly  
 20 25 30  
 Gln Val Phe Arg Lys Ile Leu Ser Ser Asp Leu Thr Ser Leu Asp Thr  
 35 40 45  
 Ser Leu Ile Thr Asp Glu Ile Ser Ser Glu Val Thr Ala Gln Thr Phe  
 50 55 60  
 Glu Gly Leu Tyr Thr Leu Gly Lys Gly Asp Lys Pro Val Leu Gly Val  
 65 70 75 80  
 Ala Lys Ala Phe Pro Glu Lys Ser Lys Asp Gly Lys Thr Leu Lys Val  
 85 90 95  
 Lys Leu Arg Ser Asp Ala Lys Trp Ser Asn Gly Asp Lys Val Thr Ala  
 100 105 110  
 Gln Asp Phe Val Tyr Ala Trp Arg Lys Thr Val Asp Pro Lys Thr Gly  
 115 120 125  
 Ser Glu Phe Ala Tyr Ile Met Gly Asp Ile Lys Asn Ala Ser Asp Ile  
 130 135 140  
 Ser Thr Gly Lys Lys Pro Val Glu Gln Leu Gly Ile Lys Ala Leu Asn  
 145 150 155 160

Asp Glu Thr Leu Gln Ile Glu Leu Glu Lys Pro Val Pro Tyr Ile Asn  
165 170 175

Gln Leu Leu Ala Leu Asn Thr Phe Ala Pro Gln Asn Glu Lys Val Ala  
180 185 190

Lys Lys Tyr Gly Lys Asn Tyr Gly Thr Ala Ala Asp Arg Ala Val Tyr  
195 200 205

Asn Gly Pro Phe Lys Val Asp Asp Trp Lys Gln Glu Asp Lys Thr Leu  
210 215 220

Leu Ser Lys Asn Gln Tyr Tyr Trp Asp Lys Lys Asn Val Lys Leu Asp  
225 230 235 240

Lys Val Asn Tyr Lys Val Ile Lys Asp Leu Gln Ala Gly Ala Ser Leu  
245 250 255

Tyr Asp Thr Glu Ser Val Asp Asp Ala Phe Ile Thr Ala Asp Gln Val  
260 265 270

Asn Lys Tyr Lys Asp Asn Lys Gly Leu Asn Phe Val Leu Thr Thr Gly  
275 280 285

Thr Phe Phe Val Lys Met Asn Glu Lys Gln Tyr Pro Asp Phe Lys Asn  
290 295 300

Lys Asn Leu Arg Leu Xaa Ser His Lys Gln  
305 310

(2) INFORMATION FOR SEQ ID NO:5195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5195:

Met Lys Arg Leu Ile Gly Leu Val Ile Val Ala Leu Val Leu Leu Ala  
1 5 10 15

Ala Cys Gly Gly Asn Asn Asp Lys Lys Val Thr Ile Gly Val Ala Ser  
20 25 30

Asn Asp Thr Lys Ala Trp Glu Lys Val Lys Glu Leu Ala Lys Lys Asp  
35 40 45

Asp Ile Asp Val Glu Ile Lys His Phe Ser Asp Tyr Asn Leu Pro Asn  
50 55 60

Lys Ala Leu Asn Asp Gly Asp Ile Asp Met Asn Ala Phe Gln His Phe  
65 70 75 80

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Ala Phe Leu Asp Gln Tyr Lys Lys Ala His Lys Gly Thr Lys Ile Ser  
85 90 95

5 Ala Leu Ser Thr Thr Val Leu Ala Pro Leu Gly Ile Tyr Ser Asp Lys  
100 105 110

Ile Lys Asp Val Lys Lys Val Lys Asp Gly Ala Lys Val Val Ile Pro  
115 120 125

10 Asn Asp Val Ser Asn Gln Ala Arg Ala Leu Lys Leu Leu Glu Ala Ala  
130 135 140

Gly Leu Ile Lys Leu Lys Lys Asp Phe Gly Leu Ala Gly Thr Val Lys  
145 150 155 160

15 Asp Ile Thr Ser Asn Pro Lys His Leu Lys Ile Thr Ala Val Asp Ala  
165 170 175

Gln Gln Thr Ala Arg Ala Leu Ser Asp Val Asp Ile Ala Val Ile Asn  
180 185 190

20 Asn Gly Val Ala Thr Lys Ala Gly Lys Asp Pro Lys Asn Asp Pro Ile  
195 200 205

25 Phe Leu Glu Lys Ser Asn Ser Asp Ala Val Lys Pro Tyr Ile Asn Ile  
210 215 220

Val Ala Val Asn Asp Lys Asp Leu Asp Asn Lys Thr Tyr Ala Lys Ile  
225 230 235 240

30 Val Glu Leu Tyr His Ser Lys Glu Ala Gln Lys Ala Leu Gln Glu Asp  
245 250 255

Val Lys Asp Gly Glu Lys Pro Val Asn Leu Ser Lys Asp Glu Ile Lys  
260 265 270

35 Ala Ile Glu Thr Ser Leu Ala Lys  
275 280

(2) INFORMATION FOR SEQ ID NO:5196:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 273 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5196:

Met Lys Lys Leu Phe Gly Leu Ile Leu Val Leu Thr Phe Ala Val Val  
1 5 10 15

55 Leu Ala Ala Cys Gly Asn Gly Asn Lys Ser Gly Ser Asp Asp Lys Lys  
20 25 30

EP 0 786 519 A2

Ile Thr Val Ser Ala Ser Pro Ala Pro His Ala Glu Ile Leu Glu Lys  
35 40 45  
Ala Lys Pro Leu Leu Glu Lys Lys Gly Tyr Glu Leu Asp Ile Lys Thr  
5 50 55 60  
Ile Asn Asp Tyr Thr Thr Pro Asn Lys Leu Leu Asp Lys Gly Glu Ile  
65 70 75 80  
Asp Ala Asn Tyr Phe Gln His Thr Pro Tyr Leu Asn Thr Glu Lys Lys  
10 85 90 95  
Asp Lys Gly Tyr Lys Ile Val Ser Ala Gly Asp Val His Leu Glu Pro  
100 105 110  
15 Met Ala Val Tyr Ser Lys Lys Tyr Lys Ser Leu Lys Glu Leu Pro Lys  
115 120 125  
Gly Ala Thr Val Tyr Val Ser Asn Asn Pro Ala Glu Gln Gly Arg Phe  
130 135 140  
20 Leu Lys Phe Phe Val Asp Ala Gly Leu Ile Lys Ile Lys Lys Gly Val  
145 150 155 160  
Lys Ile Glu Asp Ala Lys Phe Ser Asp Ile Thr Glu Asn Lys Lys Asp  
25 165 170 175  
Ile Lys Phe Asn Asn Lys Gln Ser Ala Glu Phe Leu Pro Lys Ile Tyr  
180 185 190  
Gln Asn Glu Asp Ala Asp Ala Val Ile Ile Asn Ser Asn Phe Ala Ile  
30 195 200 205  
Glu Gln Lys Leu Asn Pro Lys Lys Asp Ser Ile Ala Val Glu Ser Ala  
210 215 220  
35 Lys Asp Asn Pro Tyr Ala Asn Leu Ile Ala Val Lys Glu Gly His Gln  
225 230 235 240  
Asp Asp Lys Lys Ile Lys Ala Leu Ile Glu Val Leu Gln Ser Lys Asp  
245 250 255  
40 Ile Gln Asp Phe Ile Asn Glu Lys Tyr Asn Gly Ala Val Ile Pro Ala  
260 265 270  
Lys

(2) INFORMATION FOR SEQ ID NO:5197:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 313 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5197:

5	Met	Lys	Lys	Ile	Lys	Tyr	Ile	Leu	Val	Val	Phe	Val	Leu	Ser	Leu	Thr	1	5	10	15
	Val	Leu	Ser	Gly	Cys	Ser	Leu	Pro	Gly	Leu	Gly	Ser	Lys	Ser	Thr	Lys	20	25	30	
10	Asn	Asp	Val	Lys	Ile	Thr	Ala	Leu	Ser	Thr	Ser	Glu	Ser	Gln	Ile	Ile	35	40	45	
	Ser	His	Met	Leu	Arg	Leu	Leu	Ile	Glu	His	Asp	Thr	His	Gly	Lys	Ile	50	55	60	
15	Lys	Pro	Thr	Leu	Val	Asn	Asn	Leu	Gly	Ser	Ser	Thr	Ile	Gln	His	Asn	65	70	75	80
	Ala	Leu	Ile	Asn	Gly	Asp	Ala	Asn	Ile	Ser	Gly	Val	Arg	Tyr	Asn	Gly	85	90	95	
20	Thr	Asp	Leu	Thr	Gly	Ala	Leu	Lys	Glu	Ala	Pro	Ile	Lys	Asn	Pro	Lys	100	105	110	
	Lys	Ala	Met	Ile	Ala	Thr	Gln	Gln	Gly	Phe	Lys	Lys	Lys	Phe	Asp	Gln	115	120	125	
25	Thr	Phe	Phe	Asp	Ser	Tyr	Gly	Phe	Ala	Asn	Thr	Tyr	Ala	Phe	Met	Val	130	135	140	
	Thr	Lys	Glu	Thr	Ala	Lys	Lys	Tyr	His	Leu	Glu	Thr	Val	Ser	Asp	Leu	145	150	155	160
	Ala	Lys	His	Ser	Lys	Asp	Leu	Arg	Leu	Gly	Met	Asp	Ser	Ser	Trp	Met	165	170	175	
35	Asn	Arg	Lys	Gly	Asp	Gly	Tyr	Glu	Gly	Phe	Lys	Lys	Glu	Tyr	Gly	Phe	180	185	190	
	Asp	Phe	Gly	Thr	Val	Arg	Pro	Met	Gln	Ile	Gly	Leu	Val	Tyr	Asp	Ala	195	200	205	
40	Leu	Asn	Ser	Glu	Lys	Leu	Asp	Val	Ala	Leu	Gly	Tyr	Ser	Thr	Asp	Gly	210	215	220	
	Arg	Ile	Ala	Ala	Tyr	Asp	Leu	Lys	Val	Leu	Lys	Asp	Asp	Lys	Gln	Phe	225	230	235	240
45	Phe	Pro	Pro	Tyr	Ala	Ala	Ser	Ala	Val	Ala	Thr	Asn	Glu	Leu	Leu	Arg	245	250	255	
	Gln	His	Pro	Glu	Leu	Lys	Thr	Thr	Ile	Asn	Lys	Leu	Thr	Gly	Lys	Ile	260	265	270	
50	Ser	Thr	Ser	Glu	Met	Gln	Arg	Leu	Asn	Tyr	Glu	Ala	Asp	Gly	Lys	Gly	275	280	285	
55	Lys	Glu	Pro	Ala	Val	Val	Ala	Glu	Glu	Phe	Leu	Lys	Lys	His	His	Tyr	290	295	300	

Phe Asp Lys Gln Lys Gly Gly His Lys  
305 310

## (2) INFORMATION FOR SEQ ID NO:5198:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 284 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5198:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala  
1 5 10 15

Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys  
20 25 30

Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr  
35 40 45

Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu  
50 55 60

Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala  
65 70 75 80

Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala  
85 90 95

Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp  
100 105 110

Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile  
115 120 125

Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys  
130 135 140

Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala  
145 150 155 160

Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp  
165 170 175

Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Glu Ile  
180 185 190

Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala  
195 200 205

Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys  
210 215 220

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Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu  
225 230 235 240

Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys  
245 250 255

Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu  
260 265 270

Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu  
275 280

(2) INFORMATION FOR SEQ ID NO:5199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5199:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala  
1 5 10 15

Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys  
20 25 30

Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr  
35 40 45

Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu  
50 55 60

Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala  
65 70 75 80

Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala  
85 90 95

Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp  
100 105 110

Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile  
115 120 125

Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys  
130 135 140

Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala  
145 150 155 160

Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp  
165 170 175

Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Glu Ile  
 180 185 190  
 Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala  
 195 200 205  
 Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys  
 210 215 220  
 Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu  
 225 230 235 240  
 Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys  
 245 250 255  
 Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu  
 260 265 270  
 Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu  
 275 280

(2) INFORMATION FOR SEQ ID NO:5200:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 208 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5200:

Met Lys Phe Lys Ala Ile Val Ala Ile Thr Leu Ser Leu Ser Leu Leu  
 1 5 10 15  
 Thr Ala Cys Gly Ala Asn Gln His Lys Glu Asn Ser Ser Lys Ser Asn  
 20 25 30  
 Asp Thr Asn Lys Lys Thr Gln Gln Thr Asp Asn Thr Thr Gln Ser Asn  
 35 40 45  
 Thr Glu Lys Gln Met Thr Pro Gln Glu Ala Glu Asp Ile Val Arg Asn  
 50 55 60  
 Asp Tyr Lys Ala Arg Gly Val Asn Glu Tyr Gln Thr Leu Asn Tyr Lys  
 65 70 75 80  
 Thr Asn Leu Glu Arg Ser Asn Glu His Glu Tyr Tyr Val Glu His Leu  
 85 90 95  
 Val Arg Asp Ala Val Gly Thr Pro Leu Lys Arg Cys Ala Ile Val Asn  
 100 105 110  
 Arg His Asn Gly Thr Ile Ile Asn Ile Phe Asp Asp Met Ser Glu Lys  
 115 120 125

Asp Lys Glu Glu Phe Glu Ala Phe Lys Lys Arg Ser Pro Lys Tyr Asn  
 130 135 140  
 Pro Gly Met Asn Asn His Asp Glu Thr Asp Gly Glu Ser Glu Asp Ile  
 145 150 155 160  
 Gln His His Asp Ile Asp Asn Asn Lys Ala Ile Gln Asn Asp Ile Pro  
 165 170 175  
 Asp Gln Lys Val Asp Asp Lys Asn Asp Lys Asn Ala Val Asn Lys Glu  
 180 185 190  
 Glu Lys His Asp Asn Gly Ala Asn Asn Ser Glu Glu Thr Lys Val Lys  
 195 200 205

## (2) INFORMATION FOR SEQ ID NO:5201:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5201:

Met Leu Lys Gly Cys Gly Gly Cys Leu Ile Ser Phe Ile Leu Leu Ile  
 1 5 10 15  
 Ile Leu Leu Ser Ala Cys Ser Met Met Phe Ser Asn Asn Asp Asn Ser  
 20 25 30  
 Thr Asn Asn Gln Ser Ser Lys Thr Gln Leu Thr Gln Lys Asp Glu Asn  
 35 40 45  
 Lys Asn Glu Asp Lys Pro Glu Glu Lys Ser Glu Thr Ala Thr Asp Glu  
 50 55 60  
 Asp Leu Gln Ser Thr Glu Glu Val Pro Ala Asn Glu Asn Thr Glu Asn  
 65 70 75 80  
 Asn Gln His Glu Ile Asp Glu Ile Thr Thr Lys Asp Gln Ser Asp Asp  
 85 90 95  
 Asp Ile Asn Thr Pro Asn Val Ala Glu Asp Lys Ser Gln Asp Asp Leu  
 100 105 110  
 Lys Asp Asp Leu Lys Glu Lys Gln Gln Ser Ser Asn His His Gln Ser  
 115 120 125  
 Thr Gln Pro Lys Thr Ser Pro Ser Thr Glu Thr Asn Thr Gln Gln Ser  
 130 135 140  
 Phe Ala Asn Cys Lys Gln Leu Arg Gln Val Tyr Pro Asn Gly Val Thr

Ala Asp His Pro Ala Tyr Arg Pro His Leu Asp Arg Asp Lys Asp Lys  
                                   165                                  170                                  175

Arg Ala Cys Glu Pro Asp Lys Tyr  
                                   180

(2) INFORMATION FOR SEQ ID NO:5202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5202:

Met	Lys	Lys	Arg	Leu	Leu	Leu	Ser	Thr	Phe	Leu	Ala	Ser	Thr	Leu	Ile	1	5	10	15
Leu	Thr	Gly	Cys	Ala	Ser	Asp	Gln	Ser	Asp	Asn	Glu	Asp	His	His	Thr	20	25	30	
Ser	Thr	Gly	Ile	His	Ala	Pro	Lys	Ser	Ala	Lys	Lys	Leu	Glu	Thr	Lys	35	40	45	
Asp	Ile	Phe	Xaa	Ser	Asp	Lys	Lys	Asn	Ser	Asp	Ile	Ser	Asp	Ala	Glu	50	55	60	
Met	Lys	Gln	Ala	Ile	Glu	Lys	Tyr	Leu	Ser	Val	Asn	Ser	Asp	Ile	Leu	65	70	75	80
Asp	Asn	Lys	Tyr	Ile	Met	Gln	His	Lys	Leu	Asp	Lys	Gln	Ile	Asp	Ser	85	90	95	
Gln	Thr	Lys	Val	Thr	Glu	Lys	Gln	Ala	Glu	Thr	Leu	Ser	His	Leu	Ser	100	105	110	
Asn	Leu	Ala	Val	Lys	Asn	Asp	Leu	His	Phe	Lys	Lys	Phe	Val	Thr	Glu	115	120	125	
Asn	Asn	Ile	Pro	Lys	Glu	Tyr	Lys	Lys	Pro	Val	Glu	Leu	Met	Met	Asn	130	135	140	
Tyr	Phe	Lys	Ala	Leu	Asn	Ser	Thr	Ile	Ala	Asn	Val	Asp	Glu	Asp	Ile	145	150	155	160
Glu	Lys	Leu	Ser	Tyr	Gln	Pro	Gln	Asn	Lys	Ile	Asn	Val	Val	Asp	Val	165	170	175	
Pro	Thr	Lys	Tyr	Ala	Gly	Asp	Val	Asn	Lys	Lys	Gln	Gln	Asp	Lys	Ile	180	185	190	
Lys	Asp	Phe	Leu	Lys	Ser	Lys	Gly	Ile	Lys	Ser	Asp	Val	Ile	Asp	Lys				

## (2) INFORMATION FOR SEQ ID NO:5203:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5203:

Met Lys Ser Lys Ile Tyr Ile Leu Leu Leu Xaa Leu Ile Phe Leu Ser  
 1 5 10 15  
 Ala Cys Ala Asn Thr Arg His Ser Glu Ser Asp Lys Asn Val Leu Thr  
 20 25 30  
 Val Tyr Ser Pro Tyr Gln Ser Asn Leu Ile Arg Pro Ile Leu Asn Glu  
 35 40 45  
 Xaa Glu Lys Gln Glu His Val Lys Ile Glu Ile Lys His Gly Ser Thr  
 50 55 60  
 Gln Val Leu Leu Ser Asn Leu His Asn Glu Asp Phe Ser Glu Arg Gly  
 65 70 75 80  
 Asp Val Phe Met Gly Gly Val Leu Ser Glu Thr Ile Asp His Pro Glu  
 85 90 95  
 Asp Phe Val Pro Tyr Gln Asp Thr Ser Val Thr Gln Gln Leu Glu Asp  
 100 105 110  
 Tyr Arg Ser Asn Asn Lys Tyr Val Thr Ser Phe Leu Leu Met Pro Thr  
 115 120 125  
 Val Ile Val Val Asn Ser Asp Leu Gln Gly Asp Ile Lys Ile Arg Gly  
 130 135 140  
 Tyr Gln Asp Leu Leu Gln Pro Ile Leu Lys Gly Lys Ile Ala Tyr Ser  
 145 150 155 160  
 Asn Pro Asn Thr Thr Thr Thr Gly Tyr Gln His Met Arg Ala Ile Tyr  
 165 170 175  
 Ser Met His His Arg Val Ser Asp Val His Gln Phe Gln Asn His Ala  
 180 185 190  
 Met Gln Leu Ser Lys Thr Ser Lys Val Ile Glu Asp Val Ala Lys Gly  
 195 200 205  
 Lys Tyr Tyr Ala Gly Leu Ser Tyr Glu Gln Asp Ala Arg Thr Trp Lys  
 210 215 220

225                      230                      235                      240  
 Leu Asn Val Asp Gly Ile Ala Leu Val Lys Asn Ala His Pro His Pro  
                                  245                      250                      255  
 5                      Lys Arg Lys Lys Leu Val Gln Tyr Leu Thr Ser Arg Ser Val Gln Gln  
                                  260                      265                      270  
 Arg Leu Val Ala Glu Phe Asp Ala Lys Ser Ile  
 10                      275                      280

## (2) INFORMATION FOR SEQ ID NO:5204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5204:

25                      Met Lys Lys Phe Ile Gly Ser Val Leu Ala Thr Thr Leu Ile Leu Gly  
                                  1                      5                      10                      15  
 Gly Cys Ser Thr Met Glu Asn Glu Ser Lys Lys Asp Thr Lys Thr Glu  
                                  20                      25                      30  
 30                      Thr Lys Ser Val Pro Glu Glu Met Glu Ala Ser Lys Tyr Val Gly Gln  
                                  35                      40                      45  
 Gly Phe Gln Pro Pro Ala Glu Lys Asn Ala Ile Glu Phe Ala Lys Lys  
                                  50                      55                      60  
 35                      His Arg Lys Glu Phe Glu Lys Val Gly Glu Gln Phe Phe Lys Asp Asn  
                                  65                      70                      75                      80  
 Phe Gly Leu Lys Val Lys Ala Thr Asn Val Val Gly Lys Asp Asp Gly  
                                  85                      90                      95  
 40                      Val Glu Val Tyr Val His Cys Glu Asp His Gly Ile Val Phe Asn Ala  
                                  100                      105                      110  
 45                      Ser Leu Pro Leu Tyr Lys Asp Ala Ile His Gln Lys Gly Ser Met Arg  
                                  115                      120                      125  
 Ser Asn Asp Asn Gly Asp Asp Met Ser Met Met Val Gly Thr Val Leu  
                                  130                      135                      140  
 50                      Ser Gly Phe Glu Tyr Arg Ala Gln Lys Glu Lys Tyr Asp Asn Leu Tyr  
                                  145                      150                      155                      160  
 Lys Phe Phe Lys Glu Asn Glu Lys Lys Tyr Gln Tyr Thr Gly Phe Thr  
                                  165                      170                      175

180 185 190  
 Phe Tyr Ile Thr Tyr Ser Ser Arg Ser Leu Lys Glu Tyr Arg Lys Tyr  
 195 200 205  
 Tyr Glu Pro Leu Ile Arg Lys Asn Asp Lys Glu Phe Lys Glu Gly Met  
 210 215 220  
 Glu Arg Ala Arg Lys Glu Val Asn Tyr Ala Ala Asn Thr Asp Ala Val  
 225 230 235 240  
 Ala Thr Leu Phe Ser Thr Lys Lys Asn Phe Thr Lys Asp Asn Thr Val  
 245 250 255  
 Asp Asp Val Ile Glu Leu Ser Asp Lys Leu Tyr Asn Leu Lys Asn Lys  
 260 265 270  
 Pro Asp Lys Ser Thr Ile Thr Ile Gln Ile Gly Lys Pro Thr Ile Asn  
 275 280 285  
 Thr Lys Lys Ala Phe Tyr Asp Asp Asn Arg Pro Ile Glu Tyr Gly Val  
 290 295 300  
 His Ser Lys Asp Glu  
 305

## (2) INFORMATION FOR SEQ ID NO:5205:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5205:

Met Lys Lys Leu Val Ser Ile Val Gly Ala Thr Leu Leu Leu Ala Gly  
 1 5 10 15  
 Cys Gly Ser Gln Asn Leu Ala Pro Leu Glu Glu Lys Thr Thr Asp Leu  
 20 25 30  
 Arg Glu Asp Asn His Gln Leu Lys Leu Asp Ile Gln Glu Leu Asn Gln  
 35 40 45  
 Gln Ile Ser Asp Ser Lys Ser Lys Ile Lys Gly Leu Glu Lys Asp Lys  
 50 55 60  
 Glu Asn Ser Lys Lys Thr Ala Ser Asn Asn Thr Lys Ile Lys Leu Met  
 65 70 75 80  
 Asn Val Thr Ser Thr Tyr Tyr Asp Lys Val Ala Lys Ala Leu Lys Ser  
 85 90 95

100 105 110  
 Val Gln Ser Lys Leu Asn Gln Ile Ser Asn Asp Ile Gln Ser Ala His  
 115 120 125  
 5 Thr Ser Tyr Lys Asp Ala Ile Asp Gly Leu Ser Leu Ser Asp Asp Asp  
 130 135 140  
 Lys Lys Thr Ser Lys Asn Ile Asp Lys Leu Asn Ser Asp Leu Asn His  
 145 150 155 160  
 10 Ala Phe Asp Asp Ile Lys Asn Gly Tyr Gln Asn Lys Asp Lys Lys Gln  
 165 170 175  
 15 Leu Thr Lys Gly Gln Gln Ala Leu Ser Lys Leu Asn Leu Asn Ala Lys  
 180 185 190  
 Ser

20 (2) INFORMATION FOR SEQ ID NO:5206:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 259 amino acids  
 (B) TYPE: amino acid  
 25 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5206:

Met Lys Arg Leu Leu Phe Val Met Ile Ala Phe Val Phe Ile Leu Ala  
 1 5 10 15  
 35 Ala Cys Gly Asn Asn Ser Ser Lys Asp Lys Glu Ala Ser Lys Asp Ser  
 20 25 30  
 40 Lys Thr Ile Asn Val Gly Thr Glu Gly Thr Tyr Ala Pro Phe Ser Phe  
 35 40 45  
 His Asp Lys Asp Gly Lys Leu Thr Gly Tyr Asp Ile Asp Val Ile Lys  
 50 55 60  
 45 Ala Val Ala Lys Glu Glu Gly Leu Lys Leu Lys Phe Asn Glu Thr Ser  
 65 70 75 80  
 Trp Asp Ser Met Phe Ala Gly Leu Asp Ala Gly Arg Phe Asp Val Ile  
 85 90 95  
 50 Ala Asn Gln Val Gly Ile Asn Pro Asp Arg Glu Lys Lys Tyr Lys Phe  
 100 105 110  
 Ser Lys Pro Tyr Thr Phe Ser Ser Ala Val Leu Val Ile Arg Glu Asn  
 115 120 125  
 55

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130

135

140

Gln Thr Phe Thr Ser Asn Tyr Gly Lys Leu Ala Lys Asp Lys Gly Ala  
145 150 155 160

Asp Ile Thr Lys Val Asp Gly Phe Asn Gln Ser Met Asp Leu Leu Leu  
165 170 175

Ser Lys Arg Val Asp Gly Thr Phe Asn Asp Ser Leu Ser Tyr Leu Asp  
180 185 190

Tyr Lys Lys Gln Lys Pro Asn Ala Lys Ile Lys Ala Ile Lys Gly Asn  
195 200 205

Ala Glu Gln Ser Arg Ser Ala Phe Ala Phe Ser Lys Lys Ala Asp Asp  
210 215 220

Glu Thr Val Gln Lys Phe Asn Asp Gly Leu Lys Lys Ile Glu Glu Asn  
225 230 235 240

Gly Glu Leu Ala Lys Ile Gly Lys Lys Trp Phe Gly Gln Asp Val Ser  
245 250 255

Lys Ser Lys

(2) INFORMATION FOR SEQ ID NO:5207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5207:

Met Gly Val His Ser Met Lys Leu Lys Arg Leu Phe Ala Val Val Ile  
1 5 10 15

Ala Met Leu Leu Val Leu Ala Gly Cys Ser Asn Ser Asn Asp Asn Asn  
20 25 30

Glu Ser Lys Lys Asp Asp Ala Asp Asn Gly Lys Lys Gln Glu Ile Gln  
35 40 45

Val Ala Ala Ala Ala Ser Leu Thr Asp Val Thr Lys Lys Leu Ala Ser  
50 55 60

Glu Phe Lys Lys Glu His Lys Asn Ala Asp Ile Lys Phe Asn Tyr Gly  
65 70 75 80

Gly Ser Gly Ala Leu Arg Lys Gln Ile Glu Ser Gly Ala Pro Val Asp  
85 90 95

100 105 110  
 Asn Lys Ala His Asp Thr Tyr Lys Tyr Ala Lys Asn Ser Leu Val Leu  
 115 120 125  
 5  
 Ile Gly Asp Lys Asp Ser Asn Tyr Thr Ser Val Lys Asp Leu Lys Asp  
 130 135 140  
 Asn Asp Lys Leu Ala Leu Gly Glu Val Lys Thr Val Pro Ala Gly Lys  
 145 150 155 160  
 10  
 Tyr Ala Lys Gln Tyr Leu Asp Asn Asn Asn Leu Phe Lys Glu Val Glu  
 165 170 175  
 Ser Xaa Ile Val Tyr Ala Lys Asp Val Lys Gln Val Leu Asn Tyr Val  
 180 185 190  
 15  
 Xaa Lys Gly Asn Ala Lys Gln Gly Phe Val Tyr  
 195 200

20 (2) INFORMATION FOR SEQ ID NO:5208:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 327 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 25

(ii) MOLECULE TYPE: protein

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5208:

Met Lys Lys Trp Gln Phe Val Gly Thr Thr Ala Leu Gly Ala Thr Leu  
 1 5 10 15  
 35  
 Leu Leu Gly Ala Cys Gly Gly Gly Asn Gly Gly Ser Gly Asn Ser Asp  
 20 25 30  
 Leu Lys Gly Glu Ala Lys Gly Asp Gly Ser Ser Thr Val Ala Pro Ile  
 35 40 45  
 40  
 Val Glu Lys Leu Asn Glu Lys Trp Ala Gln Asp His Ser Asp Ala Lys  
 50 55 60  
 Ile Ser Ala Gly Gln Ala Gly Thr Gly Ala Gly Phe Gln Lys Phe Ile  
 65 70 75 80  
 45  
 Ala Gly Asp Ile Asp Phe Ala Asp Ala Ser Arg Pro Ile Lys Asp Glu  
 85 90 95  
 50  
 Glu Lys Gln Lys Leu Gln Asp Lys Asn Ile Lys Tyr Lys Glu Phe Lys  
 100 105 110  
 Ile Ala Gln Asp Gly Val Thr Val Ala Val Asn Lys Glu Asn Asp Phe  
 115 120 125  
 55

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130 135 140

Ala Lys Thr Trp Lys Asp Val Asn Ser Lys Trp Pro Asp Lys Lys Ile  
145 150 155 160

Asn Ala Val Ser Pro Asn Ser Ser His Gly Thr Tyr Asp Phe Phe Glu  
165 170 175

Asn Glu Val Met Asn Lys Glu Asp Ile Lys Ala Glu Lys Asn Ala Asp  
180 185 190

Thr Asn Ala Ile Val Ser Ser Val Thr Lys Asn Lys Glu Gly Ile Gly  
195 200 205

Tyr Phe Gly Tyr Asn Phe Tyr Val Gln Asn Lys Asp Lys Leu Lys Glu  
210 215 220

Val Lys Ile Lys Asp Glu Asn Gly Lys Ala Thr Glu Pro Thr Lys Lys  
225 230 235 240

Thr Ile Gln Asp Asn Ser Tyr Ala Leu Ser Arg Pro Leu Phe Ile Tyr  
245 250 255

Val Asn Glu Lys Ala Leu Lys Asp Asn Lys Val Met Ser Glu Phe Ile  
260 265 270

Lys Phe Val Leu Glu Asp Lys Gly Lys Ala Ala Glu Glu Ala Gly Tyr  
275 280 285

Val Ala Ala Pro Glu Lys Thr Tyr Lys Ser Gln Leu Asp Asp Leu Lys  
290 295 300

Ala Phe Ile Asp Lys Asn Gln Lys Ser Asp Asp Lys Lys Ser Asp Asp  
305 310 315 320

Lys Lys Ser Glu Asp Lys Lys  
325

(2) INFORMATION FOR SEQ ID NO:5209:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 324 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5209:

Met Lys Arg Leu Ser Ile Ile Val Ile Ile Gly Ile Phe Ile Ile Thr  
1 5 10 15

Gly Cys Asp Trp Gln Arg Thr Ser Lys Glu Arg Ser Lys Asn Ala Gln  
20 25 30

	35	40	45
5	Asn L u Met Met Thr Lys Lys Leu Leu Ser Gln Tyr Asn His Pro Lys 50 55 60		
	Tyr Lys Leu Glu Leu Val Lys Phe Asn Asn Trp Pro Asp Leu Met Asp 65 70 75 80		
10	Ala Leu Asn Ser Gly Arg Ile Asp Gly Ala Ser Thr Leu Ile Glu Leu 85 90 95		
	Ala Met Lys Ser Lys Gln Lys Gly Ser Asn Ile Lys Ala Val Ala Leu 100 105 110		
15	Gly His His Glu Gly Asn Val Ile Met Gly Gln Lys Gly Met His Leu 115 120 125		
	Asn Glu Phe Asn Asn Asn Gly Asp Asp Tyr His Phe Gly Ile Pro His 130 135 140		
20	Arg Tyr Ser Thr His Tyr Leu Leu Leu Glu Glu Leu Arg Lys Gln Leu 145 150 155 160		
	Lys Ile Lys Pro Gly His Phe Ser Tyr His Glu Met Ser Pro Ala Glu 165 170 175		
25	Met Pro Ala Ala Leu Ser Glu His Arg Ile Thr Gly Tyr Ser Val Ala 180 185 190		
	Glu Pro Phe Gly Ala Leu Gly Glu Lys Leu Gly Lys Gly Lys Thr Leu 195 200 205		
30	Lys His Gly Asp Asp Val Ile Pro Asp Ala Tyr Cys Cys Val Leu Val 210 215 220		
	Leu Arg Gly Glu Leu Leu Asp Gln His Lys Asp Val Ala Gln Ala Phe 225 230 235 240		
35	Val Gln Asp Tyr Lys Lys Ser Gly Phe Lys Met Asn Asp Arg Lys Gln 245 250 255		
	Ser Val Asp Ile Met Thr His His Phe Lys Gln Ser Arg Asp Val Leu 260 265 270		
40	Thr Gln Ser Ala Ala Trp Thr Ser Tyr Gly Asp Leu Thr Ile Lys Pro 275 280 285		
	Ser Gly Tyr Gln Glu Ile Thr Thr Leu Val Lys Gln His His Leu Phe 290 295 300		
45	Asn Pro Pro Ala Tyr Asp Asp Phe Val Glu Pro Ser Leu Tyr Lys Glu 305 310 315 320		
50	Ala Ser Arg Ser		

## (2) INFORMATION FOR SEQ ID NO:5210:

## (i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5210:

Met Lys Lys Thr Leu Gly Cys Leu Leu Leu Ile Met Leu Leu Val Val  
 1 5 10 15  
 Ala Gly Cys Ser Phe Gly Gly Asn His Lys Leu Ser Ser Lys Lys Ser  
 15 20 25 30  
 Glu Glu Ser Lys Gln Glu Thr Val Lys Lys Glu Ser Glu Glu Glu Lys  
 35 40 45  
 Asp Pro Asp Leu Glu Lys Tyr Glu Glu Ile Glu Lys Lys Met Lys Gly  
 20 50 55 60  
 Ile Lys Asp Ala Pro Ser Leu Asp Lys Leu Asp Pro Leu Met Thr Glu  
 65 70 75 80  
 Lys Ser Phe Thr Asn Ser Lys Gly Ile Gln Gly Trp Lys Asp Tyr Lys  
 25 85 90 95  
 Glu Leu Met Gly Lys Val Glu Leu Ala Asp Tyr Arg Phe Thr Lys Asp  
 100 105 110  
 Ser Lys Gly Ser Ser Ile Lys Asp Val Asp Ala Phe Phe Lys Gly Lys  
 30 115 120 125  
 Lys Gly Ile Lys Arg Lys Val Ile Glu Thr His Asp Asp Val Lys Gln  
 35 130 135 140  
 Val Asp Tyr Trp  
 145

(2) INFORMATION FOR SEQ ID NO:5211:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5211:

Trp Pro Cys Ala Thr Xaa Gln Glx Glu Trp Trp Ser Arg His Xaa Trp  
 1 5 10 15

55

20

25

30

His

5

## (2) INFORMATION FOR SEQ ID NO:5212:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 490 amino acids

10

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5212:

20

Met Ser Ile Ile Met Glu Val Ala Thr Met Gln Ala Lys Leu Thr Lys  
 1 5 10 15

Asn Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys Gln Phe Asn  
 20 25 30

25

Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala Gly  
 35 40 45

Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly Ala Lys Asp  
 50 55 60

30

Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn  
 65 70 75 80

Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser  
 85 90 95

35

Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr  
 100 105 110

Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly Trp  
 115 120 125

40

Thr Asp Gly Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr Arg  
 130 135 140

Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn Phe  
 145 150 155 160

45

Lys Ser Glu Thr Ala Pro Arg Ser Val Gln Ser Pro Thr Gln Ala Pro  
 165 170 175

Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys Ile  
 180 185 190

50

Ile Lys Asp Val Val Lys Gly Tyr Asp Leu Pro Lys Arg Gly Ser Asn  
 195 200 205

55

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	210	215	220
	Ala Glu Ala Tyr Arg Asn Gly Leu Val Asn Ala Pro Leu Ser Arg Leu		
	225	230	235 240
5	Glu Ala Gly Ile Ala His Ser Tyr Val S r Gly Asn Thr Val Trp Gln		
		245	250 255
	Ala Leu Asp Glu Ser Gln Val Gly Trp His Thr Ala Asn Gln Ile Gly		
10		260	265 270
	Asn Lys Tyr Tyr Tyr Gly Ile Glu Val Cys Gln Ser Met Gly Ala Asp		
		275	280 285
	Asn Ala Thr Phe Leu Lys Asn Glu Gln Ala Thr Phe Gln Glu Cys Ala		
15		290	295 300
	Arg Leu Leu Lys Lys Trp Gly Leu Pro Ala Asn Arg Asn Thr Ile Arg		
		305	310 315 320
	Leu His Asn Glu Phe Thr Ser Thr Ser Cys Pro His Arg Ser Ser Val		
20		325	330 335
	Leu His Thr Gly Phe Asp Pro Val Thr Arg Gly Leu Leu Pro Glu Asp		
		340	345 350
	Lys Arg Leu Gln Leu Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala Tyr		
25		355	360 365
	Met Asp Gly Lys Ile Pro Val Ala Thr Val Ser Asn Glu Ser Ser Ala		
		370	375 380
30	Ser Ser Asn Thr Val Lys Pro Val Ala Ser Ala Trp Lys Arg Asn Lys		
		385	390 395 400
	Tyr Gly Thr Tyr Tyr Met Glu Glu Ser Ala Arg Phe Thr Asn Gly Asn		
		405	410 415
35	Gln Pro Ile Thr Val Arg Lys Val Gly Pro Phe Leu Ser Cys Pro Val		
		420	425 430
	Gly Tyr Gln Phe Gln Pro Gly Gly Tyr Cys Asp Tyr Thr Glu Val Met		
40		435	440 445
	Leu Gln Asp Gly His Val Trp Val Gly Tyr Thr Trp Glu Gly Gln Arg		
		450	455 460
	Tyr Tyr Leu Pro Ile Arg Thr Trp Asn Gly Ser Ala Pro Pro Asn Gln		
45		465	470 475 480
	Ile Leu Gly Asp Leu Trp Gly Glu Ile Ser		
		485	490

(2) INFORMATION FOR SEQ ID NO:5213:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 299 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5213:

5  
 10 Gly Asp Lys Met Asn Lys Ile Ser Lys Tyr Ile Ala Ile Ala Ser Leu  
 1 5 10 15  
 Ser Val Ala Val Thr Val Ser Ala Pro Gln Thr Thr Asn Ser Thr Ala  
 20 25 30  
 15 Phe Ala Lys Ser Ser Ala Glu Val Gln Gln Thr Gln Gln Ala Ser Ile  
 35 40 45  
 Pro Ala Ser Gln Lys Ala Asn Leu Gly Asn Gln Asn Ile Met Ala Val  
 50 55 60  
 20 Ala Trp Tyr Gln Asn Ser Ala Glu Ala Lys Ala Leu Tyr Leu Gln Gly  
 65 70 75 80  
 Tyr Asn Ser Ala Lys Thr Gln Leu Asp Lys Glu Ile Lys Lys Asn Lys  
 85 90 95  
 25 Gly Lys His Lys Leu Ala Ile Ala Leu Asp Leu Asp Glu Thr Val Leu  
 100 105 110  
 Asp Asn Ser Pro Tyr Gln Gly Tyr Ala Ser Ile His Asn Lys Pro Phe  
 115 120 125  
 30 Pro Glu Gly Trp His Glu Trp Val Gln Ala Ala Lys Ala Lys Pro Val  
 130 135 140  
 35 Tyr Gly Ala Lys Glu Phe Leu Lys Tyr Ala Asp Lys Lys Gly Val Asp  
 145 150 155 160  
 Ile Tyr Tyr Ile Ser Asp Arg Asp Lys Glu Lys Asp Leu Lys Ala Thr  
 165 170 175  
 40 Gln Lys Asn Leu Lys Gln Gln Gly Ile Pro Gln Ala Lys Lys Ser His  
 180 185 190  
 Ile Leu Leu Lys Gly Lys Asp Asp Lys Ser Lys Glu Ser Arg Arg Gln  
 195 200 205  
 45 Met Val Gln Lys Asp His Lys Leu Val Met Leu Phe Gly Asp Asn Leu  
 210 215 220  
 50 Leu Asp Phe Thr Asp Pro Lys Glu Ala Thr Ala Glu Ser Arg Glu Ala  
 225 230 235 240  
 Leu Ile Glu Lys His Lys Asp Asp Phe Gly Lys Lys Tyr Ile Ile Phe  
 245 250 255  
 55 Pro Asn Pro Met Tyr Gly Ser Trp Glu Ala Thr Ile Tyr Asn Asn Asn  
 260 265 270

275

280

285

Lys Gln Phe Asp Pro Lys Thr Gly Glu Val Lys  
290 295

## (2) INFORMATION FOR SEQ ID NO:5214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5214:

Leu Asn Lys Cys Lys Ile Ile Ile Trp Arg Ile Ile Asn Met Lys Asn  
1 5 10 15  
Lys Leu Ile Ala Lys Ser Leu Leu Thr Leu Ala Ala Ile Gly Ile Thr  
20 25 30  
Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly Tyr Gly Pro  
35 40 45  
Arg Glu Lys Lys Pro Val Ser Ile Asn His Asn Ile Val Glu Tyr Asn  
50 55 60  
Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn Ser Thr Pro  
65 70 75 80  
Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu Phe Asn Asp  
85 90 95  
Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys Pro Ala Ala  
100 105 110  
Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile Gln Ala Gln  
115 120 125  
Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser Ala His Arg  
130 135 140  
Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr Lys Val Lys  
145 150 155 160  
Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu Lys Gln Gly Leu  
165 170 175  
Val Lys

## (2) INFORMATION FOR SEQ ID NO:5215:

## (i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5215:

Lys Glu Arg Val Leu Met Lys Lys Leu Leu Thr Ala Ser Ile Ile Ala  
 1 5 10 15  
 Cys Ser Val Val Met Gly Val Gly Leu Val Asn Thr Ser Ala Glu Ala  
 15 20 25 30  
 Ala Ser Gly Asn Ser Ile Asp Thr Val Lys Gln Leu Ile Lys Gly Asp  
 35 40 45  
 Gln Ser Leu Glu Asn Val Lys Ile Gly Glu Ser Ile Lys Asp Val Leu  
 50 55 60  
 Thr Lys Tyr Lys Asn Pro Met Tyr Ser Tyr Asn Glu Asp Gly Thr Glu  
 65 70 75 80  
 His Tyr Tyr Glu Phe His Thr Lys Lys Gly Met Leu Leu Val Thr Thr  
 85 90 95  
 Asp Gly Lys Lys Asn Asn Gly Lys Val Thr His Ile Ser Met Met Tyr  
 100 105 110  
 Asn Asp Ala Asn Gly Pro Thr Tyr Gln Ala Val Lys Asn Tyr Val Gly  
 115 120 125  
 Lys Ala Val Thr His Thr Glu Tyr Ser Lys Val Ala Gly Asn Phe Gly  
 130 135 140  
 Tyr Ile Glu Lys Gly Lys Thr Thr Tyr Gln Phe Ala Ser Ala Pro Lys  
 145 150 155 160  
 Asp Lys Asn Ile Lys Leu Tyr Arg Ile Asp Leu Glu Lys  
 165 170

(2) INFORMATION FOR SEQ ID NO:5216:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 167 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5216:

EP 0 786 519 A2

1 5 10 15  
 Asn Glu Asp Gly Ser Lys Lys Lys Met Ser Thr Thr Ala Lys Val Val  
 20 25 30  
 5 Ser Ile Ala Thr Val Leu Leu Leu Leu Gly Gly Leu Val Phe Ala Ile  
 35 40 45  
 10 Phe Ala Tyr Val Asp His Ser Asn Lys Ala Lys Glu Arg Met Leu Asn  
 50 55 60  
 Glu Gln Lys Gln Glu Gln Lys Glu Lys Arg Gln Lys Glu Asn Ala Glu  
 65 70 75 80  
 15 Lys Glu Arg Lys Lys Lys Gln Gln Glu Glu Lys Glu Gln Asn Glu Leu  
 85 90 95  
 Asp Ser Gln Ala Asn Gln Tyr Gln Gln Leu Pro Gln Gln Asn Gln Tyr  
 100 105 110  
 20 Gln Tyr Val Pro Pro Gln Gln Gln Ala Pro Thr Lys Gln Arg Pro Ala  
 115 120 125  
 Lys Glu Glu Asn Asp Asp Lys Ala Ser Lys Asp Glu Ser Lys Asp Lys  
 130 135 140  
 25 Asp Asp Lys Ala Ser Gln Asp Lys Ser Asp Asp Asn Gln Lys Lys Thr  
 145 150 155 160  
 Asp Asp Asn Lys Gln Pro Ala  
 165  
 30

(2) INFORMATION FOR SEQ ID NO:5217:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 115 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 35

(ii) MOLECULE TYPE: protein  
 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5217:

45 Met Lys Arg Asn Phe Pro Lys Leu Ile Ala Leu Ser Leu Ile Phe Ser  
 1 5 10 15  
 Leu Ser Val Thr Pro Ile Ala Asn Ala Glu Ser Asn Ser Asn Ile Lys  
 20 25 30  
 50 Ala Lys Asp Lys Lys His Val Gln Val Asn Val Glu Asp Lys Ser Val  
 35 40 45  
 55 Pro Thr Asp Val Arg Asn Leu Ala Gln Lys Asp Tyr Leu Ser Tyr Val  
 50 55 60

[illegible]

(2) INFORMATION FOR SEQ ID NO:5218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5218:

Asn	Phe	Lys	Met	Gln	Glu	Val	Lys	Tyr	Met	Thr	Glu	Ile	Thr	Phe	Lys
1			5						10					15	
Gly	Gly	Pro	Ile	His	Leu	Lys	Gly	Gln	Gln	Ile	Asn	Glu	Gly	Asp	Phe
			20					25					30		
Ala	Pro	Asp	Phe	Thr	Val	Leu	Asp	Asn	Asp	Leu	Asn	Gln	Val	Thr	Leu
		35					40					45			
Ala	Asp	Tyr	Ala	Gly	Lys	Lys	Lys	Leu	Ile	Ser	Val	Val	Pro	Ser	Ile
	50					55					60				
Asp	Thr	Gly	Val	Cys	Asp	Gln	Gln	Thr	Arg	Lys	Phe	Asn	Ser	Asp	Ala
65					70					75					80
Ser	Lys	Glu	Glu	Gly	Ile	Val	Leu	Thr	Ile	Ser	Ala	Asp	Leu	Pro	Phe
				85					90					95	
Ala	Gln	Lys	Arg	Trp	Cys	Ala	Ser	Ala	Gly	Leu	Asp	Asn	Val	Ile	Thr
			100					105						110	
Leu	Ser	Asp	His	Arg	Asp	Leu	Ser	Phe	Gly	Glu	Asn	Tyr	Gly	Val	Val
		115					120					125			
Met	Glu	Glu	Leu	Arg	Leu	Leu	Ala	Arg	Ala	Val	Phe	Val	Leu	Asp	Ala
	130					135					140				
Asp	Asn	Lys	Val	Val	Tyr	Lys	Glu	Ile	Val	Ser	Glu	Gly	Thr	Asp	Phe
145					150					155					160
Pro	Asp	Phe	Asp	Ala	Ala	Leu	Ala	Ala	Tyr	Lys	Asn	Ile			
				165					170						

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5219:

Ile Glu Ser Arg Phe Ile Met Ala Lys Ile Asn Phe Asp Ala Ala Thr  
 1 5 10 15  
 Lys Gly Asn Pro Gly Ile Ser Thr Cys Ala Ile Val Ile Lys Glu Asp  
 20 25 30  
 Glu Gln His Tyr Thr Tyr Thr His Glu Leu Gly Glu Met Asp Asn His  
 35 40 45  
 Thr Ala Glu Trp Ala Ala Cys Ile Tyr Ala Leu Glu His Ala Arg Glu  
 50 55 60  
 Leu Asn Val Gln Asn Ala Leu Leu Tyr Thr Asp Ser Lys Leu Ile Ala  
 65 70 75 80  
 Asp Ser Ile Glu Ala Gly Tyr Val Lys Asn Ala Asn Phe Lys Pro Tyr  
 85 90 95  
 Phe Asp Gln Ile Glu Ile Phe Glu Lys Asp Phe Asp Leu Leu Phe Val  
 100 105 110  
 Lys Trp Ile Pro Arg Glu Gln Asn Lys Glu Ala Asn Gln His Ala Gln  
 115 120 125  
 Gln Ala Leu Tyr Lys Leu Ile Lys Lys Asn Lys  
 130 135

## (2) INFORMATION FOR SEQ ID NO:5220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5220:

Met Pro Gly Thr Val Leu Asp Pro Gln Met Ile Lys Asn Glu Asp Val  
 1 5 10 15

20                      25                      30  
 Gly Val Asn Thr Ser Met Asp Trp Asp Arg Lys Tyr Pro Tyr Gly Asp  
                     35                      40                      45  
 5 Thr Leu Arg Gly Ile Phe Gly Asp Val Ser Thr Pro Ala Glu Gly Ile  
                     50                      55                      60  
 10 Pro Lys Glu Leu Thr Glu His Tyr Leu Ser Lys Gly Tyr Ser Arg Asn  
      65                      70                      75                      80  
 Asp Arg Val Gly Lys Ser Tyr Leu Glu Tyr Gln Tyr Glu Asp Val Leu  
                     85                      90                      95  
 15 Arg Gly Lys Lys Lys Glu Met Lys Tyr Thr Thr Asp Lys Ser Gly Lys  
                     100                      105                      110  
 Val Thr Ser Ser Glu Val Leu Xaa Pro Gly Ala Arg Gly Gln Asp Leu  
                     115                      120                      125  
 20 Lys Leu Thr Ile Asp Ile Asp Leu Gln Lys Glu Val Glu Ala Leu Leu  
                     130                      135                      140  
 Asp Lys Gln Ile Lys Lys Leu Ala Val Lys Val Pro Lys Ile Trp Ile  
      145                      150                      155                      160  
 25 Met Gln

## (2) INFORMATION FOR SEQ ID NO:5221:

30 (i) SEQUENCE CHARACTERISTICS:  
      (A) LENGTH: 311 amino acids  
      (B) TYPE: amino acid  
      (C) STRANDEDNESS: single  
      (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5221:

Ile Met Ala Tyr Asp Gly Leu Phe Thr Lys Lys Met Val Glu Ser Leu  
 1                      5                      10                      15  
 45 Gln Phe Leu Thr Thr Gly Arg Val His Lys Ile Asn Gln Pro Asp Asn  
                     20                      25                      30  
 Asp Thr Ile Leu Met Val Val Arg Gln Asn Arg Gln Asn His Gln Leu  
                     35                      40                      45  
 50 Leu Leu Ser Ile His Pro Asn Phe Ser Arg Leu Gln Leu Thr Thr Lys  
                     50                      55                      60  
 55 Lys Tyr Asp Asn Pro Phe Asn Pro Pro Met Phe Ala Arg Val Phe Arg  
      65                      70                      75                      80

	85	90	95
5	Asp Arg Arg Ile Glu Ile Asp Ile Lys Ser Lys Asp Glu Ile Gly Asp 100 105 110		
	Thr Ile Tyr Arg Thr Val Ile Leu Glu Ile Met Gly Lys His Ser Asn 115 120 125		
10	Leu Ile Leu Val Asp Glu Asn Arg Lys Ile Ile Glu Gly Phe Lys His 130 135 140		
	Leu Thr Pro Asn Thr Asn His Tyr Arg Thr Val Met Pro Gly Phe Asn 145 150 155 160		
15	Tyr Glu Ala Pro Pro Thr Gln His Lys Ile Asn Pro Tyr Asp Ile Thr 165 170 175		
	Gly Ala Glu Val Leu Lys Tyr Ile Asp Phe Asn Ala Gly Asn Ile Ala 180 185 190		
20	Lys Gln Leu Leu Asn Gln Phe Glu Gly Phe Ser Pro Leu Ile Thr Asn 195 200 205		
	Glu Ile Val Ser Arg Arg Gln Phe Met Thr Ser Ser Thr Leu Pro Glu 210 215 220		
25	Ala Phe Asp Glu Val Met Ala Glu Thr Lys Leu Pro Pro Thr Pro Ile 225 230 235 240		
	Phe His Lys Asn His Glu Thr Gly Lys Glu Asp Phe Tyr Phe Ile Lys 245 250 255		
30	Leu Asn Gln Phe Asn Asp Asp Thr Val Thr Tyr Asp Ser Leu Asn Asp 260 265 270		
	Leu Leu Asp Arg Phe Tyr Asp Ala Arg Gly Glu Arg Glu Arg Val Lys 275 280 285		
35	Gln Arg Ala Asn Asp Leu Val Arg Phe Val Gln Gln Gln Leu His Lys 290 295 300		
40	Tyr Gln Asn Lys Leu Ala Ser 305 310		

## (2) INFORMATION FOR SEQ ID NO:5222:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 245 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: protein
- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5222:

	1		5		10		15									
	Glu	Gln	Leu	Tyr	Gly	Glu	Leu	Ile	Thr	Ala	Asn	Ile	Tyr	Arg	Ile	Lys
5				20				25					30			
	Gln	Gly	Asp	Lys	Glu	Val	Thr	Ala	Leu	Asn	Tyr	Tyr	Thr	Asn	Glu	Glu
			35				40						45			
10	Val	Val	Ile	Pro	Leu	Asn	Pro	Thr	Lys	Ser	Pro	Ser	Ala	Asn	Ala	Gln
	50					55					60					
	Tyr	Tyr	Tyr	Lys	Gln	Tyr	Xaa	Arg	Met	Lys	Thr	Arg	Xaa	Arg	Glu	Leu
	65				70						75				80	
15	Gln	His	Gln	Ile	Gln	Leu	Thr	Lys	Asp	Asn	Ile	Asp	Tyr	Phe	Ser	Thr
			85						90					95		
	Ile	Glu	Gln	Gln	Leu	His	His	Ile	Ser	Val	His	Asp	Ile	Asp	Glu	Ile
20			100					105					110			
	Arg	Asp	Glu	Leu	Ala	Glu	Gln	Gly	Phe	Met	Lys	Gln	Arg	Lys	Asn	Gln
			115					120					125			
25	Thr	Lys	Lys	Lys	Lys	Ala	Gln	Ile	Gln	Leu	Gln	His	Tyr	Val	Ser	Thr
	130						135					140				
	Asp	Gly	Asp	Asp	Ile	Tyr	Val	Gly	Lys	Asn	Asn	Lys	Gln	Asn	Asp	Tyr
	145				150					155					160	
30	Leu	Thr	Asn	Lys	Lys	Ala	Lys	Lys	Thr	His	Thr	Trp	Leu	His	Thr	Lys
			165						170					175		
	Asp	Ile	Pro	Gly	Ser	His	Val	Val	Ile	Phe	Asn	Asp	Ala	Pro	Ser	Asp
			180					185					190			
35	Thr	Thr	Ile	Lys	Glu	Ala	Ala	Met	Leu	Ala	Gly	Tyr	Phe	Ser	Lys	Ala
	195						200					205				
	Gly	Asn	Ser	Gly	Gln	Ile	Pro	Val	Asp	Tyr	Thr	Leu	Ile	Lys	Asn	Val
40		210				215						220				
	His	Lys	Pro	Ser	Gly	Ala	Lys	Pro	Gly	Phe	Val	Thr	Tyr	Asp	Asn	Gln
	225				230					235					240	
45	Lys	Thr	Leu	Tyr	Ala											
				245												

## (2) INFORMATION FOR SEQ ID NO:5223:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 99 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5223:

Tyr Ile Thr Asn Pro Gln Asn Pro Lys Ile Lys Ile Thr Gly Ile Ser  
 1 5 10 15  
 Leu Ser Ser Gly Val Gly Asn Phe Phe Ile Ile Thr Asn Gly Lys Arg  
 20 25 30  
 Ile Ile Val Ala Lys Ile Lys Arg Asn Ala Asp Asn Asp Ser Ala Leu  
 35 40 45  
 Lys Ser Phe Asn Ala Ile Phe Ile Ile Gly Asn Ala Asp Pro His Asn  
 50 55 60  
 Met Ile Val Asn Lys Tyr Asp Arg Lys Val Val Ser Arg Ser Leu Phe  
 65 70 75 80  
 Ile Asn Ile Ile Thr Pro Leu Ile Met Cys Phe Tyr Ile Lys Lys Tyr  
 85 90 95  
 Asp Leu Lys

## (2) INFORMATION FOR SEQ ID NO:5224:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5224:

Glu Asn Val Leu Ala Lys Glu Tyr Ala Val Lys Tyr Asn Ala Val Glu  
 1 5 10 15  
 Ala Ile Gln His Arg Gly Glu Thr Val Thr Glu Gly Ser Ser Ser Asn  
 20 25 30  
 Ala Tyr Ala Ile Lys Asp Gly Val Ile Tyr Thr His Pro Ile Asn Asn  
 35 40 45  
 Tyr Ile Leu Asn Gly Ile Thr Arg Ile Val Ile Lys Lys Ile Ala Glu  
 50 55 60  
 Asp Tyr Asn Ile Pro Phe Lys Glu Glu Thr Phe Thr Val Asp Phe Leu  
 65 70 75 80  
 Lys Asn Ala Asp Glu Val Ile Val Ser Ser Thr Ser Ala Glu Val Thr  
 85 90 95  
 Pro Val Ile Lys Leu Asp Gly Glu Pro Val Asn Asp Gly Lys Val Gly  
 100 105 110

115

120

125

His Ser Ile  
130

## (2) INFORMATION FOR SEQ ID NO:5225:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5225:

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn  
1 5 10 15  
Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile  
20 25 30  
Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr  
35 40 45  
Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala  
50 55 60  
Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln  
65 70 75 80  
Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro  
85 90 95  
Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly  
100 105 110  
Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp  
115 120 125  
Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala  
130 135 140  
Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala  
145 150 155 160  
Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln  
165 170 175  
Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala  
180 185 190  
Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp  
195 200 205

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	210	215	220
	Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly		
5	225	230	235 240
	Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn		
		245	250 255
10	Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val		
		260	265 270
	Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys		
		275	280 285
15	Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr		
		290	295 300
	Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp		
		305	310 315 320
20	Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly		
		325	330 335
	Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu		
		340	345 350
25	Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr		
		355	360 365
	Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly		
30		370	375 380
	Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro		
		385	390 395 400
35	Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn		
		405	410 415
	Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu		
		420	425 430
40	Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr		
		435	440 445
	Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr		
		450	455 460
45	Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly		
		465	470 475 480
	Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp		
		485	490 495
50	Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr		
		500	505 510
55	Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser		
		515	520 525

530

535

540

## (2) INFORMATION FOR SEQ ID NO:5226:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5226:

Tyr Lys Glu Leu Ser His Gly Arg Leu Ile Gly Gly Thr Lys Met His  
 1 5 10 15

Lys Lys Tyr Phe Ile Gly Thr Ser Ile Leu Ile Ala Val Phe Val Val  
 20 25 30

Ile Phe Asp Gln Val Thr Lys Tyr Ile Ile Ala Thr Thr Met Lys Ile  
 35 40 45

Gly Asp Ser Phe Glu Val Ile Pro His Phe Leu Asn Ile Thr Ser His  
 50 55 60

Arg Asn Asn Gly Ala Ala Trp Gly Ile Leu Ser Gly Lys Met Thr Phe  
 65 70 75 80

Phe Phe Ile Ile Thr Ile Ile Ile Leu Ile Ala Leu Val Tyr Phe Phe  
 85 90 95

Ile Lys Asp Ala Gln Tyr Asn Leu Phe Met Gln Val Ala Ile Ser Leu  
 100 105 110

Leu Phe Ala Gly Ala Leu Gly Asn Phe Ile Asp Arg Ile Leu Thr Gly  
 115 120 125

Glu Val Val Asp Phe Ile Asp Thr Asn Ile Phe Gly Tyr Asp Phe Pro  
 130 135 140

Ile Phe Asn Ile Ala Asp Ser Ser Leu Thr Ile Gly Val Ile Leu Ile  
 145 150 155 160

Ile Ile Ala Leu Leu Lys Asp Thr Ser Asn Lys Lys Glu Lys Glu Val  
 165 170 175

Lys

## (2) INFORMATION FOR SEQ ID NO:5227:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5227:

Ala Gly Lys Ser Ser Leu Ile Lys Ser Leu Ile Gly Glu Phe Asn Ala  
1 5 10 15  
Thr Gly Thr Lys Leu Leu Tyr Asn Lys Pro Ile Gln Gln Gln Leu Gln  
20 25 30  
His Ile Thr Tyr Ile Pro Gln Lys Ala His Ile Asp Leu Asp Phe Pro  
35 40 45  
Ile Ser Val Glu Gln Val Ile Leu Ser Gly Cys Tyr Lys Glu Ile Gly  
50 55 60  
Trp Phe Arg Arg Pro Asn Lys Ser Ala Arg Asp Lys Leu Lys Gln Leu  
65 70 75 80  
Leu Ser Asp Leu Glu Leu Glu Ser Leu Arg His Arg Gln Ile Ser Glu  
85 90 95  
Leu Ser Gly Gly Gln Leu Gln Arg Val Leu Val Ala Arg Ala Leu Met  
100 105 110  
Ser Xaa Ser Glu Val Tyr Phe Leu Asp Glu Pro Phe Val Gly Ile Asp  
115 120 125  
Phe Ser Ser Glu Lys Leu Ile Met Thr Lys Ile Glu Asn Leu Lys Gln  
130 135 140  
Gln Gly Lys Leu Ile Leu Ile Ile His His Asp Leu Ser Lys Ala Lys  
145 150 155 160  
Gln Tyr Phe Asp Arg Ile Ile Leu Leu Asn Gln Thr Leu Arg Tyr Phe  
165 170 175  
Gly Asp Ser Glu Glu Ala Met Ser Val Thr Arg Leu Asn Glu Thr Phe  
180 185 190  
Met Ser Ser Thr Asp Cys Ser Asp Pro Ser Gln Arg Ser Asn Ile Thr  
195 200 205  
Cys

(2) INFORMATION FOR SEQ ID NO:5228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5228:

5	Thr	Phe	Arg	Ile	Ile	Phe	Leu	Leu	Ser	Ile	Arg	Lys	Arg	Ser	Asn	Arg	1	5	10	15
	Thr	His	Val	Ser	Ile	His	Trp	Ser	Thr	Val	Asn	Lys	Glu	Glu	Ile	Cys	20	25	30	
10	Leu	Arg	Val	Lys	Asp	Asn	Leu	Gln	Gln	Ile	Ser	Thr	Gln	Ile	Asn	Asp	35	40	45	
	Lys	Ser	Glu	Lys	Asn	Asn	Phe	Ser	Thr	Lys	Pro	Asn	Val	Ile	Ala	Val	50	55	60	
15	Thr	Lys	Tyr	Val	Thr	Ile	Glu	Arg	Ala	Lys	Glu	Ala	Tyr	Glu	Ala	Gly	65	70	75	80
	Ile	Arg	His	Phe	Gly	Glu	Asn	Arg	Leu	Glu	Gly	Phe	Phe	Gln	Lys	Lys	85	90	95	
20																				
	Glu	Ala	Leu	Pro	Ser	Asp	Ala	Val	Ile	His	Phe	Ile	Gly	Ser	Leu	Gln	100	105	110	
25	Ser	Arg	Lys	Val	Lys	Asp	Val	Ile	Asn	Asp	Val	Asp	Tyr	Phe	His	Ala	115	120	125	
	Leu	Asp	Arg	Leu	Ser	Leu	Ala	Lys	Glu	Ile	Asn	Lys	Arg	Ala	Glu	His	130	135	140	
30	Lys	Ile	Lys	Cys	Phe	Leu	Gln	Val	Asn	Val	Ser	Gly	Glu	Ala	Ser	Lys	145	150	155	160
	His	Gly	Ile	Ala	Leu	Glu	Asp	Val	Asp	Gln	Phe	Ile	Asp	Asp	Leu	Lys	165	170	175	
35	Lys	Tyr	Asp	Lys	Ile	Glu	Ile	Val	Gly	Leu	Met	Thr	Met	Ala	Pro	Leu	180	185	190	
	Thr	Asp	Asp	Glu	Ala	Tyr	Ile	Arg	Ser	Leu	Phe	Lys	Gln	Leu	Arg	Leu	195	200	205	
40	Lys	Lys	Glu	Glu	Ile	Gln	Arg	Leu	Asn	Leu	Glu	Tyr	Ala	Pro	Cys	Asp	210	215	220	
45	Glu	Leu	Ser	Met	Gly	Met	Ser	Asn	Asp	Tyr	Leu	Ile	Ala	Val	Glu	Glu	225	230	235	240
	Gly	Ala	Thr	Phe	Val	Arg	Ile	Gly	Thr	Lys	Leu	Val	Gly	Glu	Glu	Glu	245	250	255	

## (2) INFORMATION FOR SEQ ID NO:5229:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5229:

10 Lys His Lys Leu Thr Ile Ile Thr Gly Gly Phe Phe Thr Met Lys Lys  
 1 5 10 15  
 Thr Ile Met Ala Ser Ser Leu Ala Val Ala Leu Gly Val Thr Gly Tyr  
 20 25 30  
 15 Ala Ala Gly Thr Gly His Gln Ala His Ala Ala Glu Val Asn Val Asp  
 35 40 45  
 Gln Ala His Leu Val Asp Leu Ala His Asn His Gln Asp Gln Leu Asn  
 50 55 60  
 20 Ala Ala Pro Ile Lys Asp Gly Ala Tyr Asp Ile His Phe Val Lys Asp  
 65 70 75 80  
 Gly Phe Gln Tyr Asn Phe Thr Ser Asn Gly Thr Thr Trp Ser Trp Ser  
 85 90 95  
 25 Tyr Glu Ala Ala Asn Gly Gln Thr Ala Gly Phe Ser Asn Val Ala Gly  
 100 105 110  
 Ala Asp Tyr Thr Thr Ser Tyr Asn Gln Gly Ser Asn Val Gln Ser Val  
 115 120 125  
 Ser Tyr Asn Ala Gln Ser Ser Asn Ser Asn Val Glu Ala Val Ser Ala  
 130 135 140  
 35 Pro Thr Tyr His Asn Tyr Ser Thr Ser Thr Thr Ser Ser Ser Val Arg  
 145 150 155 160  
 Leu Ser Asn Gly Asn Thr Ala Gly Ala Thr Gly Ser Ser Ala Ala Gln  
 165 170 175  
 40 Ile Met Ala Gln Arg Thr Gly Val Ser Ala Ser Thr Trp Ala Ala Ile  
 180 185 190  
 Ile Ala Arg Glu Ser Asn Gly Gln Val Asn Ala Tyr Asn Pro Ser Gly  
 195 200 205  
 45 Ala Ser Gly Leu Phe Gln Thr Met Pro Gly Trp Gly Pro Thr Asn Thr  
 210 215 220  
 Val Asp Gln Gln Ile Asn Ala Ala Val Lys Ala Tyr Lys Ala Gln Gly  
 225 230 235 240  
 Leu Gly Ala Trp Gly Phe  
 245

(2) INFORMATION FOR SEQ ID NO:5230:

(A) LENGTH: 519 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5230:

Lys	Glu	Pro	His	Lys	Met	Lys	Lys	Ile	Tyr	Lys	Ser	Leu	Thr	Val	Ser	1	5	10	15
Ala	Ile	Val	Ala	Thr	Val	Ser	Leu	Ser	Ala	Leu	Pro	Gln	Ser	Leu	Ala	20	25	30	
Ile	Thr	His	Glu	Ser	Gln	Pro	Thr	Lys	Gln	Gln	Arg	Thr	Val	Leu	Phe	35	40	45	
Asp	Arg	Ser	His	Gly	Gln	Thr	Ala	Gly	Ala	Ala	Asp	Trp	Val	Ser	Asp	50	55	60	
Gly	Ala	Phe	Ser	Asp	Tyr	Ala	Asp	Ser	Ile	Gln	Lys	Gln	Gly	Tyr	Asp	65	70	75	80
Val	Lys	Ala	Ile	Asp	Gly	His	Ser	Asn	Ile	Thr	Glu	Ala	Ser	Leu	Lys	85	90	95	
Ser	Ser	Lys	Ile	Phe	Val	Ile	Pro	Glu	Ala	Asn	Ile	Pro	Phe	Lys	Glu	100	105	110	
Ser	Glu	Gln	Ala	Ala	Ile	Val	Lys	Tyr	Val	Lys	Gln	Gly	Gly	Asn	Val	115	120	125	
Val	Phe	Ile	Ser	Asp	His	Tyr	Asn	Ala	Asp	Arg	Asn	Leu	Asn	Arg	Ile	130	135	140	
Asp	Ser	Ser	Glu	Ala	Met	Asn	Gly	Tyr	Arg	Arg	Gly	Ala	Tyr	Glu	Asp	145	150	155	160
Met	Ser	Lys	Gly	Met	Asn	Ala	Glu	Glu	Lys	Ser	Ser	Thr	Ala	Met	Gln	165	170	175	
Gly	Val	Lys	Ser	Ser	Asp	Trp	Leu	Ser	Thr	Asn	Phe	Gly	Val	Arg	Phe	180	185	190	
Arg	Tyr	Asn	Ala	Leu	Gly	Asp	Leu	Asn	Thr	Ser	Asn	Ile	Val	Ser	Ser	195	200	205	
Lys	Glu	Ser	Phe	Gly	Ile	Thr	Glu	Gly	Val	Lys	Ser	Val	Ser	Met	His	210	215	220	
Ala	Gly	Ser	Thr	Leu	Ala	Ile	Thr	Asn	Pro	Glu	Lys	Ala	Lys	Gly	Ile	225	230	235	240
Val	Tyr	Thr	Pro	Glu	Gln	Leu	Pro	Ala	Lys	Ser	Lys	Trp	Ser	His	Ala	245	250	255	

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Val Asp Gln Gly Ile Tyr Asn Gly Gly Gly Lys Ala Glu Gly Pro Tyr  
260 265 270

5 Val Ala Ile Ser Lys Val Gly Lys Gly Lys Ala Ala Phe Ile Gly Asp  
275 280 285

Ser Ser Leu Val Glu Asp Ser Ser Pro Lys Tyr Val Arg Glu Asp Asn  
290 295 300

10 Gly Glu Lys Lys Lys Thr Tyr Asp Gly Phe Lys Glu Gln Asp Asn Gly  
305 310 315 320

Lys Leu Leu Asn Asn Ile Thr Ala Trp Met Ser Lys Asp Asn Asp Gly  
325 330 335

15 Lys Ser Leu Lys Ala Ser Ser Leu Thr Leu Asp Thr Lys Thr Lys Leu  
340 345 350

Leu Asp Phe Glu Arg Pro Glu Arg Ser Thr Glu Pro Glu Lys Glu Pro  
355 360 365

20 Trp Ser Gln Pro Pro Ser Gly Tyr Lys Trp Tyr Asp Pro Thr Thr Phe  
370 375 380

Lys Ala Gly Ser Tyr Gly Ser Glu Lys Gly Ala Asp Pro Gln Pro Asn  
385 390 395 400

25 Thr Pro Asp Asp His Thr Pro Pro Asn Gln Asn Glu Lys Val Thr Phe  
405 410 415

30 Asp Ile Pro Gln Asn Val Ser Val Asn Glu Pro Phe Glu Met Thr Ile  
420 425 430

His Leu Lys Gly Phe Glu Ala Asn Gln Thr Leu Glu Asn Leu Arg Val  
435 440 445

35 Gly Ile Tyr Lys Glu Gly Gly Arg Gln Ile Gly Gln Phe Ser Ser Lys  
450 455 460

Asp Asn Asp Tyr Asn Pro Pro Gly Tyr Ser Thr Leu Pro Thr Val Lys  
465 470 475 480

40 Ala Asp Glu Asn Gly Asn Val Thr Ile Lys Val Asn Ala Lys Val Leu  
485 490 495

45 Glu Ser Met Glu Gly Ser Lys Ile Arg Leu Lys Leu Gly Asp Lys Thr  
500 505 510

Leu Ile Thr Thr Asp Phe Lys  
515

(2) INFORMATION FOR SEQ ID NO:5231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5231:

5	Arg	Asp	Glu	Arg	Ile	Lys	Thr	Met	Thr	Asn	Ser	Ser	Lys	Ser	Phe	Thr	1	5	10	15
	Lys	Phe	Met	Ala	Ala	Ser	Ala	Val	Phe	Thr	Met	Gly	Phe	Leu	Ser	Val	20	25	30	
10	Pro	Thr	Ala	Gly	Ala	Glu	Gln	Thr	Asn	Gln	Ile	Ala	Asn	Lys	Pro	Gln	35	40	45	
	Ala	Ile	Gln	Trp	His	Thr	Asn	Leu	Thr	Asn	Glu	Arg	Phe	Thr	Thr	Ile	50	55	60	
15	Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Ala	Pro	Glu	His	Thr	Phe	Gln	Ala	65	70	75	80
	Tyr	Asp	Lys	Ser	His	Asn	Glu	Leu	Lys	Ala	Ser	Tyr	Ile	Glu	Ile	Asp	85	90	95	
20	Leu	Gln	Arg	Thr	Lys	Asp	Gly	His	Leu	Val	Ala	Met	His	Asp	Glu	Thr	100	105	110	
25	Val	Asn	Arg	Thr	Thr	Asn	Gly	His	Gly	Lys	Val	Glu	Asp	Tyr	Thr	Leu	115	120	125	
	Asp	Glu	Leu	Lys	Gln	Leu	Asp	Ala	Gly	Ser	Trp	Phe	Asn	Lys	Lys	Tyr	130	135	140	
30	Pro	Lys	Tyr	Ala	Arg	Ala	Ser	Tyr	Lys	Asn	Ala	Lys	Val	Pro	Thr	Leu	145	150	155	160
	Asp	Glu	Ile	Leu	Glu	Arg	Tyr	Gly	Pro	Asn	Ala	Asn	Tyr	Tyr	Ile	Glu	165	170	175	
35	Thr	Lys	Ser	Pro	Asp	Val	Tyr	Pro	Gly	Met	Glu	Glu	Gln	Leu	Leu	Ala	180	185	190	
40	Ser	Leu	Lys	Lys	His	His	Leu	Leu	Asn	Asn	Asn	Lys	Leu	Lys	Asn	Gly	195	200	205	
	His	Val	Met	Ile	Gln	Ser	Phe	Ser	Asp	Glu	Ser	Leu	Lys	Lys	Ile	His	210	215	220	
45	Arg	Gln	Asn	Lys	His	Val	Pro	Leu	Val	Lys	Leu	Val	Asp	Lys	Gly	Glu	225	230	235	240
	Leu	Gln	Gln	Phe	Asn	Asp	Gln	Arg	Leu	Lys	Glu	Ile	Arg	Ser	Tyr	Ala	245	250	255	
50	Ile	Gly	Leu	Gly	Pro	Asp	Tyr	Thr	Asp	Leu	Thr	Glu	Gln	Asn	Thr	His	260	265	270	
55	His	Leu	Lys	Asp	Leu	Gly	Phe	Ile	Val	His	Pro	Tyr	Thr	Val	Asn	Glu	275	280	285	

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Lys Ala Asp Met Leu Arg Leu Asn Lys Tyr Gly Val Asp Gly Val Phe  
290 295 300

Thr Asn Phe Ala Asp Lys Tyr Lys Glu Val Ile Lys  
305 310 315

(2) INFORMATION FOR SEQ ID NO:5232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5232:

Arg Phe Met Lys Asn Leu Ile Ser Ile Ile Ile Ile Leu Cys Leu Thr  
1 5 10 15

Leu Ser Ile Met Thr Pro Tyr Ala Gln Ala Thr Asn Ser Asp Val Thr  
20 25 30

Pro Val Gln Ala Ala Asn Gln Tyr Gly Tyr Ala Gly Leu Ser Ala Ala  
35 40 45

Tyr Glu Pro Thr Ser Ala Val Asn Val Ser Gln Thr Gly Gln Leu Leu  
50 55 60

Tyr Gln Tyr Asn Ile Asp Thr Lys Trp Asn Pro Ala Ser Met Thr Lys  
65 70 75 80

Leu Met Thr Met Tyr Leu Thr Leu Glu Ala Val Asn Lys Gly Gln Leu  
85 90 95

Ser Leu Asp Asp Thr Val Thr Met Thr Asn Lys Glu Tyr Ile Met Ser  
100 105 110

Thr Leu Pro Glu Leu Ser Asn Thr Lys Leu Tyr Pro Gly Gln Val Trp  
115 120 125

Thr Ile Ala Asp Leu Leu Gln Ile Thr Val Ser Asn Ser Ser Asn Ala  
130 135 140

Ala Ala Leu Ile Leu Ala Lys Lys Val Ser Lys Asn Thr Ser Asp Phe  
145 150 155 160

Val Asp Leu Met Asn Asn Lys Ala Lys Ala Ile Gly Met Lys Asn Thr  
165 170 175

His Phe Val Asn Pro Thr Gly Ala Glu Asn Ser Arg Leu Arg Thr Phe  
180 185 190

Ala Pro Thr Lys Tyr Lys Asp Gln Glu Arg Thr Val Thr Thr Ala Arg  
195 200 205

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Asp Tyr Ala Ile Leu Asp Leu His Val Ile Lys Glu Thr Pro Lys Ile  
210 215 220

Leu Asp Phe Thr Lys Gln Leu Ala Pro Thr Thr His Ala Val Thr Tyr  
225 230 235 240

Tyr Thr Phe Asn Phe Ser Leu Glu Gly Ala Lys Met Ser Leu Pro Gly  
245 250 255

Thr Asp Gly Leu Lys Thr Gly Ser Ser Asp Thr Ala Asn Tyr Asn His  
260 265 270

Thr Ile Thr Thr Lys Arg Gly Lys Phe Arg Ile Asn Gln Val Ile Met  
275 280 285

Gly Ala Gly Asp Tyr Lys Asn Leu Gly Gly Glu Lys Gln Arg Asn Met  
290 295 300

Met Gly Asn Ala Leu Met Glu Arg Ser Phe Asp Gln Tyr Lys Tyr Val  
305 310 315 320

Lys Ile Leu Ser Lys Gly Glu Gln Arg Ile Asn Gly Lys Lys Tyr Tyr  
325 330 335

Val Glu Asn Asp Leu Tyr Asp Val Leu Pro Ser Asp Phe Ser Lys Lys  
340 345 350

Asp Tyr Lys Leu Val Val Glu Asp Gly Lys Val His Ala Asp Tyr Pro  
355 360 365

Arg Glu Phe Ile Asn Lys Asp Tyr Gly Pro Pro Thr Val Glu Val His  
370 375 380

Gln Pro Ile Ile Gln Lys Ala Asn Thr Val Ala Lys Ser Met Trp Glu  
385 390 395 400

Glu His Pro Leu Phe Thr Ile Ile Gly Gly Thr Cys Leu Val Ala Gly  
405 410 415

Leu Ala Leu Ile Val His Met Ile Ile Asn Arg Leu Phe Arg Lys Arg  
420 425 430

Lys

(2) INFORMATION FOR SEQ ID NO:5233:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 151 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5233:

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Leu Thr Lys Glu Arg Glu Tyr Met Lys Leu Lys Ser Phe Ile Thr Val  
1 5 10 15

Thr Leu Ala Leu Gly Met Ile Ala Thr Thr Gly Ala Thr Val Ala Gly  
20 25 30

Asn Glu Val Ser Ala Ala Glu Lys Asp Lys Leu Pro Ala Thr Gln Lys  
35 40 45

Ala Lys Glu Met Gln Asn Val Pro Tyr Thr Ile Ala Val Asp Gly Ile  
50 55 60

Met Ala Phe Asn Gln Ser Tyr Leu Asn Leu Pro Lys Asp Ser Gln Leu  
65 70 75 80

Ser Tyr Leu Asp Leu Gly Asn Lys Val Lys Ala Leu Leu Tyr Asp Glu  
85 90 95

Arg Gly Val Thr Pro Glu Lys Ile Arg Asn Ala Lys Ser Ala Val Tyr  
100 105 110

Thr Ile Thr Trp Lys Asp Gly Ser Lys Lys Glu Val Asp Leu Lys Lys  
115 120 125

Asp Ser Tyr Thr Ala Asn Leu Phe Asp Ser Asn Ser Ile Lys Gln Ile  
130 135 140

Asp Ile Asn Val Lys Thr Lys  
145 150

(2) INFORMATION FOR SEQ ID NO:5234:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 497 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5234:

Asn His Cys Asn Arg Ile Glu Arg Lys Met Ala Met Ser Asn Asn Phe  
1 5 10 15

Lys Asp Asp Phe Glu Lys Asn Arg Gln Ser Ile Asp Thr Asn Ser His  
20 25 30

Gln Asp His Thr Glu Asp Val Glu Lys Asp Gln Ser Glu Leu Glu His  
35 40 45

Gln Asp Thr Ile Glu Asn Thr Glu Gln Gln Phe Pro Pro Arg Asn Ala  
50 55 60

Gln Arg Arg Lys Arg Arg Arg Asp Leu Ala Thr Asn His Asn Lys Gln  
65 70 75 80

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	Val	His	Asn	Glu	Ser	Gln	Thr	Ser	Glu	Asp	Asn	Val	Gln	Asn	Glu	Ala	
					85					90					95		
5	Gly	Thr	Ile	Asp	Asp	Arg	Gln	Val	Glu	Ser	Ser	His	Ser	Thr	Glu	Ser	
				100					105					110			
	Gln	Glu	Pro	Ser	His	Gln	Asp	Ser	Thr	Pro	Gln	His	Glu	Glu	Glu	Tyr	
			115					120					125				
10	Tyr	Asn	Lys	Asn	Ala	Phe	Ala	Met	Asp	Lys	Ser	His	Pro	Glu	Pro	Ile	
		130					135					140					
	Glu	Asp	Asn	Asp	Lys	His	Asp	Thr	Ile	Lys	Asn	Ala	Glu	Asn	Asn	Thr	
	145					150					155				160		
15	Glu	His	Ser	Thr	Val	Ser	Asp	Lys	Ser	Glu	Ala	Glu	Gln	Ser	Gln	Gln	
					165					170					175		
	Pro	Lys	Pro	Tyr	Phe	Thr	Thr	Gly	Ala	Asn	Gln	Ser	Glu	Thr	Ser	Lys	
				180				185						190			
20	Asn	Glu	His	Asp	Asn	Asp	Ser	Val	Lys	Gln	Asp	Gln	Asp	Glu	Pro	Lys	
			195					200					205				
25	Glu	His	His	Asn	Gly	Lys	Lys	Ala	Ala	Ala	Ile	Gly	Ala	Gly	Thr	Ala	
		210					215					220					
	Gly	Val	Ala	Gly	Ala	Ala	Gly	Ala	Met	Ala	Ala	Ser	Lys	Ala	Lys	Lys	
	225				230					235					240		
30	His	Ser	Asn	Asp	Ala	Gln	Asn	Lys	Ser	Asn	Ser	Gly	Lys	Ala	Asn	Asn	
					245					250				255			
	Ser	Thr	Glu	Asp	Lys	Ala	Ser	Gln	Asp	Lys	Ser	Lys	Asp	His	His	Asn	
				260					265					270			
35	Gly	Lys	Lys	Gly	Ala	Ala	Ile	Gly	Ala	Gly	Thr	Ala	Gly	Leu	Ala	Gly	
		275					280						285				
	Gly	Ala	Ala	Ser	Lys	Ser	Ala	Ser	Ala	Ala	Ser	Lys	Pro	His	Ala	Ser	
		290					295					300					
40	Asn	Asn	Ala	Ser	Gln	Asn	His	Asp	Glu	His	Asp	Asn	His	Asp	Arg	Asp	
	305					310					315					320	
	Lys	Glu	Arg	Lys	Lys	Gly	Gly	Met	Ala	Lys	Val	Leu	Leu	Pro	Leu	Ile	
				325						330					335		
45	Ala	Ala	Val	Leu	Ile	Ile	Gly	Ala	Leu	Ala	Ile	Phe	Gly	Gly	Met	Ala	
			340						345					350			
50	Leu	Asn	Asn	His	Asn	Asn	Gly	Thr	Lys	Glu	Asn	Lys	Ile	Ala	Asn	Thr	
		355					360						365				
	Asn	Lys	Asn	Asn	Ala	Asp	Glu	Ser	Lys	Asp	Lys	Asp	Thr	Ser	Lys	Asp	
		370					375					380					
55	Ala	Ser	Lys	Asp	Lys	Ser	Lys	Ser	Thr	Asp	Ser	Asp	Lys	Ser	Lys	Glu	
		385				390					395				400		

Asp Gln Asp Lys Ala Thr Lys Asp Glu Ser Asp Asn Asp Gln Asn Asn  
 405 410 415  
 Ala Asn Gln Ala Asn Asn Gln Ala Gln Asn Asn Gln Asn Gln Gln Gln  
 420 425 430  
 Ala Asn Gln Asn Gln Gln Gln Gln Gln Gln Arg Gln Gly Gly Gly Gln  
 435 440 445  
 Arg His Thr Val Asn Gly Gln Glu Asn Leu Tyr Arg Ile Ala Ile Gln  
 450 455 460  
 Tyr Tyr Gly Ser Gly Ser Pro Glu Asn Val Glu Lys Ile Arg Arg Ala  
 465 470 475 480  
 Asn Gly Leu Ser Gly Asn Asn Ile Arg Asn Gly Gln Gln Ile Val Ile  
 485 490 495  
 Pro

## (2) INFORMATION FOR SEQ ID NO:5235:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5235:

Leu Leu Ser Ile Lys Tyr Asn Leu Ile Gly Val Val Asn Asn Met Asn  
 1 5 10 15  
 Lys His His Pro Lys Leu Arg Ser Phe Tyr Ser Ile Arg Lys Ser Thr  
 20 25 30  
 Leu Gly Val Ala Ser Val Ile Val Ser Thr Leu Phe Leu Ile Thr Ser  
 35 40 45  
 Gln His Gln Ala Gln Ala Ala Glu Asn Thr Asn Thr Ser Asp Lys Ile  
 50 55 60  
 Ser Glu Asn Gln Asn Asn Asn Ala Thr Thr Thr Gln Pro Pro Lys Asp  
 65 70 75 80  
 Thr Asn Gln Thr Gln Pro Ala Thr Gln Pro Ala Asn Thr Ala Lys Asn  
 85 90 95  
 Tyr Pro Ala Ala Asp Glu Ser Leu Lys Asp Ala Ile Lys Asp Pro Ala  
 100 105 110  
 Leu Glu Asn Lys Glu His Asp Ile Gly Pro Arg Glu Gln Val Asn Phe  
 115 120 125

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	Gln	Leu	Leu	Asp	Lys	Asn	Asn	Glu	Thr	Gln	Tyr	Tyr	His	Phe	Phe	Ser
	130						135					140				
5	Ile	Lys	Asp	Pro	Ala	Asp	Val	Tyr	Tyr	Thr	Lys	Lys	Lys	Ala	Glu	Val
	145					150					155				160	
	Glu	Leu	Asp	Ile	Asn	Thr	Ala	Ser	Thr	Trp	Lys	Lys	Phe	Glu	Val	Tyr
				165						170					175	
10	Glu	Asn	Asn	Gln	Lys	Leu	Pro	Val	Arg	Leu	Val	Ser	Tyr	Ser	Pro	Val
				180					185					190		
	Pro	Glu	Asp	His	Ala	Tyr	Ile	Arg	Phe	Pro	Val	Ser	Asp	Gly	Thr	Gln
			195					200					205			
15	Glu	Leu	Lys	Ile	Val	Ser	Ser	Thr	Gln	Ile	Asp	Asp	Gly	Glu	Glu	Thr
	210						215					220				
	Asn	Tyr	Asp	Tyr	Thr	Lys	Leu	Val	Phe	Ala	Lys	Pro	Ile	Tyr	Asn	Asp
	225					230					235				240	
20	Pro	Ser	Leu	Val	Lys	Ser	Asp	Thr	Asn	Asp	Ala	Val	Val	Thr	Asn	Asp
					245					250					255	
25	Gln	Ser	Ser	Ser	Val	Ala	Ser	Asn	Gln	Thr	Asn	Thr	Asn	Thr	Ser	Asn
				260					265						270	
	Gln	Asn	Ile	Ser	Thr	Ile	Asn	Asn	Ala	Asn	Asn	Gln	Pro	Gln	Ala	Thr
			275				280						285			
30	Thr	Asn	Met	Ser	Gln	Pro	Ala	Gln	Pro	Lys	Ser	Ser	Thr	Asn	Ala	Asp
	290						295					300				
	Gln	Ala	Ser	Ser	Gln	Pro	Ala	His	Glu	Thr	Asn	Ser	Asn	Gly	Asn	Thr
	305					310					315				320	
35	Asn	Asp	Lys	Thr	Asn	Glu	Ser	Ser	Asn	Gln	Ser	Asp	Val	Asn	Gln	Gln
				325						330					335	
	Tyr	Pro	Pro	Ala	Asp	Glu	Ser	Leu	Gln	Asp	Ala	Ile	Lys	Asn	Pro	Ala
				340					345					350		
40	Ile	Ile	Asp	Lys	Glu	His	Thr	Ala	Asp	Asn	Trp	Arg	Pro	Ile	Asp	Phe
			355					360					365			
	Gln	Met	Lys	Asn	Asp	Lys	Gly	Glu	Arg	Gln	Phe	Tyr	His	Tyr	Ala	Ser
	370						375					380				
45	Thr	Val	Glu	Pro	Ala	Thr	Val	Ile	Phe	Thr	Lys	Thr	Gly	Pro	Ile	Ile
	385					390					395				400	
	Glu	Leu	Gly	Leu	Lys	Thr	Ala	Ser	Thr	Trp	Lys	Lys	Phe	Glu	Val	Tyr
				405						410					415	
50	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Val	Glu	Leu	Val	Ser	Tyr	Asp	Ser	Asp
				420					425					430		
55	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Pro	Val	Ser	Asn	Gly	Thr	Arg	Glu
				435				440					445			

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	Val	Lys	Ile	Val	Ser	Ser	Ile	Glu	Tyr	Gly	Glu	Asn	Ile	His	Glu	Asp	
	450						455					460					
5	Tyr	Asp	Tyr	Thr	Leu	Met	Val	Phe	Ala	Gln	Pro	Ile	Thr	Asn	Asn	Pro	
	465					470					475					480	
	Asp	Asp	Tyr	Val	Asp	Glu	Glu	Thr	Tyr	Asn	Leu	Gln	Lys	Leu	Leu	Ala	
					485					490					495		
10	Pro	Tyr	His	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Glu	
				500					505					510			
	Lys	Leu	Gln	Glu	Lys	Leu	Pro	Glu	Lys	Tyr	Lys	Ala	Glu	Tyr	Lys	Lys	
			515					520					525				
15	Lys	Leu	Asp	Gln	Thr	Arg	Val	Glu	Leu	Ala	Asp	Gln	Val	Lys	Ser	Ala	
	530						535					540					
	Val	Thr	Glu	Phe	Glu	Asn	Val	Thr	Pro	Thr	Asn	Asp	Gln	Leu	Thr	Asp	
	545					550					555					560	
20	Leu	Gln	Glu	Ala	His	Phe	Val	Val	Phe	Glu	Ser	Glu	Glu	Asn	Ser	Glu	
					565					570					575		
	Ser	Val	Met	Asp	Gly	Phe	Val	Glu	His	Pro	Phe	Tyr	Thr	Ala	Thr	Leu	
25				580					585					590			
	Asn	Gly	Gln	Lys	Tyr	Val	Val	Met	Lys	Thr	Lys	Asp	Asp	Ser	Tyr	Trp	
			595					600					605				
30	Lys	Asp	Leu	Ile	Val	Glu	Gly	Lys	Arg	Val	Thr	Thr	Val	Ser	Lys	Asp	
	610						615					620					
	Pro	Lys	Asn	Asn	Ser	Arg	Thr	Leu	Ile	Phe	Pro	Tyr	Ile	Pro	Asp	Lys	
	625					630					635					640	
35	Ala	Val	Tyr	Asn	Ala	Ile	Val	Lys	Val	Val	Val	Ala	Asn	Ile	Gly	Tyr	
				645						650					655		
	Glu	Gly	Gln	Tyr	His	Val	Arg	Ile	Ile	Asn	Gln	Asp	Ile	Asn	Thr	Lys	
				660					665					670			
40	Asp	Asp	Asp	Thr	Ser	Gln	Asn	Asn	Thr	Ser	Glu	Pro	Leu	Asn	Val	Gln	
			675					680					685				
	Thr	Gly	Gln	Glu	Gly	Lys	Val	Ala	Asp	Thr	Asp	Val	Ala	Glu	Asn	Ser	
45		690				695						700					
	Ser	Thr	Ala	Thr	Asn	Pro	Lys	Asp	Ala	Ser	Asp	Lys	Ala	Asp	Val	Ile	
	705					710					715					720	
	Glu	Pro	Glu	Ser	Asp	Val	Val	Lys	Asp	Ala	Asp	Asn	Asn	Ile	Asp	Lys	
50					725					730					735		
	Asp	Val	Gln	His	Asp	Val	Asp	His	Leu	Ser	Asp	Met	Ser	Asp	Asn	Asn	
				740					745					750			
55	His	Phe	Asp	Lys	Tyr	Asp	Leu	Lys	Glu	Met	Asp	Thr	Gln	Ile	Ala	Lys	
	755							760					765				

Asp Thr Asp Arg Asn Val Asp Lys Asp Ala Asp Asn Ser Val Gly Met  
 770 775 780  
 Ser Ser Asn Val Asp Thr Asp Lys Asp Ser Asn Lys Asn Lys Asp Lys  
 785 790 795 800  
 Val Ile Gln Leu Asn His Ile Ala Asp Lys Asn Asn His Thr Gly Lys  
 805 810 815  
 Ala Ala Lys Leu Asp Val Val Lys Gln Asn Tyr Asn Asn Thr Asp Lys  
 820 825 830  
 Val Thr Asp Lys Lys Thr Thr Glu His Leu Pro Ser Asp Ile His Lys  
 835 840 845  
 Thr Val Asp Lys Thr Val Lys Thr Lys Glu Lys Ala Gly Thr Pro Ser  
 850 855 860  
 Lys Glu Asn Lys Leu Ser Gln Ser Lys Met Leu Thr Lys Asn Trp Arg  
 865 870 875 880  
 Asn Asn Xaa Gln Ala Asn  
 885

## (2) INFORMATION FOR SEQ ID NO:5236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 236 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5236:

Asn Met Asn Lys Asn Val Met Val Lys Gly Leu Thr Ala Leu Thr Ile  
 1 5 10 15  
 Leu Thr Ser Leu Gly Phe Ala Glu Asn Ile Ser Asn Gln Xaa His Ser  
 20 25 30  
 Ile Ala Lys Ala Glu Lys Asn Val Lys Glu Ile Thr Asp Ala Thr Lys  
 35 40 45  
 Glu Pro Tyr Asn Ser Val Val Ala Phe Val Gly Gly Thr Gly Val Val  
 50 55 60  
 Val Gly Lys Asn Thr Ile Val Thr Asn Lys His Ile Ala Lys Ser Asn  
 65 70 75 80  
 Asp Ile Phe Lys Asn Arg Val Ser Ala His His Ser Ser Lys Gly Lys  
 85 90 95  
 Gly Gly Gly Asn Tyr Asp Val Lys Asp Ile Val Glu Tyr Pro Gly Lys  
 100 105 110

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Glu Asp Leu Ala Ile Val His Val His Glu Thr Ser Thr Glu Gly Leu  
115 120 125  
Asn Phe Asn Lys Asn Val Ser Tyr Thr Lys Phe Ala Asp Gly Ala Lys  
130 135 140  
Val Lys Asp Arg Ile Ser Val Ile Gly Tyr Pro Lys Gly Ala Gln Thr  
145 150 155 160  
Lys Tyr Lys Met Phe Glu Ser Thr Gly Thr Ile Asn His Ile Ser Gly  
165 170 175  
Thr Phe Met Glu Phe Asp Ala Tyr Ala Gln Pro Gly Asn Ser Gly Ser  
180 185 190  
Pro Val Leu Asn Ser Lys His Xaa Leu Ile Gly Ile Leu Tyr Ala Gly  
195 200 205  
Ser Gly Lys Asp Glu Ser Glu Lys Asn Phe Gly Val Tyr Phe Thr Pro  
210 215 220  
Gln Leu Xaa Xaa Phe Ile Pro Asn Asn Ile Glu Lys  
225 230 235

(2) INFORMATION FOR SEQ ID NO:5237:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 363 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5237:

Tyr Arg Leu Glu His Thr Ile Met Lys Met Arg Thr Ile Ala Lys Thr  
1 5 10 15  
Ser Leu Ala Leu Gly Leu Leu Thr Thr Gly Ala Ile Thr Val Thr Thr  
20 25 30  
Gln Ser Val Lys Ala Glu Lys Ile Gln Ser Thr Lys Val Asp Lys Val  
35 40 45  
Pro Thr Leu Lys Ala Glu Arg Leu Ala Met Ile Asn Ile Thr Ala Gly  
50 55 60  
Ala Asn Ser Ala Thr Thr Gln Ala Ala Asn Thr Arg Gln Glu Arg Thr  
65 70 75 80  
Pro Lys Leu Glu Lys Ala Pro Asn Thr Asn Glu Glu Lys Thr Ser Ala  
85 90 95  
Ser Lys Ile Glu Lys Ile Ser Gln Pro Lys Gln Glu Glu Gln Lys Thr  
100 105 110

	Leu	Asn	Ile	Ser	Ala	Thr	Pro	Ala	Pro	Lys	Gln	Glu	Gln	Ser	Gln	Thr	
			115					120					125				
5	Thr	Thr	Glu	Ser	Thr	Thr	Pro	Lys	Thr	Lys	Val	Thr	Thr	Pro	Pro	Ser	
			130					135					140				
	Thr	Asn	Thr	Pro	Gln	Pro	Met	Gln	Ser	Thr	Lys	Ser	Asp	Thr	Pro	Gln	
			145				150					155				160	
10	Ser	Pro	Thr	Ile	Lys	Gln	Ala	Gln	Thr	Asp	Met	Thr	Pro	Lys	Tyr	Glu	
					165					170					175		
	Asp	Leu	Arg	Ala	Tyr	Tyr	Thr	Lys	Pro	Ser	Phe	Glu	Phe	Glu	Lys	Gln	
				180					185					190			
15	Phe	Gly	Phe	Met	Leu	Lys	Pro	Trp	Thr	Thr	Val	Arg	Phe	Met	Asn	Val	
			195					200					205				
	Ile	Pro	Asn	Arg	Phe	Ile	Tyr	Lys	Ile	Ala	Leu	Val	Gly	Lys	Asp	Glu	
20			210					215					220				
<hr/>																	
	Lys	Lys	Tyr	Lys	Asp	Gly	Pro	Tyr	Asp	Asn	Ile	Asp	Val	Phe	Ile	Val	
			225				230				235					240	
25	Leu	Glu	Asp	Asn	Lys	Tyr	Gln	Leu	Lys	Lys	Tyr	Ser	Val	Gly	Gly	Ile	
					245					250					255		
	Thr	Lys	Thr	Asn	Ser	Lys	Lys	Val	Asn	His	Lys	Val	Glu	Leu	Ser	Ile	
				260					265					270			
30	Thr	Lys	Lys	Asp	Asn	Gln	Gly	Met	Ile	Ser	Arg	Asp	Val	Ser	Glu	Tyr	
			275					280					285				
	Met	Ile	Thr	Lys	Glu	Glu	Ile	Ser	Leu	Lys	Glu	Leu	Asp	Phe	Lys	Leu	
			290				295					300					
35	Arg	Lys	Gln	Leu	Ile	Glu	Lys	His	Asn	Leu	Tyr	Gly	Asn	Met	Gly	Ser	
			305				310				315					320	
	Gly	Thr	Ile	Val	Ile	Lys	Met	Lys	Asn	Gly	Gly	Lys	Tyr	Thr	Phe	Glu	
40					325					330					335		
	Leu	His	Lys	Lys	Leu	Gln	Glu	His	Arg	Met	Ala	Asp	Val	Ile	Asp	Gly	
				340					345					350			
45	Thr	Asn	Ile	Asp	Asn	Ile	Glu	Val	Asn	Ile	Lys						
			355					360									

## (2) INFORMATION FOR SEQ ID NO:5238:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5238:

5 Phe Met Lys Phe Lys Ser Leu Ile Thr Thr Thr Leu Ala Leu Gly Val  
 1 5 10 15  
 Leu Ala Ser Thr Gly Ala Asn Phe Asn Asn Asn Glu Ala Ser Ala Ala  
 20 25 30  
 10 Ala Lys Pro Leu Asp Lys Ser Ser Ser Ser Leu His His Gly Tyr Ser  
 35 40 45  
 Lys Val His Val Pro Tyr Ala Ile Thr Val Asn Gly Thr Ser Gln Asn  
 50 55 60  
 15 Ile Leu Ser Ser Leu Thr Phe Asn Lys Asn Gln Asn Ile Ser Tyr Lys  
 65 70 75 80  
 Asp Leu Glu Asp Arg Val Lys Ser Val Leu Lys Ser Asp Arg Gly Ile  
 85 90 95  
 20 Ser Asp Ile Asp Leu Arg Leu Ser Lys Gln Ala Lys Tyr Thr Val Tyr  
 100 105 110  
 Phe Lys Asn Gly Thr Lys Lys Val Ile Asp Leu Lys Ala Gly Ile Tyr  
 115 120 125  
 25 Thr Ala Asp Leu Ile Asn Thr Ser Glu Ile Lys Ala Ile Asn Ile Asn  
 130 135 140  
 Val Asp Thr Lys Lys Gln  
 145 150  
 30

## (2) INFORMATION FOR SEQ ID NO:5239:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 239 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5239:

45 Glu Lys Arg Phe Met Gln Met Ala Arg Lys Val Val Val Val Asp Asp  
 1 5 10 15  
 Glu Lys Pro Ile Ala Asp Ile Leu Glu Phe Asn Leu Lys Lys Glu Gly  
 20 25 30  
 50 Tyr Asp Val Tyr Cys Ala Tyr Asp Gly Asn Asp Ala Val Asp Leu Ile  
 35 40 45  
 Tyr Glu Glu Glu Pro Asp Ile Val Leu Leu Asp Ile Met Leu Pro Gly  
 50 55 60  
 55

Arg Asp Gly Met Glu Val Cys Arg Glu Val Arg Lys Lys Tyr Glu Met  
 65 70 75 80  
 5 Pro Ile Ile Met Leu Thr Ala Lys Asp Ser Glu Ile Asp Lys Val Leu  
 85 90 95  
 Gly Leu Glu Leu Gly Ala Asp Asp Tyr Val Thr Lys Pro Phe Ser Thr  
 100 105 110  
 10 Arg Glu Leu Ile Ala Arg Val Lys Ala Asn Leu Arg Arg His Tyr Ser  
 115 120 125  
 Gln Pro Ala Gln Asp Thr Gly Asn Val Thr Asn Glu Ile Thr Ile Lys  
 130 135 140  
 15 Asp Ile Val Ile Tyr Pro Asp Ala Tyr Ser Ile Lys Lys Arg Gly Glu  
 145 150 155 160  
 Asp Ile Glu Leu Thr His Arg Glu Phe Glu Leu Phe His Tyr Leu Ser  
 165 170 175  
 20 Lys His Met Gly Gln Val Met Thr Arg Glu His Leu Leu Gln Thr Val  
 180 185 190  
 Trp Gly Tyr Asp Tyr Phe Gly Asp Val Arg Thr Val Asp Val Thr Ile  
 195 200 205  
 25 Arg Arg Leu Arg Glu Lys Ile Glu Asp Asp Pro Ser His Pro Glu Tyr  
 210 215 220  
 Ile Val Thr Arg Arg Gly Val Gly Tyr Phe Leu Gln Gln His Glu  
 225 230 235  
 30

## (2) INFORMATION FOR SEQ ID NO:5240:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5240:

Xaa Leu Ser Thr Val Ile Gly Ala Xaa Leu Phe Phe Lys Ser Ser Val  
 1 5 10 15  
 Ser Leu Val Phe Lys Met Val Lys Lys Phe Arg Xaa Gly Val Ile Ser  
 20 25 30  
 Val Asn Asp Val Met Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys  
 35 40 45  
 Asn Ala Phe Ser Leu Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val  
 50 55 60

Ser Val Leu Cys Phe Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu  
 65 70 75 80  
 Ile Lys Tyr Thr Ala Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys  
 85 90 95  
 Ala Asn Gln Leu Ala Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe  
 100 105 110  
 Tyr Asn Tyr Lys Glu Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu  
 115 120 125  
 Phe Asp Val Lys Ala  
 130

## (2) INFORMATION FOR SEQ ID NO:5241:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5241:

Glu Ile Tyr Ile Ile Ala Asn Lys Gln Arg Arg Asp Asn Met Ala Val  
 1 5 10 15  
 Asn Val Arg Asp Tyr Ile Ala Glu Asn Tyr Gly Leu Phe Ile Asn Gly  
 20 25 30  
 Glu Phe Val Lys Gly Ser Ser Asp Glu Thr Ile Glu Val Thr Asn Pro  
 35 40 45  
 Ala Thr Gly Glu Thr Leu Ser His Ile Thr Arg Ala Lys Asp Lys Asp  
 50 55 60  
 Val Asp His Ala Val Lys Val Ala Gln Glu Ala Phe Glu Ser Trp Ser  
 65 70 75 80  
 Leu Thr Ser Lys Ser Glu Arg Ala Gln Met Leu Arg Asp Ile Gly Asp  
 85 90 95  
 Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn  
 100 105 110  
 Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala  
 115 120 125  
 Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly  
 130 135 140  
 Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu  
 145 150 155 160

Pro Ile Gly Val Val Gly Ala Val Val Ala Trp Asn Phe Pro Met Leu  
 165 170 175  
 5 Leu Ala Ala Trp Lys Ile Ala Pro Ala Ile Ala Ala Gly Asn Thr Ile  
 180 185 190  
 Val Ile Gln Pro Ser Ser Ser Thr Pro Leu Ser Leu Leu Glu Val Ala  
 195 200 205  
 10 Lys Ile Phe Gln Glu Val Leu Pro Lys Gly Val Val Asn Ile Leu Thr  
 210 215 220  
 Gly Lys Gly Ser Glu Ser Gly Asn Ala Ile Phe Asn His Asp Gly Val  
 225 230 235 240  
 15 Asp Lys Leu Ser Phe Thr Gly Ser Thr Asp Val Gly Tyr Gln Val Ala  
 245 250 255  
 Glu Ala Ala Ala Lys His Leu Val Pro Ala Thr Leu Glu Leu Gly Gly  
 260 265 270  
 20 Lys Ser Ala Asn Ile Ile Leu Asp Asp Ala Asn Leu Asp Leu Ala Val  
 275 280 285  
 Glu Gly Ile Gln Leu Gly Ile Leu Phe Asn Gln Gly Glu Val Cys Ser  
 290 295 300  
 25 Ala Gly Ser Arg Leu Leu Val His Glu Lys Ile Tyr Asp Gln Leu Val  
 305 310 315 320  
 Pro Arg Leu Gln Glu Ala Phe Ser Asn Ile Lys Val Gly Asn Pro Gln  
 325 330 335  
 30 Asp Glu Ala Thr Gln Met Gly Ser Gln Thr Gly Lys Asp Gln Leu Asp  
 340 345 350  
 35 Lys Ile Gln Ser Tyr Ile Asp Ala Ala Lys Glu Ser Asp Ala Gln Ile  
 355 360 365  
 Leu Ala Gly Gly His Arg Leu Thr Glu Asn Gly Leu Asp Lys Gly Phe  
 370 375 380  
 40 Phe Phe Glu Pro Thr Leu Ile Ala Val Pro Asp Asn His His Lys Leu  
 385 390 395 400  
 Ala Gln Glu Glu Ile Phe Gly Pro Val Leu Thr Val Ile Lys Val Lys  
 405 410 415  
 45 Asp Asp Gln Glu Ala Ile Asp Ile Ala Asn Asp Ser Glu Tyr Gly Leu  
 420 425 430  
 Ala Gly Gly Val Phe Ser Gln Asn Ile Thr Arg Ala Leu Asn Ile Ala  
 435 440 445  
 50 Lys Ala Val Arg Thr Gly Arg Ile Trp Ile Asn Thr Tyr Asn Gln Val  
 450 455 460  
 55 Pro Glu Gly Ala Pro Phe Gly Gly Tyr Lys Lys Ser Gly Ile Gly Arg  
 465 470 475 480

Glu Thr Tyr Lys Gly Ala Leu Ser Asn Tyr Gln Gln Val Lys Asn Ile  
                                     485                                    490                                    495

Tyr Ile Asp Thr Ser Asn Ala Leu Lys Gly Leu Tyr  
                                     500                                    505

(2) INFORMATION FOR SEQ ID NO:5242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5242:

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn  
 1                                    5                                    10                                    15

Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile  
                                     20                                    25                                    30

Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr  
                                     35                                    40                                    45

Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala  
                                     50                                    55                                    60

Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln  
 65                                    70                                    75                                    80

Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro  
                                     85                                    90                                    95

Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly  
                                     100                                    105                                    110

Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp  
                                     115                                    120                                    125

Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala  
                                     130                                    135                                    140

Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala  
 145                                    150                                    155                                    160

Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln  
                                     165                                    170                                    175

Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala  
                                     180                                    185                                    190

Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp  
                                     195                                    200                                    205

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Pro Ala Ile Ser Thr Asp Glu Asn Arg Gln Asp Pro Thr Val Thr Val  
210 215 220

5 Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly  
225 230 235 240

Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn  
245 250 255

10 Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val  
260 265 270

Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys  
275 280 285

15 Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr  
290 295 300

Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp  
305 310 315 320

20 Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly  
325 330 335

25 Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu  
340 345 350

Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr  
355 360 365

30 Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly  
370 375 380

Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro  
385 390 395 400

35 Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn  
405 410 415

Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu  
420 425 430

40 Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr  
435 440 445

Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr  
450 455 460

45 Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly  
465 470 475 480

Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp  
485 490 495

50 Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr  
500 505 510

55 Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser  
515 520 525

Asp Val Val Ile Asn Asn Ala Gln Pro Glu Val His  
530 535 540

## (2) INFORMATION FOR SEQ ID NO:5243:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5243:

Ile Thr Leu Lys Thr Val Ser Gln Leu Ile Asp Met Lys Gln Lys Gln  
1 5 10 15  
Thr Lys Ile Ser Met Val Thr Ala Tyr Asp Phe Pro Ser Ala Lys Gln  
20 20 25 30  
Val Glu Ala Ala Gly Ile Asp Met Ile Leu Val Gly Asp Ser Leu Gly  
25 35 40 45  
Met Thr Val Leu Gly Tyr Glu Ser Thr Val Gln Val Thr Leu Ala Asp  
50 55 60  
Met Ile His His Gly Arg Ala Val Arg Arg Gly Ala Pro Asn Thr Phe  
30 65 70 75 80  
Val Val Val Asp Met Pro Ile Gly Ala Val Gly Ile Ser Met Thr Gln  
85 90 95  
Asp Leu Asn His Ala Leu Lys Leu Tyr Gln Glu Thr Asn Ala Asn Ala  
35 100 105 110  
Ile Lys Ala Glu Gly Ala His Ile Thr Pro Phe Ile Glu Lys Ala Thr  
115 120 125  
Ala Ile Gly Ile Pro Val Val Ala His Leu Gly Leu Thr Pro Gln Ser  
40 130 135 140  
Val Gly Val Met Gly Tyr Lys Leu Gln Gly Ala Thr Lys Glu Ala Ala  
45 145 150 155 160  
Glu Gln Leu Ile Leu Asp Ala Lys Asn Val Glu Gln Ala Gly Ala Val  
165 170 175  
Ala Leu Val Leu Glu Ala Ile Pro Asn Asp Leu Ala Glu Glu Ile Ser  
50 180 185 190  
Lys His Leu Thr Ile Pro Val Ile Gly Ile Gly Ala Gly Lys Gly Thr  
195 200 205  
Asp Gly Gln Val Leu Val Tyr His Asp Met Leu Asn Tyr Gly Val Glu  
55 210 215 220

His Lys Ala Lys Phe Val Lys Gln Phe Ala Asp Phe Ser Val Gly Val  
225 230 235 240

Asp Gly Leu Lys Gln Tyr Asp Gln Glu Val Lys Ser Gly Ala Ph Pro  
245 250 255

Ser Glu Glu Tyr Thr Tyr Lys Lys Lys Ile Met Asn Glu Val Asn Asn  
260 265 270

Asn Asp

(2) INFORMATION FOR SEQ ID NO:5244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5244:

Ser Asp Asp Trp Pro Lys Ser Ile Thr Ser Leu Ser Ile Arg Gly Val  
1 5 10 15

Arg Met Lys His Gln Glu Thr Thr Ser Gln Gln Tyr Asn Phe Ser Ile  
20 25 30

Ile Lys His Gly Asp Ile Ser Thr Pro Gln Gly Phe Thr Ala Gly Gly  
35 40 45

Met His Ile Gly Leu Arg Ala Asn Lys Lys Asp Phe Gly Trp Ile Tyr  
50 55 60

Ser Ser Ser Leu Ala Ser Ala Ala Ala Val Tyr Thr Leu Asn Gln Phe  
65 70 75 80

Lys Ala Ala Pro Leu Ile Val Thr Glu Asp Thr Leu Gln Lys Ser Lys  
85 90 95

Gly Lys Leu Gln Ala Leu Val Val Asn Ser Ala Asn Ala Asn Ser Cys  
100 105 110

Thr Gly Gln Gln Gly Ile Asp Asp Ala Arg Gln Thr Gln Thr Trp Val  
115 120 125

Ala Gln Gln Leu Gln Ile Pro Ser Glu His Val Ala Val Ala Ser Thr  
130 135 140

Gly Val Ile Gly Glu Tyr Leu Pro Met Asp Lys Ile Lys Thr Gly Thr  
145 150 155 160

Glu His Ile Lys Asp Ala Asn Phe Ala Thr Pro Gly Ala Phe Asn Glu  
165 170 175

Ala Ile Leu Thr Thr Asp Thr Cys Thr Lys His Ile Ala Val Ser Leu  
180 185 190

5 Lys Ile Asp Gly Lys Thr Val Thr Ile Gly Gly Ser Thr Lys Gly Ser  
195 200 205

Gly Met Ile His Pro Asn Met Ala Thr Met Leu Ala Phe Ile Thr Thr  
210 215 220

10 Asp Ala Ser Ile Glu Ser Asn Thr Leu His Gln Leu Leu Lys Ser Ser  
225 230 235 240

Thr Asp His Thr Phe Asn Met Ile Thr Val Asp Gly Asp Thr Ser Thr  
245 250 255

15 Asn Asp Met Val Leu Val Met Ala Asn His Gln Val Glu His Gln Ile  
260 265 270

Leu Ser Gln Asp His Pro Gln Trp Glu Thr Phe Val Asp Ala Phe Asn  
275 280 285

20 Phe Val Cys Thr Phe Leu Ala Lys Ala Ile Ala Arg Asp Gly Glu Gly  
290 295 300

Ala Thr Lys Leu Ile Ser Val Asn Val Ser Gly Ala Lys Ser Ile Ser  
305 310 315 320

Asp Ala Arg Lys Ile Gly Lys Thr Ile Val Ser Ser Asn Leu Val Lys  
325 330 335

30 Ser Ala Ile Phe Gly Glu Asp Ala Asn Phe Gly Arg Ile Ile Thr Ala  
340 345 350

Ile Gly Tyr Ser Gly Cys Glu Ile Asp Pro Asn Cys Thr Tyr Val Gln  
355 360 365

35 Leu Asn Gln Ile Pro Val Val Asp Lys Gly Met Ala Val Leu Phe Asp  
370 375 380

Glu Gln Ala Met Ser Asn Thr Leu Thr His Glu Asn Val Thr Ile Asp  
385 390 395 400

40 Val Gln Leu Gly Leu Gly Asn Ala Ala Thr Ala Tyr Gly Cys Asp  
405 410 415

45 Leu Ser Tyr Asp Tyr Val Arg Ile Asn Ala Ser Tyr Arg Thr  
420 425 430

## (2) INFORMATION FOR SEQ ID NO:5245:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5245:

5	Asn	Pro	Ala	Leu	Thr	Val	Phe	Ala	Phe	Ile	Met	Ile	Ile	Ser	Ile	Leu	1	5	10	15
	Leu	Ala	Tyr	Val	Phe	Lys	Trp	Leu	Gly	Leu	Val	Asp	Asp	Val	Leu	Leu	20	25	30	
10	Met	Val	Ile	Ile	Ile	Ser	Thr	Ile	Ser	Leu	Gly	Val	Val	Val	Pro	Thr	35	40	45	
	Leu	Lys	Glu	Met	Asn	Ile	Met	Arg	Thr	Thr	Ile	Gly	Gln	Phe	Ile	Leu	50	55	60	
15	Leu	Val	Ala	Val	Leu	Ala	Asp	Leu	Val	Thr	Met	Ile	Leu	Leu	Thr	Val	65	70	75	80
	Tyr	Gly	Ala	Ile	Asn	Gly	Gln	Gly	Gly	Ser	Thr	Ile	Trp	Leu	Ile	Gly	85	90	95	
20	<del>Ile</del>	<del>Leu</del>	<del>Val</del>	<del>Val</del>	<del>Phe</del>	<del>Thr</del>	<del>Ala</del>	<del>Ile</del>	<del>Ser</del>	<del>Tyr</del>	<del>Ile</del>	<del>Leu</del>	<del>Gly</del>	<del>Val</del>	<del>Gln</del>	<del>Phe</del>	100	105	110	
	Lys	Arg	Met	Ser	Phe	Leu	Gln	Lys	Leu	Met	Asp	Gly	Thr	Thr	Gln	Ile	115	120	125	
25	Gly	Ile	Arg	Ala	Val	Phe	Ala	Leu	Ile	Ile	Leu	Leu	Val	Ala	Leu	Ala	130	135	140	
	Glu	Gly	Val	Gly	Ala	Glu	Asn	Ile	Leu	Gly	Ala	Phe	Leu	Ala	Gly	Val	145	150	155	160
30	Val	Val	Ser	Leu	Leu	Asn	Pro	Asp	Glu	Glu	Met	Val	Glu	Lys	Leu	Asp	165	170	175	
	Ser	Phe	Gly	Tyr	Gly	Phe	Phe	Ile	Pro	Ile	Phe	Phe	Ile	Met	Xaa	Gly	180	185	190	
35	Val	Asp	Leu	Asn	Ile	Pro	Ser	Leu	Ile	Lys	Glu	Pro	Lys	Leu	Leu	Ile	195	200	205	
40	Ile	Ile	Pro	Ile	Leu	Ile	Val	Ala	Phe	Ile	Ile	Ser	Lys	Leu	Ile	Pro	210	215	220	
	Val	Met	Phe	Ile	Arg	Arg	Trp	Phe	Asp	Met	Lys	Thr	Thr	Ile	Ala	Ser	225	230	235	240
45	Ala	Phe	Leu	Leu	Thr	Ser	Thr	Leu	Ser	Leu	Val	Ile	Ala	Ala	Ala	Lys	245	250	255	
	Ile	Ser	Glu	Arg	Leu	Asn	Ala	Ile	Ser	Ala	Glu	Thr	Ser	Gly	Ile	Leu	260	265	270	
50	Ile	Leu	Ser	Ala	Val	Ile	Thr	Cys	Val	Phe	Val	Pro	Ile	Ile	Phe	Lys	275	280	285	
55	Lys	Leu	Phe	Pro	Val	Pro	Asp	Glu	Phe	Asn	Arg	Lys	Ile	Glu	Val	Ser	290	295	300	

Leu Ile Gly Lys Asn Gln Leu Thr Ile Pro Ile Ala Gln Asn Leu Thr  
 305 310 315 320  
 Ser Gln Leu Tyr Asp Val Thr Leu Tyr Tyr Arg Lys Asp Leu Ser Asp  
 5 325 330 335  
 Arg Arg Gln Leu Ser Asp Asp Ile Thr Met Ile Glu Ile Ala Asp Tyr  
 340 345 350  
 Glu Gln Asp Val Leu Glu Arg Leu Gly Leu Phe Asp Arg Asp Ile Val  
 10 355 360 365  
 Val Cys Ala Thr Asn Asp Asp Asp Ile Asn Arg Lys Val Ala Lys Leu  
 370 375 380  
 Ala Lys Ala His Gln Val Glu Arg Val Ile Cys Arg Leu Glu Ser Thr  
 15 385 390 395 400  
 Thr Asp Asp Thr Glu Leu Val Asp Ser Gly Ile Glu Ile Phe Ser Ser  
 20 405 410 415  
 Tyr Leu Ser Asn Lys Ile Leu Leu Lys Gly Leu Ile Glu Thr Pro Asn  
 420 425 430  
 Met Leu Asn Leu Leu Ser Asn Val Glu Thr Ser Leu Tyr Glu Ile Gln  
 25 435 440 445  
 Met Leu Asn Tyr Lys Tyr Glu Asn Ile Gln Leu Arg Asn Phe Pro Phe  
 450 455 460  
 Gly Gly Asp Ile Ile  
 30 465

## (2) INFORMATION FOR SEQ ID NO:5246:

(i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 414 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5246:

Ala Ile Ile Val Ile Leu Leu Phe Leu Arg Asn Ile Arg Thr Thr Ala  
 1 5 10 15  
 Ile Ser Ile Ile Ser Ile Pro Leu Ser Leu Leu Met Ala Leu Ile Ala  
 50 20 25 30  
 Leu Lys Leu Ser Asp Val Ser Leu Asn Ile Leu Thr Leu Gly Ala Leu  
 35 40 45  
 Thr Val Ala Ile Gly Arg Val Ile Asp Asp Ser Ile Val Val Val Glu  
 55 50 55 60

	Asn	Ile	Tyr	Arg	Arg	Leu	Thr	Asp	Ser	Glu	Glu	Gln	Leu	Lys	Gly	Glu	
	65					70					75					80	
5	Asn	Leu	Ile	Ile	Ser	Ala	Thr	Thr	Glu	Val	Phe	Lys	Pro	Ile	Met	Ser	
					85					90					95		
	Ser	Thr	Leu	Val	Thr	Ile	Ile	Val	Phe	Leu	Pro	Leu	Val	Phe	Val	Ser	
				100					105					110			
10	Gly	Ser	Val	Gly	Glu	Met	Phe	Arg	Pro	Phe	Ala	Leu	Ala	Ile	Ala	Phe	
			115					120					125				
	Ser	Leu	Leu	Ala	Ser	Leu	Leu	Val	Ser	Ile	Thr	Leu	Val	Pro	Ala	Leu	
			130					135					140				
15	Ala	Ala	Thr	Leu	Phe	Lys	Lys	Gly	Val	Lys	Arg	Arg	Asn	Lys	Gln	His	
	145					150					155					160	
	Gln	Glu	Gly	Leu	Gly	Val	Val	Ser	Thr	Thr	Tyr	Lys	Lys	Val	Leu	His	
				165						170						175	
20	Trp	Ser	Leu	Asn	His	Lys	Trp	Ile	Val	Ile	Ile	Leu	Ser	Thr	Leu	Ile	
				180					185					190			
25	Leu	Val	Ala	Thr	Ile	Val	Phe	Gly	Gly	Pro	Arg	Leu	Gly	Thr	Ser	Phe	
			195					200					205				
	Ile	Ser	Ala	Gly	Asp	Asp	Lys	Phe	Leu	Ala	Ile	Thr	Tyr	Thr	Pro	Lys	
		210					215					220					
30	Pro	Gly	Glu	Thr	Glu	Gln	Ala	Val	Leu	Asn	His	Ala	Lys	Asp	Val	Glu	
	225					230					235					240	
	Lys	Tyr	Leu	Lys	Gln	Lys	Lys	His	Val	Lys	Thr	Ile	Gln	Tyr	Ser	Val	
				245						250					255		
35	Gly	Gly	Ser	Ser	Pro	Val	Asp	Pro	Thr	Gly	Ser	Thr	Asn	Ser	Met	Ala	
				260					265					270			
	Ile	Met	Val	Glu	Tyr	Asp	Asn	Asp	Thr	Pro	Asn	Phe	Asp	Val	Glu	Ala	
			275					280					285				
40	Asp	Lys	Val	Ile	Lys	His	Ala	Asp	Gly	Phe	Lys	His	Pro	Gly	Glu	Trp	
		290					295					300					
	Lys	Asn	Gln	Asp	Leu	Gly	Thr	Gly	Ala	Gly	Asn	Lys	Ser	Val	Glu	Val	
45		305				310					315					320	
	Thr	Val	Lys	Gly	Pro	Ser	Met	Asp	Ala	Ile	Lys	Ser	Thr	Val	Lys	Asp	
				325						330					335		
50	Ile	Glu	Gln	Lys	Met	Lys	Gln	Val	Lys	Gly	Leu	Ala	Asn	Val	Lys	Ser	
			340					345					350				
	Asp	Leu	Ser	Gln	Thr	Tyr	Asp	Gln	Tyr	Glu	Ile	Lys	Val	Asp	Gln	Asn	
			355					360					365				
55	Lys	Ala	Ala	Glu	Asn	Gly	Ile	Ser	Ala	Ser	Gln	Leu	Ala	Met	His	Leu	
			370				375					380					

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Asn Glu Asn Leu Pro Glu Lys Thr Val Thr Thr Val Lys Glu Asn Gly  
385 390 395 400

Lys Thr Val Asp Val Lys Val Lys Gln Asn Lys Gln Thr Ala  
405 410

(2) INFORMATION FOR SEQ ID NO:5247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5247:

Gly Lys Pro Phe Ile Ile Gly Leu Gly Asp Ile Ile Val Lys Lys Leu  
1 5 10 15

Thr Thr Ile Leu Phe Gln Tyr Lys Ile Phe Pro Val Leu Met Phe Leu  
20 25 30

Val Ser Thr Gly Leu Gly Ile Ile Val Ile Thr Gln Asn Ile Leu Ile  
35 40 45

Ala Asp Phe Leu Ala Lys Ile Ile Arg His Gln Phe Gln Gly Leu Trp  
50 55 60

Ile Val Leu Phe Ile Leu Leu Gly Val Leu Leu Leu Arg Ala Thr Val  
65 70 75 80

Gln Phe Leu Asn Gln Trp Leu Gly Asp Thr Leu Ala Phe Lys Val Lys  
85 90 95

His Met Leu Arg Gln Arg Val Ile Tyr Lys Asn Asn Gly His Pro Ile  
100 105 110

Gly Glu Gln Met Thr Ile Leu Thr Glu Asn Ile Asp Gly Leu Ala Pro  
115 120 125

Phe Tyr Lys Ser Tyr Leu Pro Gln Val Phe Lys Ser Met Met Val Pro  
130 135 140

Leu Ile Ile Ile Ile Ala Met Phe Phe Ile His Phe Asn Thr Ala Leu  
145 150 155 160

Ile Met Leu Ile Thr Ala Pro Phe Ile Pro Leu Phe Tyr Ile Ile Phe  
165 170 175

Gly Leu Lys Thr Arg Asp Glu Ser Lys Asp Gln Met Thr Tyr Leu Asn  
180 185 190

Gln Phe Ser Gln Arg Phe Leu Asn Ile Ala Lys Gly Leu Val Thr Leu  
195 200 205

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	Lys	Leu	Phe	Asn	Arg	Thr	Glu	Gln	Thr	Glu	Lys	His	Ile	Tyr	Asp	Asp	
	210						215					220					
5	Ser	Thr	Gln	Phe	Arg	Thr	Leu	Thr	Met	Arg	Ile	Leu	Arg	Ser	Ala	Phe	
	225					230					235					240	
	Leu	Ser	Gly	Leu	Met	Leu	Glu	Phe	Ile	Ser	Met	Leu	Gly	Ile	Gly	Leu	
					245					250					255		
10	Val	Ala	Leu	Glu	Ala	Thr	Leu	Ser	Leu	Val	Val	Phe	His	Asn	Ile	Asp	
				260					265					270			
	Phe	Lys	Thr	Ala	Ala	Ile	Ala	Ile	Ile	Leu	Ala	Pro	Glu	Phe	Tyr	Asn	
			275					280					285				
15	Ala	Ile	Lys	Asp	Leu	Gly	Gln	Ala	Phe	His	Thr	Gly	Lys	Gln	Ser	Glu	
		290					295					300					
	Gly	Ala	Ser	Asp	Val	Val	Phe	Glu	Phe	Leu	Glu	Gln	Pro	Asn	Tyr	Asn	
	305					310					315					320	
20	Asn	Glu	Phe	Leu	Leu	Lys	Tyr	Glu	Glu	Asn	Gln	Lys	Pro	Phe	Ile	Gln	
				325						330					335		
	Leu	Thr	Asp	Ile	Ser	Phe	Arg	Tyr	Asp	Asp	Ser	Asp	Arg	Leu	Val	Leu	
25				340					345					350			
	Asn	Asp	Leu	Asn	Leu	Glu	Ile	Phe	Lys	Gly	Asp	Gln	Ile	Ala	Leu	Val	
			355					360					365				
30	Gly	Pro	Ser	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Thr	His	Leu	Ile	Ala	Gly	
		370					375					380					
	Val	Tyr	Gln	Pro	Thr	Ile	Gly	Thr	Ile	Ser	Thr	Asn	Gln	Arg	Asp	Leu	
	385					390					395					400	
35	Asn	Ile	Gly	Ile	Leu	Ser	Gln	Gln	Pro	Tyr	Ile	Phe	Ser	Ala	Ser	Ile	
					405					410					415		
	Lys	Glu	Asn	Ile	Thr	Met	Phe	Lys	Asp	Ile	Glu	Asn	Asn	Thr	Ile	Glu	
				420					425					430			
40	Glu	Val	Leu	Asp	Glu	Val	Gly	Leu	Leu	Asp	Lys	Val	Gln	Ser	Phe	Thr	
			435					440					445				
	Lys	Gly	Ile	Asn	Thr	Ile	Ile	Gly	Glu	Gly	Gly	Glu	Met	Leu	Ser	Gly	
		450					455					460					
45	Gly	Gln	Met	Arg	Arg	Ile	Glu	Leu	Cys	Arg	Leu	Leu	Val	Met	Lys	Pro	
	465					470				475						480	
	Asp	Leu	Val	Ile	Phe	Asp	Glu	Pro	Ala	Thr	Gly	Leu	Asp	Ile	Gln	Thr	
					485					490					495		
50	Glu	His	Met	Ile	Gln	Asn	Val	Leu	Phe	Gln	His	Phe	Lys	Asp	Thr	Thr	
				500					505					510			
	Met	Ile	Val	Ile	Ala	His	Arg	Asp	Asn	Thr	Ile	Arg	His	Leu	Gln	Arg	
55			515					520					525				

Arg Leu Tyr Ile Glu Asn Gly Arg Leu Ile Ala Asp Asp Arg Asn Ile  
530 535 540

Ser Val Asn Ile Thr Glu Asn Gly Asp Asp Leu  
545 550 555

## (2) INFORMATION FOR SEQ ID NO:5248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5248:

Val Trp Lys Leu Lys Met Arg Trp Ile Lys Arg Lys Lys Lys Asn Phe  
1 5 10 15  
Leu Asn Ser Lys Phe Asn Phe Asn Asn Gly Lys Ile Ala Thr Tyr Leu  
20 25 30  
Tyr Lys Glu Arg Thr Ala Met Trp Asn Lys Asn Arg Leu Thr Gln Met  
35 40 45  
Leu Ser Ile Glu Tyr Pro Ile Ile Gln Ala Gly Met Ala Gly Ser Thr  
50 55 60  
Thr Pro Lys Leu Val Ala Ser Val Ser Asn Ser Gly Gly Leu Gly Thr  
65 70 75 80  
Ile Gly Ala Gly Tyr Phe Asn Thr Gln Gln Leu Glu Asp Glu Ile Asp  
85 90 95  
Tyr Val Arg Gln Leu Thr Ser Asn Ser Phe Gly Val Asn Val Phe Val  
100 105 110  
Pro Ser Gln Gln Ser Tyr Thr Ser Ser Gln Ile Glu Asn Met Asn Ala  
115 120 125  
Trp Leu Lys Pro Tyr Arg Arg Ala Leu His Leu Glu Glu Pro Val Val  
130 135 140  
Lys Ile Thr Glu Glu Gln Gln Phe Lys Cys His Ile Asp Thr Ile Ile  
145 150 155 160  
Lys Lys Gln Val Pro Val Cys Cys Phe Thr Phe Gly Ile Pro Ser Glu  
165 170 175  
Gln Ile Ile Ser Arg Leu Lys Ala Ala Asn Val Lys Leu Ile Gly Thr  
180 185 190  
Ala Thr Ser Val Asp Glu Ala Ile Ala Asn Glu Lys Ala Gly Met Asp  
195 200 205

Ala Ile Val Ala Gln Gly Ser Glu Ala Gly Gly His Arg Gly Ser Phe  
210 215 220

5 Leu Lys Pro Lys Asn Gln Leu Pro Met Val Gly Thr Ile Ser Leu Val  
225 230 235 240

Pro Gln Ile Val Asp Val Val Ser Ile Pro Val Ile Ala Ala Gly Gly  
245 250 255

10 Ile Met Asp Gly Arg Gly Val Leu Ala Ser Ile Val Leu Gly Ala Glu  
260 265 270

Gly Val Gln Met Gly Thr Ala Phe Leu Thr Ser Gln Asp Ser Asn Ala  
275 280 285

15 Ser Glu Leu Leu Arg Asp Ala Ile Ile Asn Ser Lys Glu Thr Asp Thr  
290 295 300

Val Ile Thr Lys Ala Phe Ser Gly Lys Leu Ala Arg Gly Ile Asn Asn  
305 310 315 320

20 Arg Phe Ile Glu Glu Met Ser Gln Tyr Glu Gly Asp Ile Pro Asp Tyr  
325 330 335

Pro Ile Gln Asn Glu Leu Thr Ser Ser Ile Arg Lys Ala Ala Ala Asn  
340 345 350

25 Ile Gly Asp Lys Glu Leu Ile His Met Trp Ser Gly Gln Ser Pro Arg  
355 360 365

Leu Ala Thr Thr His Pro Ala Asn Thr Ile Met Ser Asn Ile Ile Asn  
370 375 380

Gln Ile Asn Gln Ile Met Gln Tyr Lys  
385 390

## (2) INFORMATION FOR SEQ ID NO:5249:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5249:

Asn Asp Phe Leu Lys Arg Gly Asn Lys Met Asn Met Lys Lys Lys Glu  
1 5 10 15

Lys His Ala Ile Arg Lys Lys Ser Ile Gly Val Ala Ser Val Leu Val  
20 25 30

Gly Thr Leu Ile Gly Phe Gly Leu Leu Ser Ser Lys Glu Ala Asp Ala  
35 40 45

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	Ser	Glu	Asn	Ser	Val	Thr	Gln	Ser	Asp	S	r	Ala	Ser	Asn	Glu	Ser	Lys
	50						55						60				
5	Ser	Asn	Asp	Ser	Ser	Ser	Val	Ser	Ala	Ala	Pro	Lys	Thr	Asp	Asp	Thr	
	65					70				75					80		
	Asn	Val	Ser	Asp	Thr	Lys	Thr	Ser	Ser	Asn	Thr	Asn	Asn	Gly	Glu	Thr	
					85					90					95		
10	Ser	Val	Ala	Gln	Asn	Pro	Ala	Gln	Gln	Glu	Thr	Thr	Gln	Ser	Ser	Ser	
				100				105						110			
	Thr	Asn	Ala	Thr	Thr	Glu	Glu	Thr	Pro	Val	Thr	Gly	Glu	Ala	Thr	Thr	
		115						120					125				
15	Thr	Thr	Thr	Asn	Gln	Ala	Asn	Thr	Pro	Ala	Thr	Thr	Gln	Ser	Ser	Asn	
		130					135					140					
	Thr	Asn	Ala	Glu	Glu	Leu	Val	Asn	Gln	Thr	Ser	Asn	Glu	Thr	Thr	Ser	
	145					150					155					160	
20	Asn	Asp	Thr	Asn	Thr	Val	Ser	Ser	Val	Asn	Ser	Pro	Gln	Asn	Ser	Thr	
					165					170					175		
	Asn	Ala	Glu	Asn	Val	Ser	Thr	Thr	Gln	Asp	Thr	Ser	Thr	Glu	Ala	Thr	
25				180					185					190			
	Pro	Ser	Asn	Asn	Glu	Ser	Ala	Pro	Gln	Ser	Thr	Asp	Ala	Ser	Asn	Lys	
			195					200					205				
30	Asp	Val	Val	Asn	Gln	Ala	Val	Asn	Thr	Ser	Ala	Pro	Arg	Met	Arg	Ala	
		210					215					220					
	Phe	Ser	Leu	Ala	Ala	Val	Ala	Ala	Asp	Ala	Pro	Val	Ala	Gly	Thr	Asp	
	225					230					235					240	
35	Ile	Thr	Asn	Gln	Leu	Thr	Asn	Val	Thr	Val	Gly	Ile	Asp	Ser	Gly	Thr	
				245						250					255		
	Thr	Val	Tyr	Pro	His	Gln	Ala	Gly	Tyr	Val	Lys	Leu	Asn	Tyr	Gly	Phe	
			260					265						270			
40	Ser	Val	Pro	Asn	Ser	Ala	Val	Lys	Gly	Asp	Thr	Phe	Lys	Ile	Thr	Val	
			275					280					285				
	Pro	Lys	Glu	Leu	Asn	Leu	Asn	Gly	Val	Thr	Ser	Thr	Ala	Lys	Val	Pro	
		290					295					300					
45	Pro	Ile	Met	Ala	Gly	Asp	Gln	Val	Leu	Ala	Asn	Gly	Val	Ile	Asp	Ser	
	305					310					315				320		
	Asp	Gly	Asn	Val	Ile	Tyr	Thr	Phe	Thr	Asp	Tyr	Val	Asn	Thr	Lys	Asp	
				325						330					335		
50	Asp	Val	Lys	Ala	Thr	Leu	Thr	Met	Pro	Ala	Tyr	Ile	Asp	Pro	Glu	Asn	
				340					345					350			
55	Val	Lys	Lys	Thr	Gly	Asn	Val	Thr	Leu	Ala	Thr	Gly	Ile	Gly	Ser	Thr	
			355					360					365				

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	Thr	Ala	Asn	Lys	Thr	Val	Leu	Val	Asp	Tyr	Glu	Lys	Tyr	Gly	Lys	Phe	
	370						375					380					
5	Tyr	Asn	Leu	Ser	Ile	Lys	Gly	Thr	Ile	Asp	Gln	Ile	Asp	Lys	Thr	Asn	
	385					390					395					400	
	Asn	Thr	Tyr	Arg	Gln	Thr	Ile	Tyr	Val	Asn	Pro	Ser	Gly	Asp	Asn	Val	
					405					410					415		
10	Ile	Ala	Pro	Val	Leu	Thr	Gly	Asn	Leu	Lys	Pro	Asn	Thr	Asp	Ser	Asn	
				420					425					430			
	Ala	Leu	Ile	Asp	Gln	Gln	Asn	Thr	Ser	Ile	Lys	Val	Tyr	Lys	Val	Asp	
		435					440						445				
15	Asn	Ala	Ala	Asp	Leu	Ser	Glu	Ser	Tyr	Phe	Val	Asn	Pro	Glu	Asn	Phe	
	450						455					460					
	Glu	Asp	Val	Thr	Asn	Ser	Val	Asn	Ile	Thr	Phe	Pro	Asn	Pro	Asn	Gln	
	465					470					475					480	
20	Tyr	Lys	Val	Glu	Phe	Asn	Thr	Pro	Asp	Asp	Gln	Ile	Thr	Thr	Pro	Tyr	
					485					490						495	
	Ile	Val	Val	Val	Asn	Gly	His	Ile	Asp	Pro	Asn	Ser	Lys	Gly	Asp	Leu	
25				500					505					510			
	Ala	Leu	Arg	Ser	Thr	Leu	Tyr	Gly	Tyr	Asn	Ser	Asn	Ile	Ile	Trp	Arg	
			515					520					525				
30	Ser	Met	Ser	Trp	Asp	Asn	Glu	Val	Ala	Phe	Asn	Asn	Gly	Ser	Gly	Ser	
	530						535					540					
	Gly	Asp	Gly	Ile	Asp	Lys	Pro	Val	Val	Pro	Glu	Gln	Pro	Asp	Glu	Pro	
	545					550					555					560	
35	Gly	Glu	Ile	Glu	Pro	Ile	Pro	Glu	Asp	Ser	Asp	Ser	Asp	Pro	Gly	Ser	
					565					570					575		
	Asp	Ser	Gly	Ser	Asp	Ser	Asn	Ser	Asp	Ser	Gly	Ser	Asp	Ser	Gly	Ser	
				580					585					590			
40	Asp	Ser	Thr	Ser	Asp	Ser	Gly	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	
			595					600					605				
	Ala	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser	
		610					615					620					
45	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Ser	Asp	Ser	
	625					630					635					640	
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	
				645						650				655			
50	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	
				660					665					670			
55	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	
				675				680					685				

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 690 695 700  
 5 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 705 710 715 720  
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 725 730 735  
 10 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 740 745 750  
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 755 760 765  
 15 Asp Ser Asp Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Asp Ser  
 770 775 780  
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 785 790 795 800  
 20 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 805 810 815  
 25 Glu Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 820 825 830  
 Asp Ser Asp Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Gly Ser  
 835 840 845  
 30 Asp Ser Asp Ser Ser Ser Asp Ser Asp Ser Glu Ser Asp Ser Asn Ser  
 850 855 860  
 Asp Ser Glu Ser Val Ser Asn Asn Asn Val Val Pro Pro Asn Ser Pro  
 865 870 875 880  
 35 Lys Asn Gly Thr Asn Ala Ser Asn Lys Asn Glu Ala Lys Asp Ser Lys  
 885 890 895  
 Glu Pro Leu Pro Asp Thr Gly Ser Glu Asp Glu Ala Asn Thr Ser Leu  
 900 905 910  
 40 Ile Trp Gly Leu Leu Ala Ser Ile Gly Ser Leu Leu Leu Phe Arg Arg  
 915 920 925  
 45 Lys Lys Glu Asn Lys Asp Lys Lys  
 930 935

## (2) INFORMATION FOR SEQ ID NO:5250:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5250:

5 Val Ser Lys Leu Lys Lys Glu Ile Leu Glu Trp Ile Ile Ser Ile Ala  
 1 5 10 15  
 Val Ala Phe Val Ile Leu Phe Ile Val Gly Lys Phe Ile Val Thr Pro  
 20 25 30  
 10 Tyr Thr Ile Lys Gly Glu Ser Met Asp Pro Thr Leu Lys Asp Gly Glu  
 35 40 45  
 Arg Val Ala Val Asn Ile Val Gly Tyr Lys Thr Gly Gly Leu Glu Lys  
 50 55 60  
 15 Gly Asn Val Val Val Phe His Ala Asn Lys Asn Asp Asp Tyr Val Lys  
 65 70 75 80  
 Arg Val Ile Gly Val Pro Gly Asp Lys Val Glu Tyr Lys Asn Asp Thr  
 85 90 95  
 20 Leu Tyr Val Asn Gly Lys Lys Gln Asp Glu Pro Tyr Leu Asn Tyr Asn  
 100 105 110  
 Leu Lys His Lys Gln Gly Asp Tyr Ile Thr Gly Thr Phe Gln Val Lys  
 115 120 125  
 25 Asp Leu Pro Asn Ala Asn Pro Lys Ser Asn Val Ile Pro Lys Gly Lys  
 130 135 140  
 Tyr Leu Val Leu Gly Asp Asn Arg Glu Val Ser Lys Asp Ser Arg Ala  
 145 150 155 160  
 30 Phe Gly Leu Ile Asp Glu Asp Gln Ile Val Gly Lys Val Ser Phe Gln  
 165 170 175  
 35 Val Leu Ala His Phe Ser Glu Phe Gln Thr Ser Ile Ser Xaa Leu Lys  
 180 185 190  
 Ile Leu

## (2) INFORMATION FOR SEQ ID NO:5251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5251:

55 Leu Lys Ala Xaa Tyr Ala Lys Leu Asp Asp Val Ser Lys Phe Glu Asp  
 1 5 10 15

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Val Thr Asp Asn Met Ser Leu Asp Phe Asp Thr Asn Gly Gly Tyr Ser  
20 25 30

5 Leu Asn Phe Asn Asn Leu Asp Gln Ser Lys Asn Tyr Val Ile Lys Tyr  
35 40 45

Glu Gly Tyr Tyr Asp Ser Asn Ala Ser Asn Leu Glu Phe Gln Thr His  
50 55 60

10 Leu Phe Gly Tyr Tyr Asn Tyr Tyr Tyr Thr Ser Asn Leu Thr Trp Lys  
65 70 75 80

Asn Gly Val Ala Phe Tyr Ser Asn Asn Ala Gln Gly Asp Gly Lys Asp  
85 90 95

15 Lys Leu Lys Glu Pro Ile Ile Glu His Ser Thr Pro Ile Glu Leu Glu  
100 105 110

Phe Lys Ser Glu Pro Pro Val Glu Lys His Glu Leu Thr Gly Thr Ile  
115 120 125

20 Glu Glu Ser Asn Asp Ser Lys Pro Ile Asp Phe Glu Tyr His Thr Ala  
130 135 140

25 Val Glu Gly Ala Glu Gly His Ala Glu Gly Thr Ile Glu Thr Glu Glu  
145 150 155 160

Asp Ser Ile His Val Asp Phe Glu Glu Ser Thr His Glu Asn Ser Lys  
165 170 175

30 His His Ala Asp Val Val Glu Tyr Glu Glu Asp Thr Asn Pro Gly Gly  
180 185 190

Gly Gln Val Thr Thr Glu Ser Asn Leu Val Glu Phe Asp Glu Asp Ser  
195 200 205

35 Thr Lys Gly Ile Val Thr Gly Ala Val Ser Asp His Thr Thr Ile Glu  
210 215 220

Asp Thr Lys Glu Tyr Thr Thr Glu Ser Asn Leu Ile Glu Leu Val Asp  
225 230 235 240

40 Glu Leu Pro Glu Glu His Gly Gln Ala Gln Gly Pro Ile Glu Glu Ile  
245 250 255

Thr Glu Asn Asn His His Ile Ser His Ser Gly Leu Gly Thr Glu Asn  
260 265 270

45 Gly His Gly Asn Tyr Gly Val Ile Glu Glu Ile Glu Glu Asn Ser His  
275 280 285

Val Asp Ile Lys Ser Glu Leu Gly Tyr Glu Gly Gly Gln Asn Ser Gly  
290 295 300

50 Asn Gln Ser Phe Glu Glu Asp Thr Glu Glu Asp Lys Pro Lys Tyr Glu  
305 310 315 320

55 Gln Gly Gly Asn Ile Val Asp Ile Asp Phe Asp Ser Val Pro Gln Ile  
325 330 335

His Gly Gln Asn Asn Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Lys  
340 345 350

Asp Lys Pro Lys Tyr Glu Gln Gly Gly Asn Ile Ile Asp Ile Asp Phe  
355 360 365

Asp Ser Val Pro His Ile His Gly Phe Asn Lys His Thr Glu Ile Ile  
370 375 380

Glu Glu Asp Thr Asn Lys Asp Lys Pro Asn Tyr Gln Phe Gly Gly His  
385 390 395 400

Asn Ser Val Asp Phe Glu Glu Asp Thr Leu Pro Gln Val Ser Gly His  
405 410 415

Asn Glu Gly Gln Gln Thr Ile Glu Glu Asp Thr Thr Pro Pro Ile Val  
420 425 430

Pro Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro  
435 440 445

Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro Thr Pro  
450 455 460

Pro Thr Pro Glu Val Pro Thr Glu Pro Gly Lys Pro Ile Pro Pro Ala  
465 470 475 480

Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro Val Glu Gln Gly Lys Val  
485 490 495

Val Thr Pro Val Ile Glu Ile Asn Glu Lys Val Lys Ala Val Val Pro  
500 505 510

Thr Lys Lys Ala Gln Ser Lys Lys Ser Glu Leu Pro Glu Thr Gly Gly  
515 520 525

Glu Glu Ser Thr Asn Asn Gly Met Leu Phe Gly Gly Leu Phe Ser Ile  
530 535 540

Leu Gly Leu Ala Leu Leu Arg Arg Asn Lys Lys Asn His Lys Ala  
545 550 555

(2) INFORMATION FOR SEQ ID NO:5252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5252:

Thr Lys Asn Glu Lys Ile Asn Asp Val Thr Ala Val Ala Glu Lys Glu  
1 5 10 15

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Val Val Glu Glu Thr Lys Ala Thr Gly Thr Asp Val Thr Asn Lys Val  
20 25 30

5 Glu Val Glu Glu Gly Ser Glu Ile Val Gly His Lys Gln Asp Thr Asn  
35 40 45

Val Val Asn Pro His Asn Ala Glu Arg Val Thr Leu Lys Tyr Lys Trp  
50 55 60

10 Lys Phe Gly Glu Gly Ile Lys Ala Gly Asp Tyr Phe Asp Phe Thr Leu  
65 70 75 80

Ser Asp Asn Val Glu Thr His Gly Ile Ser Thr Leu Arg Lys Val Pro  
85 90 95

15 Glu Ile Lys Ser Thr Asp Gly Gln Val Met Ala Thr Gly Glu Ile Ile  
100 105 110

Gly Glu Arg Lys Val Arg Tyr Thr Phe Lys Glu Tyr Val Gln Glu Lys  
115 120 125

20 Lys Asp Leu Thr Ala Glu Leu Ser Leu Asn Leu Phe Ile Asp Pro Thr  
130 135 140

25 Thr Val Thr Gln Lys Gly Asn Gln Asn Val Glu Val Lys Leu Gly Glu  
145 150 155 160

Thr Thr Val Ser Lys Ile Phe Asn Ile Gln Tyr Leu Gly Gly Val Arg  
165 170 175

30 Asp Asn Trp Gly Val Thr Ala Asn Gly Arg Ile Asp Thr Leu Asn Lys  
180 185 190

Val Asp Gly Lys Phe Ser His Phe Ala Tyr Met Lys Pro Asn Asn Gln  
195 200 205

35 Ser Leu Ser Ser Val Thr Val Thr Gly Gln Val Thr Lys Gly Asn Lys  
210 215 220

Pro Gly Val Asn Asn Pro Thr Val Lys Val Tyr Lys His Ile Gly Ser  
225 230 235 240

40 Asp Asp Leu Ala Glu Ser Xaa Xaa Cys Lys Ala  
245 250

(2) INFORMATION FOR SEQ ID NO:5253:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 163 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5253:

1 Ile Leu His Leu Arg Glu Asn Ile Ile Val Lys Ser Asn Leu Arg Tyr  
 5 Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr  
 Met Ile Val Val Gly Met Gly Gln Glu Lys Glu Ala Ala Ala Ser Glu  
 10 Gln Asn Asn Thr Thr Val Glu Glu Ser Gly Ser Ser Ala Thr Glu Ser  
 Lys Ala Ser Glu Thr Gln Thr Thr Thr Asn Asn Val Asn Thr Ile Asp  
 15 Glu Thr Gln Ser Tyr Ser Ala Thr Ser Thr Glu Gln Pro Ser Gln Ser  
 Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Thr Val Gln Ala Pro Lys  
 20 Val Glu Thr Ser Arg Val Asp Leu Pro Ser Glu Lys Val Ala Asp Lys  
 Glu Thr Thr Gly Thr Gln Val Asp Ile Ala Gln Pro Ser Asn Val Ser  
 25 Glu Ile Lys Pro Arg Met Lys Arg Ser Met Thr Leu Gln Gln Leu Gln  
 Arg Lys Lys

## (2) INFORMATION FOR SEQ ID NO:5254:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5254:

1 Ile Leu His Leu Lys Gly Asp Ile Ile Val Lys Asn Asn Leu Arg Tyr  
 5 Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr  
 20 Met Ile Val Val Gly Met Gly Gln Asp Lys Glu Ala Ala Ala Ser Glu  
 35 Gln Lys Thr Thr Thr Val Glu Glu Asn Gly Asn Ser Ala Thr Asp Asn  
 50

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	Lys	Thr	Ser	Glu	Thr	Gln	Thr	Thr	Ala	Thr	Asn	Val	Asn	His	Ile	Glu	65	70	75	80
5	Glu	Thr	Gln	Ser	Tyr	Asn	Ala	Thr	Val	Thr	Glu	Gln	Pro	Ser	Asn	Ala	85	90	95	
	Thr	Gln	Val	Thr	Thr	Glu	Glu	Ala	Pro	Lys	Ala	Val	Gln	Ala	Pro	Gln	100	105	110	
10	Thr	Ala	Gln	Pro	Ala	Asn	Ile	Glu	Thr	Val	Lys	Glu	Glu	Val	Val	Lys	115	120	125	
	Glu	Glu	Ala	Lys	Pro	Gln	Val	Lys	Glu	Thr	Thr	Gln	Ser	Gln	Asp	Asn	130	135	140	
15	Ser	Gly	Asp	Gln	Arg	Gln	Val	Asp	Leu	Thr	Pro	Lys	Lys	Ala	Thr	Gln	145	150	155	160
	Asn	Gln	Val	Ala	Glu	Thr	Gln	Val	Glu	Val	Ala	Gln	Pro	Arg	Thr	Ala	165	170		175
20	Ser	Glu	Ser	Lys	Pro	Arg	Val	Thr	Arg	Ser	Ala	Asp	Val	Ala	Glu	Ala	180	185		190
	Lys	Glu	Ala	Ser	Asn	Ala	Lys	Val	Glu	Thr	Gly	Thr	Asp	Val	Thr	Ser	195	200	205	
25	Lys	Val	Thr	Val	Glu	Ile	Gly	Ser	Ile	Glu	Gly	His	Asn	Asn	Thr	Asn	210	215	220	
	Lys	Val	Glu	Pro	His	Ala	Gly	Gln	Arg	Ala	Val	Leu	Lys	Tyr	Lys	Leu	225	230	235	240
	Lys	Phe	Glu	Asn	Gly	Leu	His	Gln	Gly	Asp	Tyr	Phe	Asp	Phe	Thr	Leu	245	250		255
35	Ser	Asn	Asn	Val	Asn	Thr	His	Gly	Val	Ser	Thr	Ala	Arg	Lys	Val	Pro	260	265	270	
	Glu	Ile	Lys	Asn	Gly	Ser	Val	Val	Met	Ala	Thr	Gly	Glu	Val	Leu	Glu	275	280	285	
40	Gly	Gly	Lys	Ile	Arg	Tyr	Thr	Phe	Thr	Asn	Asp	Ile	Glu	Asp	Lys	Val	290	295	300	
	Asp	Val	Thr	Ala	Glu	Leu	Glu	Ile	Asn	Leu	Phe	Ile	Asp	Pro	Lys	Thr	305	310	315	320
45	Val	Gln	Thr	Asn	Gly	Asn	Gln	Thr	Ile	Thr	Ser	Thr	Leu	Asn	Glu	Glu	325	330		335
	Gln	Thr	Ser	Lys	Glu	Leu	Asp	Val	Lys	Tyr	Lys	Asp	Gly	Ile	Gly	Asn	340	345	350	
50	Tyr	Tyr	Ala	Asn	Leu	Asn	Gly	Ser	Ile	Glu	Thr	Phe	Asn	Lys	Ala	Asn	355	360	365	
55	Asn	Arg	Phe	Ser	His	Val	Ala	Phe	Ile	Lys	Pro	Asn	Asn	Gly	Lys	Thr	370	375	380	

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	Thr	Ser	Val	Thr	Val	Thr	Gly	Thr	L	u	Met	Lys	Gly	Ser	Asn	Gln	Asn	385	390	395	400
5	Gly	Asn	Gln	Pro	Lys	Val	Arg	Ile	Phe	Glu	Tyr	Leu	Gly	Asn	Asn	Glu	405	410	415		
	Asp	Ile	Ala	Lys	Ser	Val	Tyr	Ala	Asn	Thr	Thr	Asp	Thr	Ser	Lys	Phe	420	425	430		
10	Lys	Glu	Val	Thr	Ser	Asn	Met	Ser	Gly	Asn	Leu	Asn	Leu	Gln	Asn	Asn	435	440	445		
	Gly	Ser	Tyr	Ser	Leu	Asn	Ile	Glu	Asn	Leu	Asp	Lys	Thr	Tyr	Val	Val	450	455	460		
15	His	Tyr	Asp	Gly	Glu	Tyr	Leu	Asn	Gly	Thr	Asp	Glu	Val	Asp	Phe	Arg	465	470	475	480	
	Thr	Gln	Met	Val	Gly	His	Pro	Glu	Gln	Leu	Tyr	Lys	Tyr	Tyr	Tyr	Asp	485	490	495		
20	Arg	Gly	Tyr	Thr	Leu	Thr	Trp	Asp	Asn	Gly	Leu	Val	Leu	Tyr	Ser	Asn	500	505	510		
25	Lys	Ala	Asn	Gly	Asn	Glu	Lys	Asn	Gly	Pro	Ile	Ile	Gln	Asn	Asn	Lys	515	520	525		
	Phe	Glu	Tyr	Lys	Glu	Asp	Thr	Ile	Lys	Glu	Thr	Leu	Thr	Gly	Gln	Tyr	530	535	540		
30	Asp	Lys	Asn	Leu	Val	Thr	Thr	Val	Glu	Glu	Glu	Tyr	Asp	Ser	Ser	Thr	545	550	555	560	
	Leu	Asp	Ile	Asp	Tyr	His	Thr	Ala	Ile	Asp	Gly	Gly	Gly	Gly	Tyr	Val	565	570	575		
35	Asp	Gly	Tyr	Ile	Glu	Thr	Ile	Glu	Glu	Thr	Asp	Ser	Ser	Ala	Ile	Asp	580	585	590		
	Ile	Asp	Tyr	His	Thr	Ala	Val	Asp	Ser	Glu	Ala	Gly	His	Val	Gly	Gly	595	600	605		
40	Tyr	Thr	Glu	Ser	Ser	Glu	Glu	Ser	Asn	Pro	Ile	Asp	Phe	Glu	Glu	Ser	610	615	620		
	Thr	His	Glu	Asn	Ser	Lys	His	His	Ala	Asp	Val	Val	Glu	Tyr	Glu	Glu	625	630	635	640	
45	Asp	Thr	Asn	Pro	Gly	Gly	Gly	Gln	Val	Thr	Thr	Glu	Ser	Asn	Leu	Val	645	650	655		
50	Glu	Phe	Asp	Glu	Glu	Ser	Thr	Lys	Gly	Ile	Val	Thr	Gly	Ala	Val	Ser	660	665	670		
	Asp	His	Thr	Thr	Val	Glu	Asp	Thr	Lys	Glu	Tyr	Thr	Thr	Glu	Ser	Asn	675	680	685		
55	Leu	Ile	Glu	Leu	Val	Asp	Glu	Leu	Pro	Glu	Glu	His	Gly	Gln	Ala	Gln	690	695	700		

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Gly Pro Val Glu Glu Ile Thr Lys Asn Asn His His Ile Ser His Ser  
 705 710 715 720  
 5 Gly Leu Gly Thr Glu Asn Gly His Gly Asn Tyr Asp Val Ile Glu Glu  
 725 730 735  
 Ile Glu Glu Asn Ser His Val Asp Ile Lys Ser Glu Leu Gly Tyr Glu  
 740 745 750  
 10 Gly Gly Gln Asn Ser Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Glu  
 755 760 765  
 Asp Lys Pro Lys Tyr Glu Gln Gly Gly Asn Ile Val Asp Ile Asp Phe  
 770 775 780  
 15 Asp Ser Val Pro Gln Ile His Gly Gln Asn Lys Gly Asn Gln Ser Phe  
 785 790 795 800  
 Glu Glu Asp Thr Glu Lys Asp Lys Pro Lys Tyr Glu His Gly Gly Asn  
 805 810 815  
 20 Ile Ile Asp Ile Asp Phe Asp Ser Val Pro His Ile His Gly Phe Asn  
 820 825 830  
 Lys His Thr Glu Ile Ile Glu Glu Asp Thr Asn Lys Asp Lys Pro Ser  
 835 840 845  
 25 Tyr Gln Phe Gly Gly His Asn Ser Val Asp Phe Glu Glu Asp Thr Leu  
 850 855 860  
 Pro Lys Val Ser Gly Gln Asn Glu Gly Gln Gln Thr Ile Glu Glu Asp  
 865 870 875 880  
 30 Thr Thr Pro Pro Ile Val Pro Pro Thr Pro Pro Thr Pro Glu Val Pro  
 885 890 895  
 35 Ser Glu Pro Glu Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu  
 900 905 910  
 Pro Glu Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu  
 915 920 925  
 40 Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ala Glu Pro Gly Lys Pro  
 930 935 940  
 Val Pro Pro Ala Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro Val Glu  
 945 950 955 960  
 45 Gln Gly Lys Val Val Thr Pro Val Ile Glu Ile Asn Glu Lys Val Lys  
 965 970 975  
 Ala Val Ala Pro Thr Lys Lys Pro Gln Ser Lys Lys Ser Glu Leu Pro  
 980 985 990  
 50 Glu Thr Gly Gly Glu Glu Ser Thr Asn Lys Gly Met Leu Phe Gly Gly  
 995 1000 1005  
 55 Leu Phe Ser Ile Leu Gly Leu Ala Leu Leu Arg Arg Asn Lys Lys Asn  
 1010 1015 1020

His Lys Ala  
1025

(2) INFORMATION FOR SEQ ID NO:5255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5255:

20	Gly	Glu	Lys	Cys	Met	Phe	Leu	Ala	Trp	Asn	Glu	Ile	Arg	Arg	Asn	Lys	1	5	10	15
	Leu	Lys	Phe	Gly	Leu	Ile	Ile	Gly	Val	Leu	Thr	Met	Ile	Ser	Tyr	Leu	20	25	30	
25	Leu	Phe	Leu	Leu	Ser	Gly	Leu	Ala	Asn	Gly	Leu	Ile	Asn	Met	Asn	Lys	35	40	45	
	Glu	Gly	Ile	Asp	Lys	Trp	Gln	Ala	Asp	Ala	Ile	Val	Leu	Asn	Lys	Asp	50	55	60	
30	Ala	Asn	Gln	Thr	Val	Gln	Gln	Ser	Val	Phe	Asn	Lys	Lys	Asp	Ile	Glu	65	70	75	80
	Asn	Lys	Tyr	Lys	Lys	Gln	Ala	Thr	Leu	Lys	Gln	Thr	Gly	Glu	Ile	Val	85	90	95	
35	Ser	Asn	Gly	His	Gln	Lys	Asp	Asn	Val	Leu	Val	Phe	Gly	Val	Glu	Lys	100	105	110	
40	Ser	Ser	Phe	Leu	Val	Pro	Ser	Leu	Ile	Glu	Gly	His	Lys	Ala	Thr	Lys	115	120	125	
	Asp	Asn	Glu	Val	Leu	Ala	Asp	Glu	Thr	Leu	Lys	Asn	Lys	Gly	Leu	Lys	130	135	140	
45	Leu	Gly	Asp	Thr	Leu	Ser	Leu	Ser	Xaa	Xaa	Arg						145	150	155	

Claims

- Computer readable medium having recorded thereon a nucleotide sequence of the Staphylococcus aureus genome as depicted in SEQ ID NOS:1-5,191, a representative fragment thereof or a nucleotide sequence at least 95 % identical to a nucleotide sequence depicted in SEQ ID NOS:1-5,191.
- Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a degenerate variant thereof.

3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
5. A computer-based system for identifying fragments of the *Staphylococcus aureus* genome of commercial importance comprising the following elements:
  - (a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-5,191;
  - (b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and
  - (c) retrieval means for obtaining said homologous sequence(s) of step (b).
6. A method for identifying commercially important nucleic acid fragments of the *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.
7. A method for identifying an expression modulating fragment of *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to the nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression.
8. A protein-encoding nucleic acid fragment of the *Staphylococcus aureus* genome, wherein said fragment comprises the nucleotide sequence of any one of the fragments of SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence, or a degenerate variant of any of the aforementioned sequences.
9. The nucleic acid fragment of claim 8 which is DNA.
10. The nucleic acid fragment of claim 8 which is RNA.
11. A vector comprising a fragment of claim 8.
12. A fragment of the *Staphylococcus aureus* genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frames depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.
13. A vector comprising a fragment of claim 12.
14. An organism which has been altered to contain any one of the fragments of the *Staphylococcus aureus* genome of claim 8.
15. A method for producing a polypeptide in a host cell comprising the steps of:
  - (a) incubating an organism of claim 14 under conditions where said fragment is expressed to produce said protein, and
  - (b) isolating said protein.
16. An organism which has been altered to contain any one of the fragments of the *Staphylococcus aureus* genome

of claim 12.

17. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 30 to 300 bases 5' to any one of the fragments of the *Staphylococcus aureus* genome depicted in SEQ ID Nos:1-5,191 and Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.

18. A nucleic acid molecule being a homolog of any of the fragments of the *Staphylococcus aureus* genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:

- (a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS: 1-5,191 and Tables 2 and 3, including fragments thereof;
- (b) identifying members of said library which contain sequences that hybridize to said target sequence;
- (c) isolating the nucleic acid molecules from said members identified in step (b).

19. A DNA molecule being a homolog of any one of the fragments of the *Staphylococcus aureus* genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:

- (a) isolating mRNA, DNA, or cDNA produced from an organism;
- (b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Staphylococcus aureus* genome to prime said amplification;
- (c) isolating said amplified sequences produced in step (b).

20. A polypeptide encoded by a fragment of claim 8.

21. An antibody which selectively binds to any one of the polypeptides of claim 20.

22. A kit for analyzing samples for the presence of polynucleotides derived from *Staphylococcus aureus*, comprising at least one polynucleotide containing a nucleotide sequence of any one of the fragments SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical thereto or a degenerate variant of any of the aforementioned sequences, that will hybridize to a *staphylococcus aureus* polynucleotide under stringent hybridization conditions, and a suitable container.

23. A *Staphylococcus aureus* polypeptide comprising an amino acid sequence identical to an amino acid sequence selected from the group consisting of SEQ ID NOS:5,192 to 5,255 or comprising an amino acid sequence having at least 95% identity to such a sequence.

24. A *Staphylococcus aureus* polypeptide antigen comprising at least one epitope derived from a *Staphylococcus aureus* polypeptide selected from the group consisting of SEQ ID NOS:5,192 to 5,255.

25. A polypeptide comprising at least one epitope encoded by a *Staphylococcus aureus* amino acid sequence selected from the group consisting of the epitopic sequences listed in Table 4.

26. The polypeptide of claim 24 or 26, wherein said polypeptide is fixed to a solid phase.

27. A diagnostic kit for detecting *Staphylococcus aureus* infection comprising

- (a) an isolated polypeptide antigen of claim 24, and
- (b) means for detecting the binding of an antibody contained in a biological fluid to said antigen.

28. A vaccine composition comprising a polypeptide of claim 24 present in a pharmaceutically acceptable carrier.

29. A method of vaccinating an individual against *Staphylococcus aureus* infection comprising, administering to an individual the vaccine composition of claim 28.

Figure 1

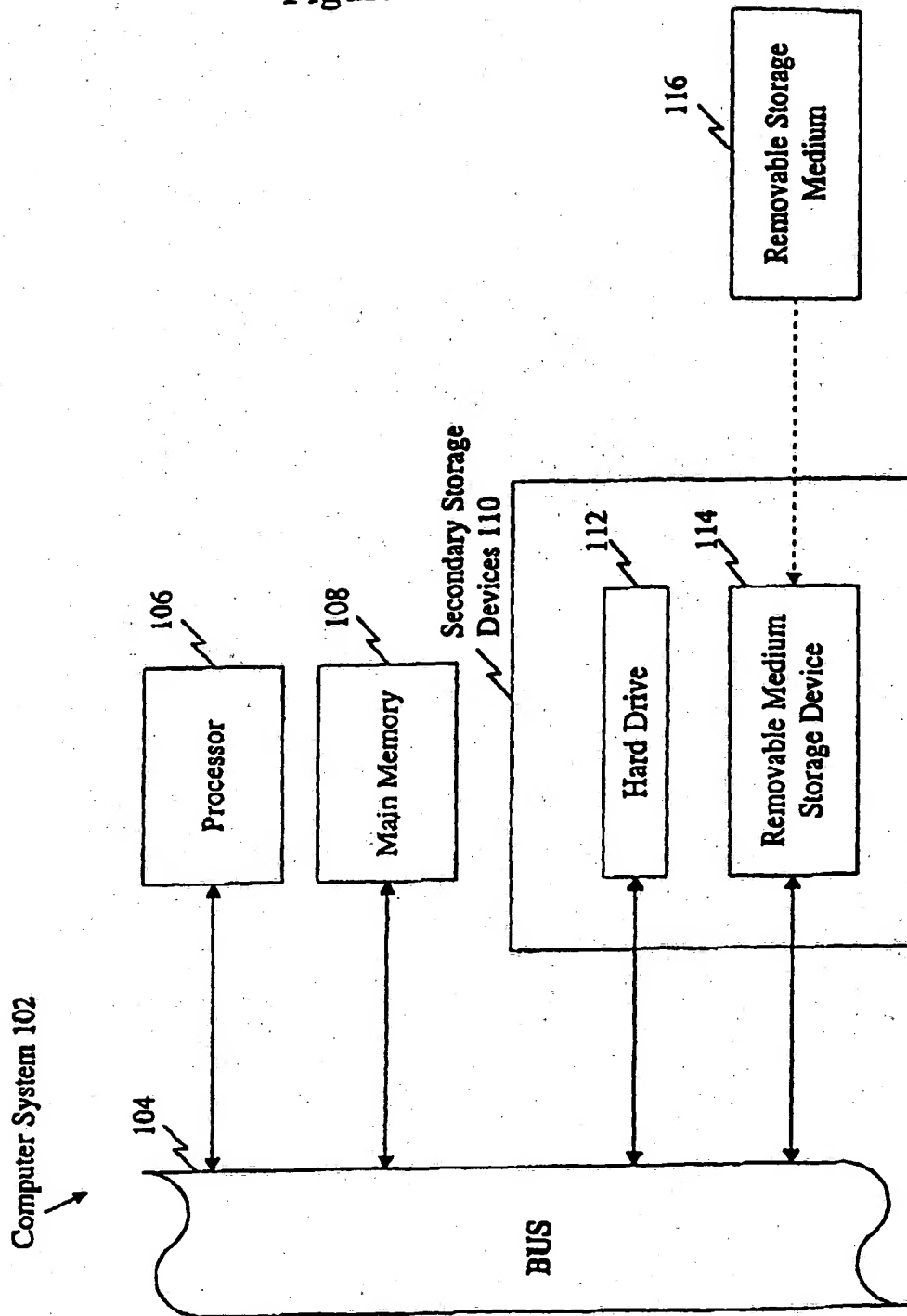


Figure 2

